

IC10 Rec'd PCT/PTO 18 JAN 2002

FORM PTO-1390 OFFICE		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK	ATTORNEY'S DOCKET NUMBER PF-0722 USN
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371			U.S. APPLICATION NO. (If known, see 37 CFR 1.5) TO BE ASSIGNED 10/031915
INTERNATIONAL APPLICATION NO. PCT/US00/19948	INTERNATIONAL FILING DATE 21 July 2000	PRIORITY DATE CLAIMED 21 July 1999	
TITLE OF INVENTION CELL CYCLE AND PROLIFERATION PROTEINS			
APPLICANT(S) FOR DO/EO/US HILLMAN, Jennifer; LAL, Preeti; TANG, Y. Tom; YUE, Henry; AU-YOUNG, Janice; BANDMAN, Olga; AZIMZAI, Yalda; YANG, Junming; LU, Dyung Aina M.; BAUGHN, Mariah R.; PATTERSON, Chandra; SHAH, Purvi			
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:			
<ol style="list-style-type: none"> 1. <input checked="" type="checkbox"/> This is the FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. 3. <input type="checkbox"/> This is an express request to promptly begin national examination procedures (35 U.S.C. 371 (f)). 4. <input type="checkbox"/> The US has been elected by the expiration of 19 months from the priority date (PCT Article 31). 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2)) <ol style="list-style-type: none"> a. <input type="checkbox"/> is attached hereto (required only if not communicated by the International Bureau) b. <input type="checkbox"/> has been communicated by the International Bureau. c. <input checked="" type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input type="checkbox"/> An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)). 7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)) <ol style="list-style-type: none"> a. <input type="checkbox"/> are attached hereto (required only if not communicated by the International Bureau). b. <input type="checkbox"/> have been communicated by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input type="checkbox"/> have not been made and will not be made. e. <input checked="" type="checkbox"/> attached hereto Article 34 Amendment 8. <input type="checkbox"/> An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). 9. <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). 10. <input type="checkbox"/> An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). 			
Items 11 to 16 below concern document(s) or information included:			
<ol style="list-style-type: none"> 11. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. 12. <input checked="" type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.27 and 3.31 is included. 13. <input checked="" type="checkbox"/> A FIRST preliminary amendment, as follows: Cancel in this application original claims #12, 14, 18, 20, 21, 23, 24, 27 before calculating the filing fee, without prejudice or disclaimer. Applicants submit that these claims were included in the application as filed in the interest of providing notice to the public of certain specific subject matter intended to be claimed, and are being canceled at this time in the interest of reducing filing costs. Applicants expressly state that these claims are not being canceled for reasons related to patentability, and are in fact fully supported by the specification as filed. Applicants expressly reserve the right to reinstate these claims or to add other claims during prosecution of this application or a continuation or divisional application. Applicants expressly do not disclaim the subject matter of any invention disclosed herein which is not set forth in the instantly filed claims. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment. 14. <input type="checkbox"/> A substitute specification. 15. <input type="checkbox"/> A change of power of attorney and/or address letter. 16. <input checked="" type="checkbox"/> Other items or information: <ol style="list-style-type: none"> 1) Transmittal Letter (2 pp, in duplicate) 2) Return Postcard 3) Express Mail Label No.: EL 856149 089 US 4) Sequence Listing Statement and Diskette 5) Article 34 Amendment 			

10031915 011902

JC13 Rec'd PCT/PTO 18 JAN 2002

U.S. APPLICATION NO. (if known, see 37 CFR 1.5) TO BE ASSIGNED 10/031915	INTERNATIONAL APPLICATION NO.: PCT/US00/19948	ATTORNEY'S DOCKET NUMBER PF-0722 USN
--	--	---

17. ☒ The following fees are submitted:

BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)):

Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO.....\$1000.00

☐ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO..\$860.00

International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO.....\$710.00

☒ International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4).....\$690.00

☐ International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4).....\$100.00

ENTER APPROPRIATE BASIC FEE AMOUNT =	\$710.00																
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).	\$																
<table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <th style="width: 20%;">CLAIMS</th> <th style="width: 20%;">NUMBER FILED</th> <th style="width: 20%;">NUMBER EXTRA</th> <th style="width: 20%;">RATE</th> <th style="width: 20%;"></th> </tr> <tr> <td>Total Claims</td> <td style="text-align: center;">20 =</td> <td style="text-align: center;">0</td> <td style="text-align: right;">X \$ 18.00</td> <td style="text-align: right;">\$</td> </tr> <tr> <td>Independent Claims</td> <td style="text-align: center;">3 =</td> <td style="text-align: center;">0</td> <td style="text-align: right;">X \$ 80.00</td> <td style="text-align: right;">\$</td> </tr> </table>	CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		Total Claims	20 =	0	X \$ 18.00	\$	Independent Claims	3 =	0	X \$ 80.00	\$		
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE														
Total Claims	20 =	0	X \$ 18.00	\$													
Independent Claims	3 =	0	X \$ 80.00	\$													
MULTIPLE DEPENDENT CLAIM(S) (if applicable)	+ \$270.00	\$															
TOTAL OF ABOVE CALCULATIONS =	\$																
<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.	\$																
SUBTOTAL	\$710.00																
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).	\$																
TOTAL NATIONAL FEE =	\$710.00																
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by the appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property	+																
TOTAL FEES ENCLOSED =	\$710.00																
	Amount to be Refunded:	\$															
	Charged:	\$															

a. ☐ A check in the amount of \$ _____ to cover the above fees is enclosed.

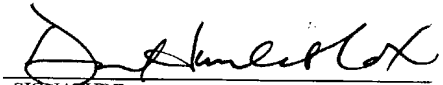
b. ☒ Please charge my Deposit Account No. 09-0108 in the amount of \$710.00 to cover the above fees.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 09-0108. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

INCYTE GENOMICS, INC.
 3160 Porter Drive
 Palo Alto, CA 94304


 SIGNATURE

NAME: Diana Hamlet-Cox

REGISTRATION NUMBER: 33,302

DATE: 18 January 2002

PF-0722 PCT

100319152

10/0319152
J613 Rec'd PCT/PTO 18 JAN 2002

"Express Mail" mailing label number EL 892 011 785 US I hereby certify that this document and referenced attachments are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR § 1.10 on the date indicated and is addressed to: Commissioner for Patents, Box PCT, USPTO, P.O. Box 2327 Arlington, Virginia 22207 on 12-6-01.

By: Nancy Ramos

Printed: Nancy Ramos

CHAPTER II

INTERNATIONAL EXAMINING AUTHORITY (IPEA/US)

PCT/US00/19948

INTERNATIONAL APPLICATION NO.

21 July 2000

INTERNATIONAL FILING DATE

21 July 1999

PRIORITY DATE CLAIMED

CELL CYCLE AND PROLIFERATION PROTEINS

TITLE OF INVENTION

INCYTE GENOMICS, INC.

APPLICANT

United States Patent and Trademark Office

P.O. Box PCT

Washington, D.C. 20231

EL 892 011 785 US

ARTICLE 34 AMENDMENT

Dear Sirs:

Please add new claims 29-192 in the above referenced international application as indicated below. A clean copy of the affected claims is attached (see pages 111/1-111/15). The replacement pages represent the new claims to be added as well as replacement page 111/1. These new claims do not go beyond the disclosure as filed.

Respectfully submitted,

INCYTE GENOMICS, INC.

Diana Hamlet-Cox

Diana Hamlet-Cox, Ph.D., Esq.

Reg. No. 33,302

Direct Dial Telephone: (650) 845-4639

Date: 05 Dec 2001

Date: 24 December 2001

Michelle M. Stempien

Michelle M. Stempien

Reg. No. 41,327

Direct Dial Telephone (650) 843-7219

with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

5 27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, and
- b) detecting altered expression of the target polynucleotide.

10 28. A method for assessing toxicity of a test compound, said method comprising:
a) treating a biological sample containing nucleic acids with the test compound;
b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific
15 hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;

- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the
20 amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

25 29. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- 30 c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

30. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

35 31. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

32. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

33. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

34. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

35. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

36. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

37. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

38. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

39. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.

40. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.

41. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.

42. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.

43. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.

44. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.

45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.

46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:23.

48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:24.

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:25.

PF-0722 PCT

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:26.

51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:28.

5 52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:29.

53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:30.

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:31.

10

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:32.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:33.

15

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:34.

58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:35.

59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:36.

20

60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:37.

61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:38.

25

62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:39.

63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:41.

64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:42.

30

65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:43.

66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:44.

35

67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:45.

PF-0722 PCT

68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:46.

69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:47.

70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:48.

71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:50.

72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:51.

73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:52.

74. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:53.

75. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:54.

76. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:55.

77. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:56.

78. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:57.

79. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:58.

80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:59.

81. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:60.

82. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:61.

PF-0722 PCT

83. A polynucleotide of claim 11, comprising the polynucleotide

NO:64.

84. A polynucleotide of claim 11, comprising the polynucleot.

NO:65.

85. A polynucleotide of claim 11, comprising the polynucleotide sequence c

NO:66.

86. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:67.

87. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:68.

88. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:69.

89. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:71.

90. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:72.

91. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:74.

92. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:76.

93. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:77.

94. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:78.

PF-0722 PCT

95. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:79.

96. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:80.

97. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:82.

98. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:83.

99. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:84.

100. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:85.

101. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:86.

102. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:87.

103. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:88.

104. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:89.

105. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:90.

106. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:91.

PF-0722 PCT

107. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:92.

108. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:93.

109. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:95.

110. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:96.

111. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:97.

112. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:98.

113. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:99.

114. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:100.

115. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:101.

116. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:102.

117. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:104.

118. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:105.

PF-0722 PCT

119. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:106.
120. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:107.
121. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:108.
122. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:1.
123. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:2.
124. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:3.
125. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:4.
126. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:5.
127. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:6.
128. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:7.
129. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:10.
130. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:11.
131. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:12.
132. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:13.
133. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:14.
134. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:15.
135. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:17.

PF-0722 PCT

136. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:18.

137. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:20.

5 138. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:22.

139. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:23.

140. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:24.

10

141. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:25.

142. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:26.

15

143. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:28.

144. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:29.

145. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:30.

20

146. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:31.

147. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:32.

25

148. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:33.

149. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:34.

150. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:35.

30

151. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:36.

152. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:37.

35

153. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:38.

PF-0722 PCT

154. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:39.

155. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:41.

5 156. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:42.

157. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:43.

158. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:44.

10

159. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:45.

160. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:46.

15

161. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:47.

162. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:48.

163. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:50.

20

164. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:51.

165. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:52.

25

166. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:53.

167. A method of claim 9, wherein the polypeptide has the sequence of SEQ ID NO:54.

168. A diagnostic test for a condition or disease associated with the expression of human cell
cycle and proliferation proteins (CCYPR) in a biological sample comprising the steps of:

30

- a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and
- b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

35

PF-0722 PCT

169. The antibody of claim 10, wherein the antibody is:

- a) a chimeric antibody.
- b) a single chain antibody.
- c) a Fab fragment.
- 5 d) a F(ab')₂ fragment, or
- e) a humanized antibody.

170. A composition comprising an antibody of claim 10 and an acceptable excipient.

10 171. A method of diagnosing a condition or disease associated with the expression of human cell cycle and proliferation proteins (CCYPR) in a subject, comprising administering to said subject an effective amount of the composition of claim 170.

172. A composition of claim 170, wherein the antibody is labeled.

15

173. A method of diagnosing a condition or disease associated with the expression of human cell cycle and proliferation proteins (CCYPR) in a subject, comprising administering to said subject an effective amount of the composition of claim 172.

20 174. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 10 comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54, or an immunogenic fragment thereof, under conditions to elicit an antibody response;
- b) isolating antibodies from said animal; and
- 35 c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid

PF-0722 PCT

5 SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5,
 SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID
 NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17,
 SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID
 NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29,
 SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID
 NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38,
 SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID
 NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48,
 10 SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ
 ID NO:54.

178. A monoclonal antibody produced by a method of claim 177.

15 179. A composition comprising the antibody of claim 178 and a suitable carrier.

180. The antibody of claim 10, wherein the antibody is produced by screening a Fab expression library.

20 181. The antibody of claim 10, wherein the antibody is produced by screening a recombinant immunoglobulin library.

25 182. A method for detecting a polypeptide having an amino acid sequence selected from the
 group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ
 ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID
 NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID
 NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID
 NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID
 30 NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID
 NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54, in a sample comprising
 the steps of:

- a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and
- 35 b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of

184. A microarray wherein at least one element of the microarray is a polynucleotide of claim 12.

185. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising the steps of:

- a) labeling the polynucleotides of the sample,
- b) contacting the elements of the microarray of claim 184 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

186. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, said target polynucleotide having a sequence of claim 11.

187. An array of claim 186, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

188. An array of claim 186, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 60 contiguous nucleotides of said target polynucleotide.

189. An array of claim 186, which is a microarray.

190. An array of claim 186, further comprising said target polynucleotide hybridized to said first oligonucleotide or polynucleotide.

191. An array of claim 186, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

192. An array of claim 186, wherein each distinct physical location on the substrate contains multiple nucleotide molecules having the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another physical location on the substrate.

TECHNICAL FIELD

BACKGROUND OF THE INVENTION

Cell division is the fundamental process by which all living things grow and reproduce. In unicellular organisms such as yeast and bacteria, each cell division doubles the number of organisms, while in multicellular species many rounds of cell division are required to replace cells lost by wear or by programmed cell death, and for cell differentiation to produce a new tissue or organ. Details of the cell division cycle may vary, but the basic process consists of three principal events. The first event, interphase, involves preparations for cell division, replication of the DNA, and production of essential proteins. In the second event, mitosis, the nuclear material is divided and separates to opposite sides of the cell. The final event, cytokinesis, is division and fission of the cell cytoplasm. The sequence and timing of cell cycle transitions are under the control of the cell cycle regulation system which controls the process by positive or negative regulatory circuits at various check points.

Mitosis marks the end of interphase and concludes with the onset of cytokinesis. There are four stages in mitosis, occurring in the following order: prophase, metaphase, anaphase and telophase. Prophase includes the formation of bi-polar mitotic spindles, composed of microtubules and associated proteins such as dynein, which originate from polar mitotic centers. During metaphase, the nuclear material condenses and develops kinetochore fibers which aid in its physical attachment to the mitotic spindles. The ensuing movement of the nuclear material to opposite poles along the mitotic spindles occurs during anaphase. Telophase includes the disappearance of the mitotic spindles and kinetochore fibers from the nuclear material. Mitosis depends on the interaction of numerous proteins. For example, mutation studies in the *Drosophila melanogaster zw10* gene show a disruption in chromosome segregation. ZW10 protein appears to function at the kinetochore as a tension-sensing checkpoint during the onset of anaphase. ZW10 appears to have a direct role in the recruitment of dynein to the kinetochore, and, dynein's involvement in the coordination of chromosome separation at the onset of anaphase and/or poleward movement (Starr, D.A. et al. (1998) J. Cell Biol. 142:763-774).

Regulated progression of the cell cycle depends on the integration of growth control pathways with the basic cell cycle machinery. Cell cycle regulators have been identified by selecting for human and yeast cDNAs that block or activate cell cycle arrest signals in the yeast mating pheromone pathway

when they are overexpressed. Known regulators include human CPR (cell cycle progression restoration) genes, such as CPR8 and CPR2, and yeast CDC (cell division control) genes, including CDC91, that block the arrest signals. The CPR genes express a variety of proteins including cyclins, tumor suppressor binding proteins, chaperones, transcription factors, translation factors, and
5 RNA-binding proteins (Edwards, M.C. et al. (1997) Genetics 147:1063-1076).

The human CDC protein, CDC23, is homologous to the S. cerevisiae protein CDC23 which functions in the transition from metaphase to anaphase as well as in the exit from mitosis (Zhao, N. et al. (1998) Genomics 53:184-190). The C. elegans gene cullin-1 (cul1) is a negative regulator of the cell cycle. cul1 regulates the G1 to S phase transition and C. elegans cul1 mutants exhibit hyperplasia of all
10 tissues through acceleration of this transition by overriding mitotic arrest. cul1 is a member of a conserved gene family that spans S. cerevisiae, nematodes and humans (Kipreos, E.T. et al. (1996) Cell 85:929-839).

Several cell cycle transitions, including the entry and exit of a cell from mitosis, are dependent upon the activation and inhibition of cyclin-dependent kinases (Cdks). The Cdks are composed of a
15 kinase subunit, Cdk, and an activating subunit, cyclin, in a complex that is subject to many levels of regulation. There appears to be a single Cdk in Saccharomyces cerevisiae and Schizosaccharomyces pombe whereas mammals have a variety of specialized Cdks. Cyclins act by binding to and activating cyclin-dependent protein kinases which then phosphorylate and activate selected proteins involved in the mitotic process. The Cdk-cyclin complex is both positively and negatively regulated by
20 phosphorylation, and by targeted degradation involving molecules such as CDC4 and CDC53. In addition, Cdks are further regulated by binding to inhibitors and other proteins such as Suc1 that modify their specificity or accessibility to regulators (Patra, D. and W.G. Dunphy (1996) Genes Dev. 10:1503-1515; and Mathias, N. et al. (1996) Mol. Cell Biol. 16:6634-6643).

Reproduction

25 The male and female reproductive systems are complex and involve many aspects of growth and development. The anatomy and physiology of the male and female reproductive systems are reviewed in Guyton, A.C. ((1991) Textbook of Medical Physiology, W.B. Saunders Co., Philadelphia PA, pp.899-928).

The male reproductive system includes the process of spermatogenesis, in which the sperm are
30 formed. Male reproductive functions are regulated by various hormones. The hormones exert their effects on accessory sexual organs, and are involved in cellular metabolism, growth, and other bodily functions.

Spermatogenesis begins at puberty as a result of stimulation by gonadotropic hormones released from the anterior pituitary. Immature sperm (spermatogonia) undergo several mitotic cell

divisions before undergoing meiosis and full maturation. The testes secrete several male sex hormones. Testosterone, the most abundant, is essential for growth and division of the immature sperm, and for the masculine characteristics of the male body. Three other male sex hormones, gonadotropin-releasing hormone (GnRH), luteinizing hormone (LH), and follicle-stimulating hormone (FSH), control sexual function.

The uterus, ovaries, fallopian tubes, vagina, and breasts comprise the female reproductive system. The ovaries and uterus are the source of ova and the location of fetal development, respectively. The fallopian tubes and vagina are accessory organs attached to the top and bottom of the uterus, respectively. Both the uterus and ovaries have additional roles in the development and loss of reproductive capability during a female's lifetime. The primary role of the breasts is lactation. Multiple endocrine signals from the ovaries, uterus, pituitary, hypothalamus, adrenal glands, and other tissues coordinate reproduction and lactation. These signals vary during the monthly menstruation cycle and during the female's lifetime. Similarly, the sensitivity of reproductive organs to these endocrine signals varies during the female's lifetime.

A combination of positive and negative feedback to the ovaries, pituitary and hypothalamus glands controls physiologic changes during the monthly ovulation and endometrial cycles. The anterior pituitary secretes two major gonadotropin hormones, follicle-stimulating hormone (FSH) and luteinizing hormone (LH), regulated by negative feedback of steroids, most notably by ovarian estradiol. If fertilization does not occur, estrogen and progesterone levels decrease. This sudden reduction of the ovarian hormones leads to menstruation, the desquamation of the endometrium.

Hormones further govern all the steps of pregnancy, parturition, lactation, and menopause. During pregnancy large quantities of human chorionic gonadotropin (hCG), estrogens, progesterone, and human chorionic somatomammotropin (hCS) are formed by the placenta. hCG, a glycoprotein similar to luteinizing hormone, stimulates the corpus luteum to continue producing more progesterone and estrogens, rather than to involute as occurs if the ovum is not fertilized. hCS is similar to growth hormone and is crucial for fetal nutrition.

The female breast also matures during pregnancy. Large amounts of estrogen secreted by the placenta trigger growth and branching of the breast milk ductal system while lactation is initiated by the secretion of prolactin by the pituitary gland.

Parturition involves several hormonal changes that increase uterine contractility toward the end of pregnancy, as follows. The levels of estrogens increase more than those of progesterone. Oxytocin is secreted by the neurohypophysis. Concomitantly, uterine sensitivity to oxytocin increases. The fetus itself secretes oxytocin, cortisol (from adrenal glands), and prostaglandins.

Menopause occurs when most of the ovarian follicles have degenerated. The ovary then

produces less estradiol, reducing the negative feedback on the pituitary and hypothalamus glands. Mean levels of circulating FSH and LH increase, even as ovulatory cycles continue. Therefore, the ovary is less responsive to gonadotropins, and there is an increase in the time between menstrual cycles. Consequently, menstrual bleeding ceases, and reproductive capability ends.

5 **Differentiation and Proliferation**

Tissue growth involves complex and ordered patterns of cell proliferation, cell differentiation, and apoptosis. Cell proliferation must be regulated to maintain both the number of cells and their spatial organization. This regulation depends upon the appropriate expression of proteins which control cell cycle progression in response to extracellular signals, such as growth factors and other mitogens, and intracellular cues, such as DNA damage or nutrient starvation. Molecules which directly or indirectly modulate cell cycle progression fall into several categories, including growth factors and their receptors, second messenger and signal transduction proteins, oncogene products, tumor-suppressor proteins, and mitosis-promoting factors.

Embryogenesis is a process in which distinct patterns of protein expression control proper development. This process involves a host of proteins each with distinct and highly coordinated expression patterns. For example, in the mouse, temporally regulated expression of two related genes *Msg1* and *Mrg1* contribute to normal embryonic development. *Msg1* is expressed in the posterior domains of the developing mesoderm, while *Mrg1* is expressed in the anterior visceral endoderm. Properly coordinated expression of each protein throughout embryogenesis is critical for proper tissue and organ formation (Dunwoodie, S.L. et al. (1998) *Mech. Dev.* 72:27-40).

Growth factors were originally described as serum factors required to promote cell proliferation. Most growth factors are large, secreted polypeptides that act on cells in their local environment. Growth factors bind to and activate specific cell surface receptors and initiate intracellular signal transduction cascades. Many growth factor receptors are classified as receptor tyrosine kinases which undergo autophosphorylation upon ligand binding. Autophosphorylation enables the receptor to interact with signal transduction proteins characterized by the presence of SH2 or SH3 domains (Src homology regions 2 or 3). These proteins then modulate the activity state of small G-proteins, such as Ras, Rab, and Rho, along with GTPase activating proteins (GAPs), guanine nucleotide releasing proteins (GNRPs), and other guanine nucleotide exchange factors. Small G-proteins act as molecular switches that activate other downstream events, such as mitogen-activated protein kinase (MAP kinase) cascades. MAP kinases ultimately activate transcription of mitosis-promoting genes.

In addition to growth factors, small signaling peptides and hormones also influence cell proliferation. These molecules bind primarily to another class of receptor, the trimeric G-protein

coupled receptor (GPCR), found predominantly on the surface of immune, neuronal and neuroendocrine cells. Upon ligand binding, the GPCR activates a trimeric G protein which in turn triggers increased levels of intracellular second messengers such as phospholipase C, Ca^{2+} , and cyclic AMP. Most GPCR-mediated signaling pathways indirectly promote cell proliferation by causing the secretion or
5 breakdown of other signaling molecules that have direct mitogenic effects. These signaling cascades often involve activation of kinases and phosphatases. Some growth factors, such as some members of the transforming growth factor beta (TGF- β) family, act on some cells to stimulate cell proliferation and on other cells to inhibit it. Growth factors may also stimulate a cell at one concentration and inhibit the same cell at another concentration. Most growth factors also have a multitude of other actions
10 besides the regulation of cell growth and division: they can control the proliferation, survival, differentiation, migration, or function of cells depending on the circumstance. For example, the tumor necrosis factor/nerve growth factor (TNF/NGF) family can activate or inhibit cell death, as well as regulate proliferation and differentiation. The cell response depends on the type of cell, its stage of differentiation and transformation status, which surface receptors are stimulated, and the types of
15 stimuli acting on the cell (Smith, A. et al. (1994) Cell 76:959-962; and Nocentini, G. et al. (1997) Proc. Natl. Acad. Sci. USA 94:6216-6221).

Neighboring cells in a tissue compete for growth factors, and when provided with "unlimited" quantities in a perfused system will grow to even higher cell densities before reaching density-dependent inhibition of cell division. Cells often demonstrate an anchorage dependence of cell division as well.
20 This anchorage dependence may be associated with the formation of focal contacts linking the cytoskeleton with the extracellular matrix (ECM). The expression of ECM components can be stimulated by growth factors. For example, TGF- β stimulates fibroblasts to produce a variety of ECM proteins, including fibronectin, collagen, and tenascin (Pearson, C.A. et al. (1988) EMBO J. 7:2977-2981). In fact, for some cell types, specific ECM molecules, such as laminin or fibronectin, may act as
25 growth factors. Tenascin-C and -R, expressed in developing and lesioned neural tissue, provide stimulatory/anti-adhesive or inhibitory properties, respectively, for axonal growth (Faissner, A. (1997) Cell Tissue Res. 290:331-341).

Cancers and immune disorders are characterized by uncoordinated cell proliferation. Cancers are associated with the activation of oncogenes which are derived from normal cellular genes. These
30 oncogenes encode oncoproteins which convert normal cells into malignant cells. Some oncoproteins are mutant isoforms of the normal protein, and other oncoproteins are abnormally expressed with respect to location or amount of expression. The latter category of oncoprotein causes cancer by altering transcriptional control of cell proliferation. Five classes of oncoproteins are known to affect cell cycle controls. These classes include growth factors, growth factor receptors, intracellular signal

transducers, nuclear transcription factors, and cell-cycle control proteins. Viral oncogenes are integrated into the human genome after infection of human cells by certain viruses. Examples of viral oncogenes include v-src, v-abl, and v-fps. Certain cell proliferation disorders can be identified by changes in the protein complexes that normally control progression through the cell cycle. A primary treatment strategy involves reestablishing control over cell cycle progression by manipulation of the proteins involved in cell cycle regulation (Nigg, E.A. (1995) BioEssays 17:471-480).

Many oncogenes have been identified and characterized. These include sis, erbA, erbB, her-2, mutated G_s, src, abl, ras, crk, jun, fos, myc, and mutated tumor-suppressor genes such as RB, p53, mdm2, Cip1, p16, and cyclin D. Transformation of normal genes to oncogenes may also occur by chromosomal translocation. The Philadelphia chromosome, characteristic of chronic myeloid leukemia and a subset of acute lymphoblastic leukemias, results from a reciprocal translocation between chromosomes 9 and 22 that moves a truncated portion of the proto-oncogene c-abl to the breakpoint cluster region (bcr) on chromosome 22.

Mutations which hyperactivate oncogenes result in cell proliferation. Stimulation of a cell by growth factors activates two sets of gene products, the early-response genes and the delayed-response genes. Early-response gene products include *myc*, *fos*, and *jun*, all of which encode gene regulatory proteins. These regulatory proteins lead to the transcriptional activation of a second set of genes, the delayed-response genes, which include the cell-cycle regulators Cdk and cyclins. For example, the human T-cell leukemia virus type I (HTLV-1) Tax transactivator protein acts as an early response gene by enhancing the activity of a cellular transcription factor. The oncogenic properties of the Tax protein include transformation of primary T-lymphocytes and fibroblasts through cooperation with the a GTP-binding protein, Ras. Recently investigators have shown that Tax interacts with several PDZ-containing proteins. The PDZ domain, originally described in the Drosophila tumor suppressor protein Discs-Large, is common to membrane proteins thought to be involved in clustering receptors in growth factor signal transduction pathways (Rousset, R. et al. (1998) Oncogene 16:643-654).

Tumor-suppressor genes are involved in regulating cell proliferation. Mutations which cause reduced or loss of function in tumor-suppressor genes result in uncontrolled cell proliferation. For example, the retinoblastoma gene product (RB), in a non-phosphorylated state, binds several early-response genes and suppresses their transcription, thus blocking cell division. Phosphorylation of RB causes it to dissociate from the genes, releasing the suppression, and allowing cell division to proceed.

Other gene products involved in cell proliferation, differentiation, and apoptosis are yet to be discovered. One method currently being utilized to help identify such new molecules involves comparisons between quiescent and proliferative tissues. For example, a subtractive hybridization screen of human placental cytotrophoblast cells identified 20 genes whose expression levels rose due to

EGF induction of cell proliferation. (Morrish, D.W. et al. (1996) Placenta 17:431-441). Another method involves identification of molecules produced in cells treated with anti-tumorigenic agents, such as dithiolethiones. Presumably, the protective action of these anti-tumorigenic agents is associated with the induction of tumor suppressor gene products (Primiano, T. et al. (1996) Carcinogenesis 17:2297-2303).

In another example, the candidate tumor-suppressor gene ING1, that codes a nuclear protein, p33ING1, is involved in the negative regulation of cell proliferation. The action of p33ING1 is dependent upon the activity of another tumor-suppressor gene, p53. p53 is a cellular stress-responsive gene requiring the activity of p33ING1 to effectively induce growth inhibition of cells. p33ING1 and p53 have been shown to physically associate through immunoprecipitation studies (Garkavtsev, I. et al. (1998) Nature 391:295-298).

Apoptosis

Apoptosis is the genetically controlled process by which unneeded or defective cells undergo programmed cell death. Selective elimination of cells is as important for morphogenesis and tissue remodeling as is cell proliferation and differentiation. Lack of apoptosis may result in hyperplasia and other disorders associated with increased cell proliferation. Apoptosis is also a critical component of the immune response. Immune cells such as cytotoxic T-cells and natural killer cells prevent the spread of disease by inducing apoptosis in tumor cells and virus-infected cells. In addition, immune cells that fail to distinguish self molecules from foreign molecules must be eliminated by apoptosis to avoid an autoimmune response.

Apoptotic cells undergo distinct morphological changes. Hallmarks of apoptosis include cell shrinkage, nuclear and cytoplasmic condensation, and alterations in plasma membrane topology. Biochemically, apoptotic cells are characterized by increased intracellular calcium concentration, fragmentation of chromosomal DNA, and expression of novel cell surface components.

The molecular mechanisms of apoptosis are highly conserved, and many of the key protein regulators and effectors of apoptosis have been identified. Apoptosis generally proceeds in response to a signal which is transduced intracellularly and results in altered patterns of gene expression and protein activity. Signaling molecules such as hormones and cytokines are known both to stimulate and to inhibit apoptosis through interactions with cell surface receptors. Transcription factors also play an important role in the onset of apoptosis. A number of downstream effector molecules, particularly proteases such as the cysteine proteases called caspases, have been implicated in the degradation of cellular components and the proteolytic activation of other apoptotic effectors.

Aging and Senescence

Studies of the aging process or senescence have shown a number of characteristic cellular and

molecular changes (Fauci, A.S. et al. (1998) Harrison's Principles of Internal Medicine, McGraw-Hill, New York NY, p.37). These characteristics include increases in chromosome structural abnormalities, DNA cross-linking, incidence of single-stranded breaks in DNA, losses in DNA methylation, and degradation of telomere regions. In addition to these DNA changes, post-translational alterations of proteins increase including deamidation, oxidation, cross-linking, and nonenzymatic glycosylation. Still further molecular changes occur in the mitochondria of aging cells through deterioration of structure. These changes eventually contribute to decreased function in every organ of the body.

The discovery of new cell cycle and proliferation proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of immune, developmental, and cell signaling disorders, and cell proliferative disorders including cancer.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, cell cycle and proliferation proteins, referred to collectively as "CCYPR" and individually as "CCYPR-1," "CCYPR-2," "CCYPR-3," "CCYPR-4," "CCYPR-5," "CCYPR-6," "CCYPR-7," "CCYPR-8," "CCYPR-9," "CCYPR-10," "CCYPR-11," "CCYPR-12," "CCYPR-13," "CCYPR-14," "CCYPR-15," "CCYPR-16," "CCYPR-17," "CCYPR-18," "CCYPR-19," "CCYPR-20," "CCYPR-21," "CCYPR-22," "CCYPR-23," "CCYPR-24," "CCYPR-25," "CCYPR-26," "CCYPR-27," "CCYPR-28," "CCYPR-29," "CCYPR-30," "CCYPR-31," "CCYPR-32," "CCYPR-33," "CCYPR-34," "CCYPR-35," "CCYPR-36," "CCYPR-37," "CCYPR-38," "CCYPR-39," "CCYPR-40," "CCYPR-41," "CCYPR-42," "CCYPR-43," "CCYPR-44," "CCYPR-45," "CCYPR-46," "CCYPR-47," "CCYPR-48," "CCYPR-49," "CCYPR-50," "CCYPR-51," "CCYPR-52," "CCYPR-53," "CCYPR-54." In one aspect, the invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-54.

The invention further provides an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-

54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-54. In another alternative, the polynucleotide is selected
5 from the group consisting of SEQ ID NO:55-108.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90%
10 sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism
15 comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, c)
20 a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b)
25 recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group
30 consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54.

The invention further provides an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of

SEQ ID NO:55-108, b) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:55-108, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous
5 nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:55-108, b) a naturally occurring polynucleotide sequence having at least 70% sequence
10 identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:55-108, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions
15 whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said
20 target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:55-108, b) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:55-108, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e)
25 an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a pharmaceutical composition comprising an effective amount
30 of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid

sequence selected from the group consisting of SEQ ID NO:1-54, and a pharmaceutically acceptable excipient. In one embodiment, the pharmaceutical composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional CCYPR, comprising administering to a patient in need of such treatment the pharmaceutical composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional CCYPR, comprising administering to a patient in need of such treatment the pharmaceutical composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional CCYPR, comprising administering to a patient in need of such treatment the pharmaceutical composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group

consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding
 5 of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, b) a naturally
 10 occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-54. The method comprises a) combining the polypeptide with at least one test compound under conditions
 15 permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

20 The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:55-108, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

25 The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID
 30 NO:55-108, ii) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:55-108, iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological
 35 sample, said target polynucleotide comprising a polynucleotide sequence selected from the group

consisting of SEQ ID NO:55-108, ii) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:55-108, iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of the above polynucleotide sequence; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

10

BRIEF DESCRIPTION OF THE TABLES

Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding CCYPR.

15

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods, algorithms, and searchable databases used for analysis of CCYPR.

Table 3 shows selected fragments of each nucleic acid sequence; the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis; diseases, disorders, or conditions associated with these tissues; and the vector into which each cDNA was cloned.

20

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding CCYPR were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

25

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

30

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

35

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described.

- 5 All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

- 10 "CCYPR" refers to the amino acid sequences of substantially purified CCYPR obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

- The term "agonist" refers to a molecule which intensifies or mimics the biological activity of CCYPR. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other
15 compound or composition which modulates the activity of CCYPR either by directly interacting with CCYPR or by acting on components of the biological pathway in which CCYPR participates.

- An "allelic variant" is an alternative form of the gene encoding CCYPR. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or
20 many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

- "Altered" nucleic acid sequences encoding CCYPR include those sequences with deletions,
25 insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as CCYPR or a polypeptide with at least one functional characteristic of CCYPR. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding CCYPR, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding CCYPR.
- 30 The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent CCYPR. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of CCYPR is retained. For example, negatively charged amino

acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and
5 valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence
10 to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of
15 CCYPR. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of CCYPR either by directly interacting with CCYPR or by acting on components of the biological pathway in which CCYPR participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof,
20 such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind CCYPR polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers
25 that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which
30 bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA;
35 peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as

phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once
5 introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical
10 functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic CCYPR, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid
15 sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution.
20 Compositions comprising polynucleotide sequences encoding CCYPR or fragments of CCYPR may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

25 "Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (PE Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap
30 (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

"Conservative amino acid substitutions" are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino

acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
5	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
10	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
15	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
20	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

A "fragment" is a unique portion of CCYPR or the polynucleotide encoding CCYPR which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment

used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected
5 from the first 250 or 500 amino acids (or first 25% or 50% of a polypeptide) as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:55-108 comprises a region of unique polynucleotide sequence that
10 specifically identifies SEQ ID NO:55-108, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:55-108 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:55-108 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:55-108 and the region of SEQ ID NO:55-108 to which the fragment corresponds are routinely
15 determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-54 is encoded by a fragment of SEQ ID NO:55-108. A fragment of SEQ ID NO:1-54 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-54. For example, a fragment of SEQ ID NO:1-54 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-54.
20 The precise length of a fragment of SEQ ID NO:1-54 and the region of SEQ ID NO:1-54 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full-length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full-
25 length" polynucleotide sequence encodes a "full-length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a
30 standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence
35 alignment program. This program is part of the LASERGENE software package, a suite of molecular

WO 01/07471

PCT/US00/19948

biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

5 The phrases “percent identity” and “% identity,” as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of
10 substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and
15 “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.12
20 (Apr-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

25 *Word Size: 3*

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance,
30 a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain

DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term "humanized antibody" refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the "washing" step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency

conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization
5 complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence
10 resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

15 An "immunogenic fragment" is a polypeptide or oligopeptide fragment of CCYPR which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of CCYPR which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides,
20 or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of CCYPR. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological,
25 functional, or immunological properties of CCYPR.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

30 "Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

35 "Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which

comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

5 "Post-translational modification" of an CCYPR may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of CCYPR.

"Probe" refers to nucleic acid sequences encoding CCYPR, their complements, or fragments
10 thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA
15 polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100,
20 or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold
25 Spring Harbor Press, Plainview NY; Ausubel, F.M. et al., 1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge
30 MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection

programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection
5 program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program
10 (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the
15 above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence
20 that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a
25 recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be use to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

30 A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid,

amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

5 An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

10 The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding CCYPR, or fragments thereof, or CCYPR itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

15 The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

20 The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

25 "Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

30 A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type

of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed
5 cells which express the inserted DNA or RNA for limited periods of time.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor
10 of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants, and animals. The isolated DNA of the present invention can be
15 introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at
20 least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95% or at least 98% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic"
25 (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting
30 polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

35 A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at

least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 98% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

The invention is based on the discovery of new human cell cycle and proliferation proteins (CCYPR), the polynucleotides encoding CCYPR, and the use of these compositions for the diagnosis, treatment, or prevention of immune, developmental, and cell signaling disorders, and cell proliferative disorders including cancer.

Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding CCYPR. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte clones in which nucleic acids encoding each CCYPR were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. In some cases, GenBank sequence identifiers are also shown in column 5. The Incyte clones and GenBank cDNA sequences, where indicated, in column 5 were used to assemble the consensus nucleotide sequence of each CCYPR and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows homologous sequences as identified by BLAST analysis along with relevant citations, all of which are expressly incorporated by reference herein in their entirety; and column 7 shows analytical methods and in some cases, searchable databases to which the analytical methods were applied. The methods of column 7 were used to characterize each polypeptide through sequence homology and protein motifs.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding CCYPR. The first column of Table 3 lists the nucleotide SEQ ID NOs. Column 2 lists fragments of the nucleotide sequences of column 1. These fragments are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:55-108 and to distinguish between SEQ ID NO:55-108 and related polynucleotide sequences. The polypeptides encoded by these fragments are useful, for example, as immunogenic peptides. Column 3 lists tissue

categories which express CCYPR as a fraction of total tissues expressing CCYPR. Column 4 lists diseases, disorders, or conditions associated with those tissues expressing CCYPR as a fraction of total tissues expressing CCYPR. Column 5 lists the vectors used to subclone each cDNA library. Of particular note is the expression of SEQ ID NO:66 in inflammatory tissues. It should be noted that

5 SEQ ID NO:76 was found to be expressed predominantly in nervous tissue.

The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding CCYPR were isolated. Column 1 references the nucleotide SEQ ID NOs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

10 SEQ ID NO:61 maps to chromosome 5 within the interval from 141.40 to 142.60 centiMorgans. This interval also contains gene(s) and/or EST(s) associated with corneal dystrophy and deafness.

SEQ ID NO:73 maps to chromosome 2 within the interval from 73.80 to 83.50 centiMorgans. This interval also contains gene(s) and/or EST(s) associated with hereditary nonpolyposis colorectal carcinoma and Muir-Torre syndrome. SEQ ID NO:74 maps to chromosome 19 within the interval

15 from 41.70 to 58.70 centiMorgans. SEQ ID NO:75 maps to chromosome 17 within the interval from 62.90 to 64.20 centiMorgans. This interval also contains gene(s) and/or EST(s) located within the human breast cancer (BRCA1) gene region. SEQ ID NO:76 maps to chromosome 1 within the interval from 143.30 to 153.90 centiMorgans, to chromosome 3 within the interval from 156.20 to

20 160.00 centiMorgans, and to chromosome X within the interval from 112.80 to 139.40 centiMorgans. The interval on chromosome X from 112.80 to 139.40 centiMorgans also contains gene(s) and/or EST(s) associated with X-linked agammaglobulinaemia.

SEQ ID NO:77 maps to chromosome 23 within the interval from 173.60 to 179.80 centiMorgans, and to chromosome 11 within the interval from 136.90 centiMorgans to q-terminus.

25 SEQ ID NO:78 maps to chromosome 3 within the interval from 200.00 to 213.70 centiMorgans. SEQ ID NO:81 maps to chromosome 7 within the interval from 167.60 centiMorgans to q-terminus. SEQ ID NO:90 maps to chromosome 2 within the interval from 236.10 to 240.20 centiMorgans, to chromosome 3 within the interval from 16.50 to 43.00 centiMorgans, and to chromosome 6 within the interval from 124.20 to 126.50 centiMorgans. SEQ ID NO:91 maps to chromosome 2 within the

30 interval from 22.40 to 40.70 centiMorgans. SEQ ID NO:98 maps to chromosome 8 within the interval from 40.30 to 60.00 centiMorgans. SEQ ID NO:100 maps to chromosome 14 within the interval from 95.50 to 103.70 centiMorgans, and to chromosome 6 within the interval from 158.50 centiMorgans to q-terminus. SEQ ID NO:104 maps to chromosome 18 within the interval from 32.40 to 42.70 centiMorgans. SEQ ID NO:105 maps to chromosome 19 within the interval from 69.90 to

35 81.20 centiMorgans.

The invention also encompasses CCYPR variants. A preferred CCYPR variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the CCYPR amino acid sequence, and which contains at least one functional or structural characteristic of CCYPR.

5 The invention also encompasses polynucleotides which encode CCYPR. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:55-108, which encodes CCYPR. The polynucleotide sequences of SEQ ID NO:55-108, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone
10 is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding CCYPR. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding CCYPR. A particular aspect of the invention encompasses a variant of a polynucleotide
15 sequence comprising a sequence selected from the group consisting of SEQ ID NO:55-108 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:55-108. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of CCYPR.

20 It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding CCYPR, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in
25 accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring CCYPR, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode CCYPR and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring CCYPR under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding CCYPR or
30 its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding CCYPR and its derivatives without altering the encoded amino acid sequences

include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode CCYPR and CCYPR derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the
5 synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding CCYPR or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID
10 NO:55-108 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the
15 embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (PE Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is
20 automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (PE Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (PE Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of
25 algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding CCYPR may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences,
30 such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) *PCR Methods Applic.* 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a

known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and
5 ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in
10 finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

15 When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

20 Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate
25 software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, PE Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which
30 encode CCYPR may be cloned in recombinant DNA molecules that direct expression of CCYPR, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express CCYPR.

The nucleotide sequences of the present invention can be engineered using methods generally

WO 01/07471

PCT/US00/19948

known in the art in order to alter CCYPR-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of CCYPR, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding CCYPR may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.) Alternatively, CCYPR itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (PE Biosystems). Additionally, the amino acid sequence of CCYPR, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.)

The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active CCYPR, the nucleotide sequences encoding CCYPR or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding CCYPR. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding CCYPR. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding CCYPR and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding CCYPR and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding CCYPR. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184; Engelhard, E.K. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945; Takamatsu,

N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding CCYPR. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding CCYPR can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding CCYPR into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of CCYPR are needed, e.g. for the production of antibodies, vectors which direct high level expression of CCYPR may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of CCYPR. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, supra; and Scorer, supra.)

Plant systems may also be used for expression of CCYPR. Transcription of sequences encoding CCYPR may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, supra; Broglie, supra; and Winter, supra.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated

transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding CCYPR may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses CCYPR in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of CCYPR in cell lines is preferred. For example, sequences encoding CCYPR can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* and *apr* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β

glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) *Methods Mol. Biol.* 55:121-131.)

5 Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding CCYPR is inserted within a marker gene sequence, transformed cells containing sequences encoding CCYPR can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding CCYPR under the control of a single
10 promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding CCYPR and that express CCYPR may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR
15 amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of CCYPR using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence
20 activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on CCYPR is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New
25 York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding CCYPR include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide.
30 Alternatively, the sequences encoding CCYPR, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega

(Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding CCYPR may be cultured under
5 conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CCYPR may be designed to contain signal sequences which direct secretion of CCYPR through a prokaryotic or eukaryotic cell membrane.

10 In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells
15 which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid
20 sequences encoding CCYPR may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric CCYPR protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of CCYPR activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity
25 matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion
30 proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the CCYPR encoding sequence and the heterologous protein sequence, so that CCYPR may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially

available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled CCYPR may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

CCYPR of the present invention or fragments thereof may be used to screen for compounds that specifically bind to CCYPR. At least one and up to a plurality of test compounds may be screened for specific binding to CCYPR. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of CCYPR, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which CCYPR binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express CCYPR, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing CCYPR or cell membrane fractions which contain CCYPR are then contacted with a test compound and binding, stimulation, or inhibition of activity of either CCYPR or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with CCYPR, either in solution or affixed to a solid support, and detecting the binding of CCYPR to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

CCYPR of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of CCYPR. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for CCYPR activity, wherein CCYPR is combined with at least one test compound, and the activity of CCYPR in the presence of a test compound is compared with the activity of CCYPR in the absence of the test compound. A change in the activity of CCYPR in the presence of the test compound is

indicative of a compound that modulates the activity of CCYPR. Alternatively, a test compound is combined with an in vitro or cell-free system comprising CCYPR under conditions suitable for CCYPR activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of CCYPR may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding CCYPR or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent No. 5,175,383 and U.S. Patent No. 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding CCYPR may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding CCYPR can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding CCYPR is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress CCYPR, e.g., by secreting CCYPR in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of CCYPR and cell cycle and proliferation proteins. In addition, the expression of CCYPR is closely associated with inflammation, trauma, cell proliferation and cancer. Therefore, CCYPR appears to play a role in immune, developmental, and cell signaling disorders, and cell proliferative disorders including cancer. In the treatment of disorders associated with increased CCYPR expression or activity, it is desirable to decrease the expression or activity of CCYPR. In the treatment of disorders associated with decreased CCYPR expression or activity, it is desirable to increase the expression or activity of CCYPR.

- Therefore, in one embodiment, CCYPR or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CCYPR. Examples of such disorders include, but are not limited to, an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, mixed connective tissue disorder (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, sensorineural hearing loss, and disorders of immune cell activation; a cell signaling disorder including

endocrine disorders such as disorders of the hypothalamus and pituitary resulting from lesions such as primary brain tumors, adenomas, infarction associated with pregnancy, hypophysectomy, aneurysms, vascular malformations, thrombosis, infections, immunological disorders, and complications due to head trauma; disorders associated with hyperpituitarism including acromegaly, gigantism, and

5 syndrome of inappropriate antidiuretic hormone (ADH) secretion (SIADH) often caused by benign adenoma; disorders associated with hypothyroidism including goiter, myxedema, acute thyroiditis associated with bacterial infection; disorders associated with hyperparathyroidism including Conn disease (chronic hypercalcemia); pancreatic disorders such as Type I or Type II diabetes mellitus and associated complications; disorders associated with the adrenals such as hyperplasia, carcinoma, or

10 adenoma of the adrenal cortex, hypertension associated with alkalosis; disorders associated with gonadal steroid hormones such as: in women, abnormal prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, perturbations of the menstrual cycle, polycystic ovarian disease, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, teratogenesis, hyperprolactinemia, isolated

15 gonadotropin deficiency, amenorrhea, galactorrhea, hermaphroditism, hirsutism and virilization, breast cancer, and fibrocystic breast disease; and, in post-menopausal women, osteoporosis; and, in men, Leydig cell deficiency, male climacteric phase, germinal cell aplasia, hypergonadal disorders associated with Leydig cell tumors, androgen resistance associated with absence of androgen receptors, syndrome of 5 α -reductase, a disruption of spermatogenesis, abnormal sperm physiology,

20 cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma,

25 myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing CCYPR or a fragment or derivative

30 thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CCYPR including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified CCYPR in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CCYPR including, but not

35 limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of CCYPR may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CCYPR including, but not limited to, those listed above.

5 In a further embodiment, an antagonist of CCYPR may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of CCYPR. Examples of such disorders include, but are not limited to, those immune, developmental, and cell signaling disorders, and cell proliferative disorders including cancer, described above. In one aspect, an antibody which specifically binds CCYPR may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express CCYPR.

10 In an additional embodiment, a vector expressing the complement of the polynucleotide encoding CCYPR may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of CCYPR including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

20 An antagonist of CCYPR may be produced using methods which are generally known in the art. In particular, purified CCYPR may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind CCYPR. Antibodies to CCYPR may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

30 For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with CCYPR or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to

CCYPR have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of CCYPR amino acids may be fused with those of another protein, such as KLH, and antibodies to the

5 chimeric molecule may be produced.

Monoclonal antibodies to CCYPR may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) *Nature* 256:495-497; Kozbor, D. et al. (1985) *J.*

10 *Immunol. Methods* 81:31-42; Cote, R.J. et al. (1983) *Proc. Natl. Acad. Sci. USA* 80:2026-2030; and Cole, S.P. et al. (1984) *Mol. Cell Biol.* 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) *Proc.*

15 *Natl. Acad. Sci. USA* 81:6851-6855; Neuberger, M.S. et al. (1984) *Nature* 312:604-608; and Takeda, S. et al. (1985) *Nature* 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce CCYPR-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton,

20 D.R. (1991) *Proc. Natl. Acad. Sci. USA* 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:3833-3837; Winter, G. et al. (1991) *Nature* 349:293-299.)

25 Antibody fragments which contain specific binding sites for CCYPR may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al.

30 (1989) *Science* 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between CCYPR and its

specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering CCYPR epitopes is generally used, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques
5 may be used to assess the affinity of antibodies for CCYPR. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of CCYPR-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple
10 CCYPR epitopes, represents the average affinity, or avidity, of the antibodies for CCYPR. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular CCYPR epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the CCYPR-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from
15 about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of CCYPR, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a
20 polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of CCYPR-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al., supra.)

25 In another embodiment of the invention, the polynucleotides encoding CCYPR, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding CCYPR. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be
30 designed from various locations along the coding or control regions of sequences encoding CCYPR. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence

complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 5 76:271; Ausubel, *supra*; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

10 In another embodiment of the invention, polynucleotides encoding CCYPR may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency 15 (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) *Science* 270:404-410; Verma, I.M. and Somia, N. (1997) *Nature* 389:239-242)), (ii) 20 express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) *Nature* 335:395-396; Poeschla, E. et al. (1996) *Proc. Natl. Acad. Sci. USA.* 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides 25 brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in CCYPR expression or regulation causes disease, the expression of CCYPR from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in 30 CCYPR are treated by constructing mammalian expression vectors encoding CCYPR and introducing these vectors by mechanical means into CCYPR-deficient cells. Mechanical transfer technologies for use with cells *in vivo* or *ex vitro* include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) *Annu. Rev. Biochem.* 62:191- 35 217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J-L. and H. Récipon (1998) *Curr. Opin. Biotechnol.*

9:445-450).

Expression vectors that may be effective for the expression of CCYPR include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, 5 PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). CCYPR may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl. Acad. Sci. USA 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) 10 Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and H.M. Blau, *supra*)), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding CCYPR from a normal individual.

15 Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. 20 (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to CCYPR expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding CCYPR under the control of an independent promoter or the retrovirus long 25 terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. USA 92:6733-6737), incorporated by reference herein. The vector is propagated in an 30 appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and A.D. Miller (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining

retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant”) discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference.

Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding CCYPR to cells which have one or more genetic abnormalities with respect to the expression of CCYPR. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano (“Adenovirus vectors for gene therapy”), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544; and Verma, I.M. and N. Somia (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding CCYPR to target cells which have one or more genetic abnormalities with respect to the expression of CCYPR. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing CCYPR to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca (“Herpes simplex virus strains for gene transfer”), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for
5 secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for
10 chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding CCYPR. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or
15 tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be
20 extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding CCYPR.
25 Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or
30 promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased CCYPR expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding CCYPR may be therapeutically useful, and in the treatment of disorders associated with decreased CCYPR expression or activity, a compound which specifically promotes expression of the polynucleotide encoding CCYPR may be therapeutically useful.

35 At least one, and up to a plurality, of test compounds may be screened for effectiveness in

altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound
5 based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding CCYPR is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding CCYPR are assayed
10 by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding CCYPR. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide
15 exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

25 Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat.
30 Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a pharmaceutical
35 composition which generally comprises an active ingredient formulated with a pharmaceutically

acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such pharmaceutical compositions may consist of CCYPR, antibodies to CCYPR, and mimetics, agonists, antagonists, or inhibitors of CCYPR.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Pharmaceutical compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

Specialized forms of pharmaceutical compositions may be prepared for direct intracellular delivery of macromolecules comprising CCYPR or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, CCYPR or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example CCYPR or fragments thereof, antibodies of CCYPR, and agonists, antagonists or inhibitors of CCYPR, which

ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED₅₀ (the dose therapeutically effective in 50% of the population) or LD₅₀ (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD₅₀/ED₅₀ ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED₅₀ with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 µg to 100,000 µg, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind CCYPR may be used for the diagnosis of disorders characterized by expression of CCYPR, or in assays to monitor patients being treated with CCYPR or agonists, antagonists, or inhibitors of CCYPR. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for CCYPR include methods which utilize the antibody and a label to detect CCYPR in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring CCYPR, including ELISAs, RIAs, and FACS, are known

in the art and provide a basis for diagnosing altered or abnormal levels of CCYPR expression. Normal or standard values for CCYPR expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibody to CCYPR under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of CCYPR expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding CCYPR may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of CCYPR may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of CCYPR, and to monitor regulation of CCYPR levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding CCYPR or closely related molecules may be used to identify nucleic acid sequences which encode CCYPR. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding CCYPR, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the CCYPR encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:55-108 or from genomic sequences including promoters, enhancers, and introns of the CCYPR gene.

Means for producing specific hybridization probes for DNAs encoding CCYPR include the cloning of polynucleotide sequences encoding CCYPR or CCYPR derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding CCYPR may be used for the diagnosis of disorders associated with expression of CCYPR. Examples of such disorders include, but are not limited to, an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome

(AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic

5 dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, mixed connective tissue disorder (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation,

10 myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections,

15 trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary

20 neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, sensorineural hearing loss, and disorders of immune cell activation; a cell signaling disorder including endocrine disorders such as disorders of the hypothalamus and pituitary resulting from lesions such as primary brain tumors,

25 adenomas, infarction associated with pregnancy, hypophysectomy, aneurysms, vascular malformations, thrombosis, infections, immunological disorders, and complications due to head trauma; disorders associated with hyperpituitarism including acromegaly, gigantism, and syndrome of inappropriate antidiuretic hormone (ADH) secretion (SIADH) often caused by benign adenoma; disorders associated with hypothyroidism including goiter, myxedema, acute thyroiditis associated

30 with bacterial infection; disorders associated with hyperparathyroidism including Conn disease (chronic hypercalcemia); pancreatic disorders such as Type I or Type II diabetes mellitus and associated complications; disorders associated with the adrenals such as hyperplasia, carcinoma, or adenoma of the adrenal cortex, hypertension associated with alkalosis; disorders associated with gonadal steroid hormones such as: in women, abnormal prolactin production, infertility, including

35 tubal disease, ovulatory defects, and endometriosis, perturbations of the menstrual cycle, polycystic

ovarian disease, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, teratogenesis, hyperprolactinemia, isolated gonadotropin deficiency, amenorrhea, galactorrhea, hermaphroditism, hirsutism and virilization, breast cancer, and fibrocystic breast disease; and, in post-menopausal women, osteoporosis; and, in
5 men, Leydig cell deficiency, male climacteric phase, germinal cell aplasia, hypergonadal disorders associated with Leydig cell tumors, androgen resistance associated with absence of androgen receptors, syndrome of 5 α -reductase, a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; and a cell proliferative disorder such as
10 actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver,
15 lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. The polynucleotide sequences encoding CCYPR may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered CCYPR expression. Such qualitative or quantitative methods are well known in the art.

20 In a particular aspect, the nucleotide sequences encoding CCYPR may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding CCYPR may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard
25 value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding CCYPR in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

30 In order to provide a basis for the diagnosis of a disorder associated with expression of CCYPR, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding CCYPR, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal
35 subjects with values from an experiment in which a known amount of a substantially purified

polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated,
5 hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or
10 overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

15 Additional diagnostic uses for oligonucleotides designed from the sequences encoding CCYPR may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding CCYPR, or a fragment of a polynucleotide complementary to the polynucleotide encoding CCYPR, and will be employed under optimized conditions for identification of a specific gene or condition.
20 Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding CCYPR may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease
25 in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding CCYPR are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary
30 and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual

overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high
5 throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of CCYPR include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be
10 accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray
15 can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described in Seilhamer, J.J. et al., "Comparative Gene Transcript Analysis," U.S. Patent No. 5,840,484, incorporated herein by reference. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor
20 progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

25 In another embodiment, antibodies specific for CCYPR, or CCYPR or fragments thereof may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of
30 gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of

5 Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

58

invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for CCYPR to quantify the levels of CCYPR expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoz, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological

sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound
5 in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized
10 by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.
15

In another embodiment of the invention, nucleic acid sequences encoding CCYPR may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal
20 mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, e.g., Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)
25

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map
35

properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific
 5 embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/145,075, U.S. Ser. No. 60/153,129, and U.S. Ser. No. 60/164,647, are hereby expressly incorporated by reference.

10

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed
 15 in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA
 20 purity. In some cases, RNA was treated with DNase. For most libraries, poly(A⁺) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA
 25 libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic
 30 oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g.,
 35 PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), pcDNA2.1 plasmid

(Invitrogen, Carlsbad CA), or pINCY plasmid (Incyte Genomics, Palo Alto CA). Recombinant plasmids were transformed into competent E. coli cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

- 5 Plasmids obtained as described in Example I were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid
10 purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-
15 well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

- Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows.
20 Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (PE Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI
25 PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (PE Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA
30 sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VI.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions,

WO 01/07471

PCT/US00/19948

references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments were generated using the default parameters specified by the clustal algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and PFAM to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:55-108. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related

molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar.

The basis of the search is the product score, which is defined as:

$$5 \times \frac{\text{BLAST Score} \times \text{Percent Identity}}{\text{minimum \{length(Seq. 1), length(Seq. 2)\}}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding CCYPR occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation, trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. Chromosomal Mapping of CCYPR Encoding Polynucleotides

The cDNA sequences which were used to assemble SEQ ID NO:55-108 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:55-108 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 5). Radiation hybrid and genetic mapping data available

from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Génethon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

5 The genetic map locations of SEQ ID NO:61, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:81, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:104, and SEQ ID NO:105 are described in The Invention as ranges, or intervals, of human chromosomes. More than one map location is reported for SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:90, and SEQ ID NO:100, indicating that
10 previously mapped sequences having similarity, but not complete identity, to SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:90, and SEQ ID NO:100 were assembled into their respective clusters. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase
15 (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Génethon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified
20 disease genes map within or in proximity to the intervals indicated above.

VI. Extension of CCYPR Encoding Polynucleotides

The full length nucleic acid sequences of SEQ ID NO:55-108 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other
25 primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

30 Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$,
35 and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme

(Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems).

In like manner, the polynucleotide sequences of SEQ ID NO:55-108 are used to obtain 5' regulatory sequences using the procedure above, along with oligonucleotides designed for such

extension, and an appropriate genomic library.

VII. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:55-108 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

VIII. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Schena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array

elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

10 Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse

15 transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to stop the reaction and degrade the RNA. Samples are purified

20 using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

25 Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5

30 μ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR

35 Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and

coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60 °C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65 °C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60 °C. The arrays are washed for 10 min at 45 °C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45 °C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

IX. Complementary Polynucleotides

Sequences complementary to the CCYPR-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring CCYPR. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of CCYPR. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the CCYPR-encoding transcript.

X. Expression of CCYPR

Expression and purification of CCYPR is achieved using bacterial or virus-based expression systems. For expression of CCYPR in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3).

Antibiotic resistant bacteria express CCYPR upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of CCYPR in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding CCYPR by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, CCYPR is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from CCYPR at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified CCYPR obtained by these methods can be used directly in the assays shown in Examples XI and XV.

XI. Demonstration of CCYPR Activity

An assay for CCYPR activity measures cell proliferation as the amount of newly initiated DNA synthesis in Swiss mouse 3T3 cells. A plasmid containing polynucleotides encoding CCYPR is transfected into quiescent 3T3 cultured cells using methods well known in the art. The transiently transfected cells are then incubated in the presence of [³H]thymidine, a radioactive DNA precursor. Where applicable, varying amounts of CCYPR ligand are added to the transfected cells. Incorporation of [³H]thymidine into acid-precipitable DNA is measured over an appropriate time interval, and the amount incorporated is directly proportional to the amount of newly synthesized DNA and CCYPR activity.

XII. Functional Assays

CCYPR function is assessed by expressing the sequences encoding CCYPR at physiologically

elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT plasmid (Life Technologies) and pCR3.1 plasmid (Invitrogen), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of CCYPR on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding CCYPR and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding CCYPR and other genes of interest can be analyzed by northern analysis or microarray techniques.

XIII. Production of CCYPR Specific Antibodies

CCYPR substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the CCYPR amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is

synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-CCYPR activity by, for example, binding the peptide or CCYPR to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIV. Purification of Naturally Occurring CCYPR Using Specific Antibodies

Naturally occurring or recombinant CCYPR is substantially purified by immunoaffinity chromatography using antibodies specific for CCYPR. An immunoaffinity column is constructed by covalently coupling anti-CCYPR antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing CCYPR are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of CCYPR (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/CCYPR binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and CCYPR is collected.

XV. Identification of Molecules Which Interact with CCYPR

CCYPR, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled CCYPR, washed, and any wells with labeled CCYPR complex are assayed. Data obtained using different concentrations of CCYPR are used to calculate values for the number, affinity, and association of CCYPR with the candidate molecules.

Alternatively, molecules interacting with CCYPR are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989, Nature 340:245-246), or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

CCYPR may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent

No. 6,057,101).

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention.

5 Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	55	116462	KIDNNOT01	116462H1 (KIDNNOT01), 116462R1 (KIDNNOT01), 116462X304D1 (KIDNNOT01), 1500439F6 (SINPBST01), 2369977F6 (ADRENOT07)
2	56	1210462	BRSTNOT02	260707H1 (HNT2RAT01), 1210462H1 (BRSTNOT02), 1458882F6 (COLNFET02), 1841248T6 (COLNNOT07), 2378362H1 (ISLTNOT01), 3728643F6 (SMCCNON03)
3	57	1305252	PLACNOT02	794067R6 (OVARNOT03), 871989R1 (LUNGAST01), 1235253F1 (LUNGFET03), 1305252F6 (PLACNOT02), 1305252H1 (PLACNOT02), 1703258T6.comp (DUODNOT02), 2678307H1.comp (OVRTUT07), 3221088H1.comp (COLNNON03), 3647280H1 (ENDINOT01)
4	58	1416289	BRAINOT12	639958R6 (BRSTNOT03), 861752H1 (BRAITUT03), 1416289H1 (BRAINOT12), 1416289X310B1 (BRAINOT12), 1416289X310D2 (BRAINOT12), 1947451R6 (PITUNOT01)
5	59	1558289	SPLNNOT04	1558289H1 (SPLNNOT04), 1852450T6 (LUNGFET03), 2396092F6 (THP1AZT01), 2593267F6 (LUNGNOT22), 2632784F6 (COLNTUT15)
6	60	1577739	LNODNOT03	181266R1 (PLACNOB01), 1577739H1 (LNODNOT03), 4180022T6 (SINITUT03), 4597046H1 (COLSTUT01), 4860616H1 (PROSTUT09), 4991290H1 (LIVRTUT11), 5059810H1 (CONDTUT02)
7	61	1752768	LIVRTUT01	256106R1 (HNT2RAT01), 258814H1 (HNT2RAT01), 1312247F1 (COLNFET02), 1344279T6 (PROSNOT11), 1350089H1 (LATRTUT02), 1440718F6 (THYRNOT03), 1752768F6 (LIVRTUT01), 1752768H1 (LIVRTUT01), 1752768T6 (LIVRTUT01), 2079106F6 (ISLTNOT01), SBYA00612U1
8	62	1887228	BLADTUT07	080294F1 (SYNORAB01), 140055F1 (TLYMNOR01), 285207X42 (EOSIHET02), 516882R6 (MMLR1DT01), 1217892T1 (NEUTGMT01), 1887228H1 (BLADTUT07), 4323029H1 (TLYMUNT01)
9	63	1988468	LUNGAST01	072147R6 (THP1PEB01), 496297H1 (HNT2NOT01), 1362109F6 (LUNGNOT12), 1726095F6 (PROSNOT14), 1726095T6 (PROSNOT14), 1988468H1 (LUNGAST01), 1988468T6 (LUNGAST01), 2232471F6 (PROSNOT16)
10	64	2049176	LIVRFET02	2049176H1 (LIVRFET02), 2049176T6 (LIVRFET02), 2049176X321D1 (LIVRFET02)
11	65	2686765	LUNGNOT23	1502858F6 (BRAITUT07), 1956694X315D1 (CONNNOT01), 2022628X307D1 (CONNNOT01), 2686765F6 (LUNGNOT23), 2686765H1 (LUNGNOT23), 2864555H1 (KIDNNOT20), 2887609F6 (SINJNOT02), 3381980H1 (ESOGNOT04)
12	66	3215187	TESTNOT07	151135R6 (FIBRAGT01), 3215187F6 (TESTNOT07), 3215187H1 (TESTNOT07)
13	67	3500375	PROSTUT13	860585R1 (BRAITUT03), 1318501F1 (BLADNOT04), 1419126F1 (KIDNNOT09), 1483246F6 (CORPNOT02), 2238114T6 (PANCUTUT02), 2272329H1 (PROSNON01), 3209746F7 (BLADNOT08), 3403213H1 (ESOGNOT03), 4176619H1 (BRAINOT22), 4614606H1 (BRAYDIT01)

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
14	68	5080410	LNODNOT11	1270372X300D1 (BRAINOT09), 3460603H1 (293TF1T01), 5080410H1 (LNODNOT11)
15	69	5218248	BRSTNOT35	1808748X15C1 (PROSTUT12), 1808748X16C1 (PROSTUT12), 3391884H1 (LUNGNOT28)
16	70	058336	MUSCNOT01	058336H1 (MUSCNOT01), 058336T6 (MUSCNOT01), g2206766, g2069225
17	71	1511488	LUNGNOT14	1436265F1 (PANCNOT08), 1511488H1 (LUNGNOT14), 1511488T6 (LUNGNOT14), 1850020F6 (LUNGFET03)
18	72	1638819	UTRSNOT06	1282638T1 (COLNNOT16), 1638819F6 (UTRSNOT06), 1638819H1 (UTRSNOT06), 3597071H1 (FIBPNOT01), SBRA03813D1, SBRA04133D1, SBRA03785D1
19	73	1655123	PROSTUT08	1271351F1 (TESTTUT02), 1353234F1 (LATRTUT02), 1655123H1 (PROSTUT08), 2132188R6 (OVARNOT03), 3296525H1 (TLYJINT01), 3354010H1 (PROSNOT28), 3741838F6 (MENTNOT01), 3741838T6 (MENTNOT01), SXAF03528V1
20	74	2553926	THYMNOT03	403261F1 (TMLR3DT01), 1869739F6 (SKINBIT01), 2197242T6 (SPLNFET02), 2553926H1 (THYMNOT03), 2553956T6 (THYMNOT03), 3935528H1 (PROSTUT09), 5263918F6 (CONDTUT02)
21	75	2800717	PENCNOT01	411179F1 (BRSTNOT01), 415284R1 (BRSTNOT01), 1458971F1 (COLNFET02), 1600810H1 (BLADNOT03), 1622005F6 (BRAITUT13), 2173076F6 (ENDCNOT03), 2520087F6 (BRAITUT21), 2800717H1 (PENCNOT01), 5184583H1 (LUNGTMT03), 5435834H1 (SPLNNOT17), 5872662H1 (COLTDIT04)
22	76	5664154	BRAUNOT01	181534F1 (PLACNOB01), SCHAA00262V1
23	77	017900	HUVELPB01	017900H1 (HUVELPB01), 092858F1 (HYPONOB01), 1353543F1 (LATRTUT02), 1353543F6 (LATRTUT02), 1428464F1 (SINTBST01), g1616429
24	78	035102	HUVENOB01	035102H1 (HUVENOB01), 077722R1 (SYNORAB01), 995133H1 (KIDNTUT01), 1356968T6 (LUNGNOT09), 1963135R6 (BRSTNOT04), 2659921F6 (LUNGTUT09), 3110603H1 (BRSTNOT17)
25	79	259983	HNT2RAT01	259131R1 (HNT2RAT01), 259983H1 (HNT2RAT01), 268205R1 (HNT2NOT01), 1305726F1 (PLACNOT02)
26	80	926810	BRAINOT04	926810H1 (BRAINOT04), 3490378T6 (EPIGNOT01), 4774848H1 (BRAQNOT01), SBIA01080D1, SBIA04006D1, SBIA02273D1, SBIA01121D1
27	81	1398816	BRAITUT08	056398F1 (FIBRNOT01), 1252138F2 (LUNGFET03), 1294556T1 (PGANNOT03), 1398816H1 (BRAITUT08), 1545328R1 (PROSTUT04)

WO 01/07471

PCT/US00/19948

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
28	82	1496820	PROSNON01	996673H1 (KIDNTUT01), 1496820H1 (PROSNON01), 2368484F6 (ADREN07), 3071781X303D1 (UTRSNOR01), 3071781X307B1 (UTRSNOR01), 3071781X316B2 (UTRSNOR01), 3071781X316D3 (UTRSNOR01)
29	83	1514559	PANCTUT01	155768H1 (THP1PLB02), 1229952H1 (BRAITUT01), 1337018X11 (COLNNOT13), 1360361H1 (LUNGNOT12), 1365811H1 (SCORNON02), 1514559F6 (PANCTUT01), 1514559H1 (PANCTUT01)
30	84	1620092	BRAITUT13	1620092F6 (BRAITUT13), 1620092H1 (BRAITUT13), 1832842H1 (BRAINON01), 1843815R6 (COLNNOT08), 1843815T6 (COLNNOT08)
31	85	1678765	STOMFET01	1678765F6 (STOMFET01), 1678765H1 (STOMFET01), 2640786H1 (LUNGTUT08), 3542276F6 (TONSNOT03), 4180591H1 (SINITUT03), 4183383H1 (LIVRDIR01), 4349212H1 (TLYMTXT01), 4718559H1 (BRAIHT02), 5023762H1 (OVARNON03), 5332272H1 (KIDNNOT34), 91665766
32	86	1708229	PROSNOT16	388493R1 (THYMNOT02), 1503519F1 (BRAITUT07), 1708229H1 (PROSNOT16), 1725267F6 (PROSNOT14), 3089258F6 (HEAONOT03)
33	87	1806454	SINTNOT13	406723H1 (EOSIHET02), 821556R1 (KERANOT02), 1649621F6 (PROSTUT09), 1710552H1 (PROSNOT16), 1806454F6 (SINTNOT13), 1806454H1 (SINTNOT13), 2526283H1 (BRAITUT21), 3869969H1 (BMARNOT03)
34	88	1806850	SINTNOT13	270548H1 (HNT2NOT01), 443885R1 (MPHGNOT03), 1257235F1 (MENITUT03), 1337438H1 (COLNNOT13), 1351820F1 (LATRTUT02), 1544066R1 (PROSTUT04), 1806850F6 (SINTNOT13), 1806850H1 (SINTNOT13), 1984108T6 (LUNGAST01), 2921419H1 (SININOT04), 3109392H1 (BRSTTUT15)
35	89	1851534	LUNGFET03	1851534H1 (LUNGFET03), 2407346R6 (BSTMNON02), 2757389R6 (THP1AZS08), 5513454H1 (BRADDIR01), 5629312H1 (PLACFER01)
36	90	1868749	SKINBIT01	1322048F1 (BLADNOT04), 1398330F1 (BRAITUT08), 1437866F6 (PANCNOT08), 1868749F6 (SKINBIT01), 1868749H1 (SKINBIT01), 2279968R6 (PROSNON01), 2684670H1 (LUNGNOT23), 4632232H1 (GBLADIT02), 4951533H2 (ENDVUNT01), 5077673H1 (LNODNOT11), 5388496H1 (BRAINOT19)
37	91	1980010	LUNGTUT03	127747R1 (TESTNOT01), 357561F1 (PROSNOT01), 357561R1 (PROSNOT01), 918017R1 (BRSTNOT04), 1428117F6 (SINTBST01), 1625080F6 (COLNPOT01), 1720753H1 (BLADNOT06), 1932038F6 (COLNNOT16), 1980010H1 (LUNGTUT03), 3112417F6 (BRSTNOT17), 4174704H1 (SINTNOT21), 4238802H1 (SYNWDIT01), 5499543H1 (BRABDIR01), 94337459

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
38	92	2259032	OVARTUT01	475134H1 (MMLR2DT01), 784284R1 (PROSNOT05), 1264124H1 (SYNORAT05), 1418710F1 (KIDNNOT09), 1697570T6 (BLADTUT05), 1874051F6 (LEUKNOT02), 2187960T6 (PROSNOT26), 2259032H1 (OVARTUT01), 2259032R6 (OVARTUT01), 3406237H1 (ESOGNOT03), 3441729H1 (PENCNOT06), 3555764H1 (LUNGNOT31), 3728010H1 (SMCCNON03), 3813639H1 (TONSNOT03), 4031501H1 (BRAINT023), 4274704H1 (PROSTT01), 4602450H1 (BRSTNOT07), g3327183
39	93	2359526	LUNGFET05	1667182F6 (BMARNOT03), 2359526H1 (LUNGFET05), 2359526X311D1 (LUNGFET05), 2555305F7 (THYMNOT03), 2654667T6 (THYMNOT04), SCHAO0290V1, SCHAO0266V1, g1748241
40	94	2456494	ENDANOT01	1860223F6 (PROSNOT18), 2456494H1 (ENDANOT01), 2564671H1 (ADRETUT01), 3618339H1 (EPIPNOT01)
41	95	2668536	ESOGTUT02	1513847H1 (PANCUTUT01), 1668943F6 (BMARNOT03), 1668943T6 (BMARNOT03), 1721443F6 (BLADNOT06), 2668536H1 (ESOGTUT02), 3438287H1 (PENCNOT05), SBFA00330F1, SCBA05255V1, SCBA01530V1
42	96	2683225	SINIUCT01	196443R6 (KIDNNOT02), 1243440R6 (LUNGNOT03), 1604540F6 (LUNGNOT15), 2072837H1 (ISLTNOT01), 2683225F6 (SINIUCT01), 2683225H1 (SINIUCT01), 3647874H1 (ENDINOT01), 4029178H1 (BRAINT023)
43	97	2797839	NPOLNOT01	460779T6 (KERANOT01), 782663H1 (MYOMNOT01), 896898R1 (BRSTNOT05), 1218533H1 (NEUTGMT01), 1312923F6 (BLADTUT02), 2473746F6 (THP1NOT03), 2481564H1 (SMCANOT01), 2797839H1 (NPOLNOT01), 3350118H1 (BRAITUT24), 4184264H1 (BRABDIR01), 4401265H1 (TESTTUT03), 4727770H1 (GBLADIT01), 5080203H1 (LNODNOT11), 5524886H1 (LIVRDIR01)
44	98	2959521	ADRENOT09	046696H1 (CORNNOT01), 087727R6 (LIVRNOT01), 138475H1 (LIVRNOT01), 167505H1 (LIVRNOT01), 647975H1 (CARCTXT02), 781084T1 (MYOMNOT01), 972191R6 (MUSCNOT02), 1309196H1 (COLNFET02), 2641117H1 (LUNGNOT08), 2913953H1 (KIDNTUT15), 2959521H1 (ADRENOT09), 2984654H1 (CARGDIT01), 2985141H1 (CARGDIT01), 3138371H1 (SMCCNOT02), 3386016H1 (ESOGNOT04), 3496187H1 (ADRETUT07), 3614426H1 (EPIPNOT01), 4287819H1 (LIVRDIR01), 5395566H1 (LIVRTUT13), g505101
45	99	3082014	BRAIUNT01	182588H1 (PLACNOB01), 645276R6 (BRSTTUT02), 1497811F1 (SINTBST01), 2051505F6 (LIVRFET02), 3082014H1 (BRAIUNT01), 3464112F6 (293TF2T01), 4603079H1 (BRSTNOT07)
46	100	3520701	LUNGNON03	971201H1 (MUSCNOT02), 1544657R6 (PROSTT04), 1545570H1 (PROSTT04), 1671030F6 (BMARNOT03), 1671030T6 (BMARNOT03), 2605263F6 (LUNGNOT07), 3520701H1 (LUNGNON03), 3520701R6 (LUNGNON03)

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
47	101	4184320	BRADDIT02	2156956F6 (BRAINOT09), 4184253F6 (BRABDIR01), 4184253T6 (BRABDIR01), 4184320H1 (BRADDIT02), 4252542F6 (BRADDIR01)
48	102	4764233	PLACNOT05	4764233H1 (PLACNOT05), 5634642H1 (PLACFER01), g1148809
49	103	4817352	HELATXT03	426993R6 (BLADNOT01), 426993T6 (BLADNOT01), 488301R6 (HNT2AGT01), 3779640H1 (BRSTNOT27), 4817352H1 (HELATXT03)
50	104	5040573	COLHTUT01	1724126F6 (PROSNOT14), 1859337F6 (PROSNOT18), 2026289R6 (KERANOT02), 2026289T6 (KERANOT02), 2122846T6 (BRSTNOT07), 3225302H1 (ADRETUT07), 3322214H1 (PTHYNOT03), 4587178H1 (BRAQNOT01), 4601227H1 (BRSTNOT07), 4885408H1 (LUNLTMT01), 5040573H1 (COLHTUT01)
51	105	5627029	PLACFER01	967988R1 (BRSTNOT05), 1534642T6 (SPLNNOT04), 1700904F6 (BLADTUT05), 1846971R6 (COLNNOT09), 2112727R6 (BRAITUT03), 2112727T6 (BRAITUT03), 2205225F6 (SPLNFET02), 2828475H1 (TLYMNOT03), 3439165F6 (PENCNOT06), 3604622H1 (LUNGNOT30)
52	106	5678487	293TF2T01	1258787F6 (MENITUT03), 1522008F1 (BLADTUT04), 1597992F6 (BLADNOT03), 2057679H1 (BEPINOT01), 2411504H1 (BSTMNON02), 2467956H1 (THYRNOT08), 2739089F6 (OVARNOT09), 2739089T6 (OVARNOT09), 2740762H1 (BRSTTUT14), 2754616H1 (THP1AZS08), 3254971R6 (OVRTUN01), 3487616H1 (EPIGNOT01), 5678487H1 (293TF2T01)
53	107	5682976	BRAENOT02	350492H1 (LVENNOT01), 825361R1 (PROSNOT06), 879866R1 (THYRNOT02), 1667502F6 (BMARNOT03), 1733323F6 (BRSTTUT08), 1876248T6 (LEUKNOT02), 1963215T6 (BRSTNOT04), 2539188H1 (BONRTUT01), 2896448H1 (KIDNTUT14), 3141553H1 (SMCCNOT02), 3374826F6 (CONNTUT05), 3773427H1 (BRSTNOT25), 3779981H1 (BRSTNOT27), 5682976H1 (BRAENOT02), 5546853H1 (TESTNOC01)
54	108	5992432	FTUBTUT02	645878R6 (BRSTTUT02), 1287660F1 (BRAINOT11), 1287660T6 (BRAINOT11), 1417373F6 (BRAINOT12), 1618868F6 (BRAITUT12), 2269980R6 (UTRSNOT02), 2793117F6 (COLNTUT16), 3246793F6 (BRAINOT19), 3592787H1 (293TF5T01), 5992432H1 (FTUBTUT02), 9821012

Table 2

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
1	145	T10 S93	N15 N38	Signal peptide: M1-Q33 Protein SH3 domain repeat: L8-R99 GLGF signal transduction-related domain: M1-R99		MOTIFS SPSCAN BLAST_PRODUM BLAST_DOMO
2	340	T39 S190 S268 T307 S88 S102 S165 S226 S230 S234 T337		P120 nuclear proliferating cell antigen: N117-K333 Proliferative cell nucleolar protein P120: E26-G293	Proliferating cell nucleolar antigen P120 (g2649749) A. fulgidus	MOTIFS BLAST_PRODUM BLAST_DOMO BLAST_GenBank
3	418	S246 S415 T142 T156 S292 S349 S369 S64 S247 S298	N190 N191 N203 N288 N306		Candidate tumor suppressor p33ING1 (g2829208) H. sapiens	MOTIFS BLAST_GenBank
4	297	T217 T82 S76 S127 S176 T207 S246 Y189	N74	Germ cell-less protein: E96-N297	Germ cell-less protein (g5814404) Mus musculus	MOTIFS BLIMPS_PPFAM BLAST_GenBank
5	184	T34 S103 S5 T136	N76		Differentiation factor MDC-3.13 (g3860093) H. sapiens	MOTIFS BLAST_GenBank
6	173	S109 S24 S59 S66 S141 S142 T152			Posterior end mark-5 (g4107015) C. savignyi	MOTIFS BLAST_GenBank

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
7	591	S582 T71 T208 S217 S339 T475 S493 T536 S45 S105 S153 T208 S305 S336 T578 Y93	N374 N425 N534 N585	Signal peptide M1-L64 TPR domain mitosis control E239-P356 TPR repeat V265-K516	Cell division cycle protein 23 homolog (g5541721) <u>A. thaliana</u>	MOTIFS SPSCAN HMMR_PFAM BLAST_DOMO BLAST_GenBank
8	463	T237 S34 T67 T117 T125 S138 T288 T321 S328 S418 T80 S186 S190 S209 S210 T232 T288 S418 T441 S445 Y416	N208	Formin limb deformity: M1-E335	Lymphocyte specific formin related protein (g4101720) <u>M. musculus</u>	MOTIFS BLAST_PRODOR BLAST_DOMO BLAST_GenBank
9	270		N64 N94 N147		Early embryogenesis MRG1 protein (g2570051) <u>M. musculus</u>	MOTIFS BLAST_GenBank
10	255	S180 T49 T53 S97 S152 T201 S210 S23 S97 T145 T216 S225 S228 T231 S242 Y106 Y240		Polyposis locus TB2 homolog: G15-T117 Polyposis locus protein: V13-T117	Similar to polyposis locus protein 1 (g849238) <u>H. sapiens</u>	MOTIFS BLAST_PRODOR BLAST_DOMO BLAST_GenBank
11	533	S227 S412 S505 S7 S17 S65 T349 S442 T29 S72 S89 S358 S442 T446 S505 Y244		TRE oncogene: R56-I277	TRE oncogene-related protein (g2286196) <u>D. melanogaster</u>	MOTIFS BLOCKS_DOMO BLAST_GenBank

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
12	160	S40		Signal peptide: M1-A30 Transmembrane domain: A6-I29 Cornichon developmental protein: M1-S160	Cornichon-like protein (g4521254) <u>M. musculus</u>	MOTIFS SPSCAN HMMR BLAST_PRODOR BLAST_DOMO BLAST_GenBank
13	531	S195 T196 S357 T45 S172 T199 S212 S322 S465 T495 T45 T241 S255 T279 T319 S328	N244 N401		Cdc 73p (g632679) <u>S. cerevisiae</u>	MOTIFS BLAST_GenBank
14	165	S3 T67 S104			Wolf-Hirschhorn syndrome candidate 2 protein (g3860187) <u>H. sapiens</u> Developmental protein DG1118 (g3789911) <u>D. discoideum</u>	MOTIFS BLAST_GenBank
15	199	S2 S21 S69 T102 S189				MOTIFS BLAST_GenBank
16	168	S141 S55 S61 T79	N77	Signal peptide M1-S61 H-Rev protein homolog P15-K166	<u>g3777529</u> retinoic acid receptor responder 3 <u>Homo sapiens</u>	BLAST_GenBank SPSCAN BLAST_PRODOR MOTIFS
17	162	S70 S85 T16 T28 T65 T80 T100 S127 Y111			<u>g207250</u> growth and transformation dependent protein <u>Rattus norvegicus</u>	BLAST_GenBank

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
18	246	T209 S227 T243 T28 S223 S51 S136 S201	N26 N158	Protein cell intergenic region FTSJ K25-K241	g2622903 cell division protein J Methanobacterium thermoauto-trophicum	BLAST-GenBank BLAST-PRODOM BLAST-DOMO MOTIFS
19	483	T394 T85 S86 S219 S225 T230 S298 T299 T472 S114 S200 T273 S371 T407 T424 T431		Signal peptide M1-G29 OS-9 precursor L54-E281	g1322234 OS-9 precursor Homo sapiens	BLAST-GenBank SPSCAN BLAST-PRODOM MOTIFS
20	280	T129 T6 T102 T119 T181 S250 S46 T72 T84 S262		Signal peptide M1-L28	g3901272 ZW10 interactor Zwint Homo sapiens	BLAST-GenBank SPSCAN MOTIFS
21	425	S122 S235 T60 S192 S203 S204 S218 S226 S307 T313 S332 S366 S370 T375 T402 S409 S89 S118 S241 S284 T360 Y399	N190 N311		g455719 Activated c-raf oncogenic fusion protein homolog Homo sapiens	BLAST-GenBank
22	128	S3 S107	N42	Prenyl group binding site (CAAX box) C125-P128 Ovarian granulosa cell 13.0 KD protein HGR74 N16-P128	g4580592 brain expressed x-linked protein 2 Mus musculus	BLAST-GenBank MOTIFS BLAST-PRODOM
23	113	S88 T20 T37		Biotin-requiring enzyme attachment site: L40-L90	LDOC-1 protein g3869127 (Homo sapiens) Nagasaki, K. et al. (1999) Cancer Lett. 140:227-234.	BLAST-GenBank PROFILES SCAN MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
24	308	S95 T79 T98 S184 S246 S251 T55 S184 S226 S294 S300 Y127	N77	Melanoma antigen gene (MAGE) family: M1-Q200, H205-D283, D91-A287	Breast cancer associated gene 1 g4928044 (Homo sapiens) Lurquin, C. et al. (1997) Genomics 46:397-408.	BLAST-GenBank BLAST-PRODOM HMMER-PFAM BLAST-DOMO MOTIFS
25	221	S145 S160 S217 S25 S31 S70 S85 T89 S153 S197 Y34	N139	Annexin VI signature: L86-V95 Sushi domain: T165-C174	Teratocarcinoma expressed gene Tera g1575505 (Mus musculus)	BLAST-GenBank BLIMPS-PRINTS BLIMPS-PFAM MOTIFS
26	402	T344 S39 S78 S109 S237 T269 S273 T376 T381 T383 S11 S49 T89 T344 S364 S11	N76 N107 N171 N362		Paraneoplastic cancer-testis-brain antigen g6179740 (Homo sapiens)	BLAST-GenBank MOTIFS
27	93				Hypoxia inducible gene-1 g4929330 (Homo sapiens)	BLAST-GenBank MOTIFS
28	353	S125 T42 S43 S85 S212 S283 S314 T42 S49 S105 S120 S133 S162 S163 S212 S290	N145 N157 N191	af-4 (FEL protein): S195-K353 E4-Q185	AF5q31 protein g6601438 (Homo sapiens)	BLAST-GenBank BLAST-PRODOM BLAST-DOMO MOTIFS
29	120	T57		Cyclin-dependent kinase inhibitor: D7-P106, M1-N114	Cyclin dependent kinase inhibitor CIP1 g2276312 (Homo sapiens)	BLAST-GenBank BLAST-PRODOM BLAST-DOMO MOTIFS

Table 2 (cont.)

Polypeptide ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
30	144	S15 S64		Transmembrane domain: I93-I110	Transformation dependent protein g207250 (Rattus norvegicus) N.Glaichenhaus and F.Cuzin (1987) Cell 50:1081-1089.	BLAST-GenBank MOTIFS HMMER
31	933	S603 T51 S109 T129 S162 S203 S223 S224 S240 S261 S266 S280 S282 S313 T328 S346 S353 S378 S394 S460 S491 S499 T531 S627 S641 S642 S725 T732 S759 S188 S309 S423 S592 S671 S675 T706 S771 Y856	N107 N238 N639 N883		Replication protein Smp2 g218488 (Saccharomyces cerevisiae) Irie, K. et al. (1993) Mol. Gen. Genet. 6:283-288.	BLAST-GenBank MOTIFS
32	268	S7 T104 T154 S169	N90	Serine-Threonine kinase Binder MPS1: L74-I230	Putative mitotic protein (Schizosaccharomyces pombe) g3947877 F.C.Luca and M.Winey (1998) Mol Biol Cell 9:29-46.	BLAST-GenBank BLAST-PRODOM MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
33	337	T29 S236 T44 T238		Leucine zipper: L259-L280, L266-L287	DNA binding protein g184390 (Homo sapiens) Weitzel, J.N. et al. (1992) Genomics 14:309-319.	BLAST-GenBank MOTIFS
34	565	T17 S34 S61 S66 T138 T142 S174 T238 S245 S265 S436 S466 S527 S106 S205 S218 S258 T297 S314 T325 S463 T470 Y460	N347 N386 N506	F-Box domain: H75-Y123, L82-N95 Disease resistance protein: G254-I270	F-box protein FLR1 g7672734 (Homo sapiens)	BLAST-GenBank HMMER_PFAM BLIMPS-PRINTS MOTIFS
35	228	S200 T47 T62 S78 S107 S188 S192 S206 S200 S205 S213	N36 N94 N225		Predicted WHSC1 protein (Wolf-Hirschhorn syndrome critical region 1) g4378022 (Homo sapiens) Stecc I. et al. (1998) Hum. Mol. Genet. 7:1071-1082.	BLAST-GenBank MOTIFS
36	495	S451 S152 S365 S478 S108 S171 S181 T192 T347 T409 S435 Y86 Y111 Y203			Malignant brain tumor protein 1(3)mbt g3811111 (Homo sapiens) Koga, H. et al. (1999) Oncogene 18:3799-3809.	BLAST-GenBank MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
37	1336	T635 T769 S902 S10 S32 S33 T76 S95 S156 T298 S313 T427 S467 T579 T626 T642 S661 T668 S680 T699 T729 S774 S834 T859 T915 S944 S959 S961 S997 S1049 T1085 S1132 S1227 T1245 S1249 T48 S94 T169 S224 T352 T379 T389 T475 T696 S867 T883 T889 S940 S961 S1220 Y631	N148 N152 N345 N385 N1213 N1247	Ribosomal protein S14 signature: R1172-N1194 Leucine zipper: L211-L232	Neuroblastoma related protein g4337460 (Homo sapiens)	BLAST-GenBank BLIMPS-PRINTS MOTIFS
38	934	T532 S11 T23 T80 S171 S202 T214 T240 S244 T275 S412 S416 S437 S518 T523 S719 S746 S753 S796 S807 S93 T279 T527 S598 T780	N8 N210 N426	SAP: I92-Q364	Sap2 family putative cell cycle dependent phosphatase g3426127 (Schizosaccharomyces pombe) Luke, M.M. et al. (1996) Mol. Cell Biol. 16:2744-2755.	BLAST-GenBank BLAST-DOMO MOTIFS

10051915 011995

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
39	515	T72 S122 S175 S272 S277 S305 T420 S422 T432 T79 S139 T189 S215 T316 S457 T486 Y13 Y383	N16 N31 N115	Metastasis-Associated Protein: E65-R230 Leucine zipper: L234-L255	Metastasis associated gene g1008544 (Homo sapiens) Toh, Y. et al. (1995) Gene 159:97-104 Toh, Y. et al. (1994) J Biol. Chem. 269:22958-22963.	BLAST-GenBank BLAST-PRODOM BLIMPS-PRINTS MOTIFS
40	146	S61		Leucine zipper: L5-L26, L12-L33, L19-L40	LDOC1 g3869127 (Homo sapiens)	BLAST-GenBank BLIMPS-PFAM MOTIFS
41	580	S324 S36 S340 S550 S86 T109 T119 T150 T226 S329 S340	N190	Cyclin: H19-K262	Cyclin K g3746549 (Homo sapiens) Edwards, M.C. et al. (1998) Mol. Cell Biol. 18:4291-4300.	BLAST-GenBank BLAST-PRODOM MOTIFS
42	131	S78 T121 T26		Presenilin: Q64-K75	Cell growth regulator DRR1 g4322559 (Homo sapiens) G.Thomas and M.N.Hall (1997) Curr. Opin. Cell Biol. 9:782-787.	BLAST-GenBank BLIMPS-PRINTS MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
43	812	S44 S588 S646 S801 S111 S120 S134 T140 S148 S150 S181 T185 S262 S279 S440 T477 S497 T520 T542 T605 S675 S40 T64 T311 T316 T319 T505 S562 S565 T566 T695 S702 S707 S708 T739 T776 S790 Y277	N503 N618	NOL1/NOP2/fmu(sun) family signature: F454-G467, F300-K585, I388-M402, G410-G433, F454-G467, K507-L532, E189-M576 Proliferating Cell Nucleolar Antigen P120: M1-S134, E135- T311, F587-G805	Proliferating cell nuclear protein P120 g287723 (Homo sapiens)	BLAST-GenBank BLAST-PRODOM BLAST-DOMO BLIMPS-BLOCKS MOTIFS HMMER-PFAM
44	537	S505 T69 S138 S194 S310 S337 S356 T386 S485 S37 T45 T282	N122 N132 N147	Transmembrane domains: I506-G532, V271-L290, W472-F490	Estrogen induced protein in breast cancer LIV-1 g1256001 (Homo sapiens)	BLAST-GenBank HMMER MOTIFS
45	584	S185 T324 S343 T537 S575 S17 T102 S128 T229 T374 S412 T450	N28	Cytochrome C motif: C283-T288 Metastasis- associated protein MTA1: R19-R143, D144-K321, G340-G483, P432-K555 Leucine zipper: L147-L168	Metastasis associated gene g1008544 (Homo sapiens) Toh, Y. et al. (1995) Gene 159:97-104 Toh, Y. et al. (1994) J. Biol. Chem. 269:22958-22963.	BLAST-GenBank BLAST-PRODOM MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
46	425	S190 T301 S12 S19 S41 S205 T206 T235 S263 S265 T315 S43 S52 S85 T93 T351 S411 Y422	N275	MLO2 mitosis-associated protein: L24-R188, P226-Y245, N308-E408		BLAST-PRODOM MOTIFS
47	255	T9 T147 S237	N144	Melastatin: M1-R172, G199-G255	Melastatin g3047242 (Mus musculus) Duncan, L.M. et al. (1998) Cancer Res. 58:1515-1520.	BLAST-GenBank BLAST-PRODOM MOTIFS
48	111	T30 S2 T8			Melanoma associated antigen GAGE-8 g3511023 (Homo sapiens) Van den Eynde, B. et al. (1995) J. Exp. Med. 182:689-698.	BLAST-GenBank MOTIFS
49	422	T110 T159 S136 S150 T163 T190 S383 T413 S9 T27 S46 S96 T347 S359 S363 S368 Y350		XPMC2 (mitosis associated inducing protein): A236-E402	Mitotic regulator XPMC2 (Xenopus gene which prevents mitotic catastrophe) g595380 (Xenopus laevis) J.Y.Su and J.L.Maller (1995) Mol. Gen. Genet. 246:387-396.	BLAST-GenBank BLAST-PRODOM BLAST-DOMO MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
50	397	S20 S21 T395 T57 S59 T64 S127 S208 T210 S262 S307 T341 T64 T168 S180 S185 S218 S231 S288 S326	N222 N260	Transmembrane motifs: I361-L380, L24-L44 Cell division control protein: K17-L347	Cell cycle protein CDC1 g550426 (Saccharomyces cerevisidae)	BLAST-GenBank HMMER BLAST-PRODOM MOTIFS
51	800	S56 S448 T721 S760 S48 S84 S111 S119 T146 T189 T235 S250 S265 T275 S321 S335 T392 S448 T466 S474 T562 S596 S598 T626 S686 S3 S4 S65 S89 S107 T123 S348 T398 T402 T716 S730 S738 T743 S789 Y102 Y316 Y569 Y685	N554 N665	Signal peptide: M1-A25 Leucine zipper: L365-L386	SART-1 g4126469 (Mus musculus)	BLAST-GenBank SPSCAN MOTIFS
52	713	S100 T631 S8 T9 S20 T42 T114 T121 T172 T177 T191 T192 S218 T231 T256 S325 S335 S381 T464 T482 T538 T581 T617 S693 S94 S166 T201 S202 S321 T568 S614 T658 Y459	N7 N49 N462	Leucine zipper: L680-L701	Colon cancer antigen NY-CO-8 g3170180 (Homo sapiens) Scanlan, M.J. et al. (1998) Int. J. Cancer 76:652-658.	BLAST-GenBank BLAST-PRODOM BLAST-DOMO MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
53	880	S18 S68 T123 T143 S159 T178 T286 S294 S327 S376 S388 T397 T403 S426 S438 S474 S563 T587 T634 T645 S659 S665 S677 S756 S799 S809 T827 S870 S82 T88 S99 T131 T165 S215 S253 S362 S487 T510 S525 S589 T593 S622	N60 N251 N338 N514 N585 N643	MybI DNA-binding domain: W808-I816 WD40 domains: L41-N79, K84-N124, T131-D170, G239-D281, A771-S809, F157-T171 Acidic Serine Cluster Repeat: A423-R697	homologous to mouse gene PC326 g458692 (Homo sapiens) Bergsagel, P.L. et al. (1992) Oncogene 7:2059-2064.	BLAST-GenBank BLAST-DOMO HMMER-PFAM BLIMPS-PRINTS MOTIFS
54	855	T460 S8 S179 S261 T288 T313 T377 T706 T719 T755 S764 S803 S851 S34 S67 T129 S190 S339 T391 S483 S502 S537 Y92	N552	Crooked neck protein (RNA processing associated, contains TPR repeat): W398-V814	Predicted TPR domain protein G2315362 (Caenorhabditis elegans) Zhang, K. et al. (1991) Genes Dev. 5:1080-1091.	BLAST-GenBank BLAST-PRODOM MOTIFS

Table 3

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition Fraction of Total	Vector
55	263-307	Cardiovascular (0.200) Gastrointestinal (0.200) Reproductive (0.200)	Cancer (0.433) Inflammation (0.267) Cell Proliferation (0.200)	PBLUESCRIPT
56	406-450	Reproductive (0.222) Cardiovascular (0.167) Gastrointestinal (0.167) Nervous (0.167)	Cancer (0.500) Inflammation (0.389) Cell Proliferation (0.167)	PSPORT1
57	1001-1045	Reproductive (0.265) Gastrointestinal (0.206) Nervous (0.206)	Cancer (0.412) Inflammation (0.324) Cell Proliferation (0.176)	pINCY
58	226-270	Nervous (0.316) Hematopoietic/Immune (0.211) Reproductive (0.211)	Cancer (0.368) Inflammation (0.368) Cell Proliferation (0.158)	pINCY
59	406-450	Hematopoietic/Immune (0.500) Cardiovascular (0.227)	Cancer (0.182) Inflammation (0.682) Cell Proliferation (0.136)	pINCY
60	56-100	Gastrointestinal (0.545) Nervous (0.182) Reproductive (0.182)	Cancer (0.545) Inflammation (0.364) Cell Proliferation (0.273)	pINCY
61	1046-1090	Nervous (0.271) Reproductive (0.220) Gastrointestinal (0.153)	Cancer (0.542) Inflammation (0.288) Cell Proliferation (0.220)	pINCY
62	226-270	Hematopoietic/Immune (0.288) Nervous (0.178) Reproductive (0.164)	Cancer (0.397) Inflammation (0.548)	pINCY
63	559-603	Reproductive (0.260) Gastrointestinal (0.145) Cardiovascular (0.130)	Cancer (0.458) Inflammation (0.359) Cell Proliferation (0.176)	PSPORT1
64	12-56	Reproductive (0.385) Gastrointestinal (0.231) Cardiovascular (0.154) Nervous (0.154)	Cancer (0.538) Inflammation (0.154) Cell Proliferation (0.154)	pINCY
65	488-532 1091-1135	Reproductive (0.308) Nervous (0.282) Gastrointestinal (0.154)	Cancer (0.487) Inflammation (0.231) Cell Proliferation (0.103)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition Fraction of Total	Vector
66	37-81	Nervous (0.500) Dermatologic (0.250) Reproductive (0.250)	Inflammation (0.500)	pINCY
67	326-370 1136-1180	Nervous (0.237) Reproductive (0.237) Hematopoietic/Immune (0.158)	Cancer (0.395) Inflammation (0.316) Cell Proliferation (0.158)	pINCY
68	451-495	Nervous (0.312) Reproductive (0.312) Developmental (0.125) Hematopoietic/Immune (0.125) Urologic (0.125)	Cancer (0.562) Inflammation (0.188) Cell Proliferation (0.312)	pINCY
69	64-108	Reproductive (0.233) Nervous (0.174) Cardiovascular (0.140)	Cancer (0.477) Inflammation (0.279) Cell Proliferation (0.198)	pINCY
70	77-121	Cardiovascular (0.500) Musculoskeletal (0.500)	Cancer (0.500) Trauma (0.500)	PBLUESCRIPT
71	164-208	Developmental (0.222) Nervous (0.222)	Cancer (0.444) Cell proliferation (0.222) Trauma (0.222)	pINCY
72	604-648	Reproductive (0.362) Gastrointestinal (0.149) Hematopoietic/Immune (0.128)	Cancer (0.426) Inflammation/Trauma (0.276) Cell proliferation (0.170)	pINCY
73	106-150 1066-1110	Reproductive (0.307) Nervous (0.202) Cardiovascular (0.114)	Cancer (0.482) Inflammation/Trauma (0.307) Cell proliferation (0.175)	pINCY
74	651-695	Hematopoietic/Immune (0.290) Reproductive (0.226) Cardiovascular (0.161)	Inflammation/Trauma (0.451) Cell proliferation (0.230) Cancer (0.320)	pINCY
75	241-285 535-579	Reproductive (0.193) Cardiovascular (0.169) Gastrointestinal (0.157)	Cancer (0.458) Inflammation/Trauma (0.337) Cell proliferation (0.169)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition Fraction of Total	Vector
76	173-217 593-637	Nervous (0.513) Reproductive (0.167)	Inflammation/Trauma (0.371) Cancer (0.333) Cell proliferation (0.141)	pINCY
77	13-57	Reproductive (0.241) Nervous (0.202) Cardiovascular (0.140)	Cancer (0.461) Inflammation (0.180) Cell Proliferation (0.167)	PBLUESCRIPT
78	176-220	Nervous (0.279) Reproductive (0.235) Gastrointestinal (0.147)	Cancer (0.500) Inflammation (0.176) Cell Proliferation (0.162)	PBLUESCRIPT
79	79-123	Nervous (0.280) Cardiovascular (0.160) Developmental (0.160)	Cancer (0.480) Cell Proliferation (0.480) Inflammation (0.160)	PBLUESCRIPT
80	870-914	Nervous (0.571) Reproductive (0.238) Developmental (0.095)	Cancer (0.238) Inflammation (0.381) Cell Proliferation (0.190)	PSPORT1
81	149-194	Nervous (0.216) Reproductive (0.201) Gastrointestinal (0.185)	Cancer (0.432) Inflammation (0.259) Cell Proliferation (0.154)	pINCY
82	150-194	Reproductive (0.375) Cardiovascular (0.125) Endocrine (0.125) Hematopoietic/Immune (0.125) Developmental (0.125) Urologic (0.125)	Cancer (0.375) Inflammation (0.375) Trauma (0.250)	PSPORT1
83	177-221	Reproductive (0.199) Gastrointestinal (0.173) Hematopoietic/Immune (0.128) Nervous (0.128)	Cancer (0.429) Inflammation (0.270) Cell Proliferation (0.186)	pINCY
84	342-386	Reproductive (0.252) Gastrointestinal (0.196) Nervous (0.161)	Cancer (0.483) Inflammation (0.238) Cell Proliferation (0.161)	pINCY
85	124-168	Hematopoietic/Immune (0.308) Cardiovascular (0.154) Nervous (0.154) Gastrointestinal (0.154)	Cancer (0.538) Inflammation (0.308)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition Fraction of Total	Vector
86	238-282	Reproductive (0.277) Cardiovascular (0.181) Nervous (0.169)	Cancer (0.434) Inflammation (0.193) Cell Proliferation (0.157)	pINCY
87	117-161	Reproductive (0.250) Gastrointestinal (0.250) Hematopoietic/Immune (0.115)	Cancer (0.558) Inflammation (0.192) Cell Proliferation (0.115) Trauma (0.115)	pINCY
88	139-183	Nervous (0.237) Reproductive (0.214) Gastrointestinal (0.168)	Cancer (0.397) Inflammation (0.298) Trauma (0.137)	pINCY
89	184-228 352-396	Reproductive (0.556) Nervous (0.222) Hematopoietic/Immune (0.111) Developmental (0.111)	Cancer (0.444) Inflammation (0.333) Cell Proliferation (0.333)	pINCY
90	69-113 879-923	Nervous (0.316) Reproductive (0.193) Hematopoietic/Immune (0.158)	Cancer (0.439) Inflammation (0.211) Cell Proliferation (0.123)	pINCY
91	72-116	Nervous (0.211) Reproductive (0.197) Gastrointestinal (0.158)	Cancer (0.461) Inflammation (0.263) Cell Proliferation (0.211)	PSPORT1
92	489-533	Reproductive (0.274) Nervous (0.217) Gastrointestinal (0.123)	Cancer (0.481) Inflammation (0.189) Cell Proliferation (0.160)	PSPORT1
93	761-805	Reproductive (0.219) Hematopoietic/Immune (0.156) Developmental (0.125)	Cancer (0.312) Cell Proliferation (0.281) Inflammation (0.188) Trauma (0.188)	PSPORT1
94	126-170	Reproductive (0.379) Nervous (0.241) Developmental (0.138)	Cancer (0.414) Cell Proliferation (0.241) Inflammation (0.103)	PBLUESCRIPT
95	1173-1217	Reproductive (0.192) Gastrointestinal (0.192) Nervous (0.173)	Cancer (0.481) Inflammation (0.250) Cell Proliferation (0.212)	pINCY
96	465-509	Hematopoietic/Immune (0.250) Cardiovascular (0.158) Gastrointestinal (0.145)	Inflammation (0.368) Cancer (0.355) Cell Proliferation (0.132)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition Fraction of Total	Vector
97	2427-2471	Nervous (0.224) Reproductive (0.197) Gastrointestinal (0.184)	Cancer (0.474) Cell Proliferation(0.263) Inflammation (0.237)	pINCY
98	23-67	Gastrointestinal (0.270) Reproductive (0.190) Cardiovascular (0.135)	Cancer (0.429) Inflammation (0.278) Cell Proliferation(0.143)	pINCY
99	106-150	Gastrointestinal (0.263) Reproductive (0.263) Nervous (0.158)	Cancer (0.474) Inflammation (0.368) Cell Proliferation(0.211)	pINCY
100	73-117 460-504	Hematopoietic/Immune (0.211) Reproductive (0.211) Cardiovascular (0.105) Developmental (0.105) Gastrointestinal (0.105) Musculoskeletal (0.105)	Cancer (0.474) Inflammation (0.263) Cell Proliferation(0.211)	PSPORT1
101	861-905	Developmental (0.333) Nervous (0.667)	Cell Proliferation(0.333) Trauma (0.333) Neurological (0.333)	pINCY
102	8-52	Developmental (1.000)	Cell Proliferation (1.000)	pINCY
103	199-243	Hematopoietic/Immune (0.143) Nervous (0.179) Reproductive (0.286)	Cancer (0.536) Inflammation (0.250) Cell Proliferation(0.214)	pINCY
104	413-457 908-952	Nervous (0.236) Reproductive (0.222) Gastrointestinal (0.125)	Cancer (0.458) Inflammation (0.236) Cell Proliferation(0.139)	pINCY
105		Reproductive (0.270) Gastrointestinal (0.169) Hematopoietic/Immune (0.101) Developmental (0.101) Nervous (0.101)	Cancer (0.449) Inflammation (0.281) Cell Proliferation(0.258)	pINCY
106	255-299 513-557	Reproductive (0.216) Gastrointestinal (0.196) Nervous (0.157)	Cancer (0.490) Inflammation (0.176) Cell Proliferation(0.176)	pINCY
107	167-211 814-859 1922-1966	Reproductive (0.263) Nervous (0.162) Gastrointestinal (0.141)	Cancer (0.455) Inflammation (0.202) Trauma (0.131)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition Fraction of Total	Vector
108	877-921 2230-2274	Reproductive (0.299) Nervous (0.206) Gastrointestinal (0.134)	Cancer (0.536) Inflammation (0.227) Cell Proliferation(0.124)	pINCY

100 21 915 01 1993

Table 4

Nucleotide SEQ ID NO:	Library	Library Description
55	KIDNNOT01	Library was constructed using RNA isolated from the kidney tissue of a 64-year-old Caucasian female, who died from an intracranial bleed. Patient history included rheumatoid arthritis.
56	BRSTNOT02	Library was constructed using RNA isolated from diseased breast tissue removed from a 55-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated proliferative fibrocystic changes characterized by apocrine metaplasia, sclerosing adenosis, cyst formation, and ductal hyperplasia without atypia. Pathology for the associated tumor tissue indicated an invasive grade 4 mammary adenocarcinoma. Patient history included atrial tachycardia and a benign neoplasm. Family history included cardiovascular and cerebrovascular disease.
57	PLACNOT02	Library was constructed using RNA isolated from the placental tissue of a Hispanic female fetus, who was prematurely delivered at 21 weeks' gestation. Serologies of the mother's blood were positive for CMV (cytomegalovirus).
58	BRAINOT12	Library was constructed using RNA isolated from brain tissue removed from the right frontal lobe of a 5-year-old Caucasian male during a hemispherectomy. Pathology indicated extensive polymicrogyria and mild to moderate gliosis (predominantly subpial and subcortical), which are consistent with chronic seizure disorder. Family history included a cervical neoplasm.
59	SPLNNOT04	Library was constructed using RNA isolated from the spleen tissue of a 2-year-old Hispanic male, who died from cerebral anoxia.
60	LNODNOT03	Library was constructed using RNA isolated from lymph node tissue obtained from a 67-year-old Caucasian male during a segmental lung resection and bronchoscopy. On microscopic exam, this tissue was found to be extensively necrotic with 10% viable tumor. Pathology for the associated tumor tissue indicated invasive grade 3-4 squamous cell carcinoma. Patient history included hemangioma. Family history included atherosclerotic coronary artery disease, benign hypertension, congestive heart failure, atherosclerotic coronary artery disease.
61	LIVRTUT01	Library was constructed using RNA isolated from liver tumor tissue removed from a 51-year-old Caucasian female during a hepatic lobectomy. Pathology indicated metastatic grade 3 adenocarcinoma consistent with colon cancer. Family history included a malignant neoplasm of the liver.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
62	BLADTUT07	Library was constructed using RNA isolated from bladder tumor tissue removed from the anterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated a grade 3 transitional cell carcinoma in the left lateral bladder. Patient history included angina, emphysema, and tobacco use. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
63	LUNGAST01	Library was constructed using RNA isolated from the lung tissue of a 17-year-old Caucasian male, who died from head trauma. Patient history included asthma.
64	LIVRFET02	Library was constructed using RNA isolated from liver tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation.
65	LUNGNOT23	Library was constructed using RNA isolated from left lobe lung tissue removed from a 58-year-old Caucasian male. Pathology for the associated tumor tissue indicated metastatic grade 3 (of 4) osteosarcoma. Patient history included soft tissue cancer, secondary cancer of the lung, prostate cancer, and an acute duodenal ulcer with hemorrhage. Family history included prostate cancer, breast cancer, and acute leukemia.
66	TESTNOT07	Library was constructed using RNA isolated from testicular tissue removed from a 31-year-old Caucasian male during an unilateral orchiectomy (excision of testis). Pathology indicated a mass containing a large subcapsular hematoma with laceration of the tunica albuginea. The surrounding testicular parenchyma was extensively necrotic.
67	PROSTUT13	Library was constructed using RNA isolated from prostate tumor tissue removed from a 59-year-old Caucasian male during a radical prostatectomy with regional lymph node excision. Pathology indicated adenocarcinoma (Gleason grade 3+3). Adenofibromatous hyperplasia was present. The patient presented with elevated prostate-specific antigen (PSA). Patient history included colon diverticuli, asbestosis, and thrombophlebitis. Family history included multiple myeloma, hyperlipidemia, and rheumatoid arthritis.
68	LNODNOT11	Library was constructed using RNA isolated from lymph node tissue removed from a 16-month-old Caucasian male who died from head trauma. Patient history included bronchitis.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
69	BRSTNOT35	Library was constructed using RNA isolated from breast tissue removed from a 46-year-old Caucasian female during a bilateral reduction mammoplasty. Pathology indicated normal breast parenchyma, bilaterally. The patient presented with hypertrophy of breast and headache. Patient history included obesity, lumbago, glaucoma, and alcohol abuse. Family history included cataract, osteoarthritis, uterine cancer, benign hypertension, hyperlipidemia, alcoholic cirrhosis of the liver, cerebrovascular disease, and type II diabetes.
70	MUSCNOT01	Library was constructed at Stratagene (STR937209), using RNA isolated from the skeletal muscle tissue of a patient with malignant hyperthermia.
71	LUNGNOT14	Library was constructed using RNA isolated from lung tissue removed from the left lower lobe of a 47-year-old Caucasian male during a segmental lung resection. Pathology for the associated tumor tissue indicated a grade 4 adenocarcinoma, and the parenchyma showed calcified granuloma. Patient history included benign hypertension and chronic obstructive pulmonary disease. Family history included type II diabetes and acute myocardial infarction.
72	UTRSNOT06	Library was constructed using RNA isolated from myometrial tissue removed from a 50-year-old Caucasian female during a vaginal hysterectomy. Pathology indicated residual atypical complex endometrial hyperplasia. Pathology for the associated tissue removed during dilation and curettage indicated fragments of atypical complex hyperplasia and a single microscopic focus suspicious for grade 1 adenocarcinoma. Patient history included benign breast neoplasm, hypothyroid disease, polypectomy, and arthralgia. Family history included cerebrovascular disease, atherosclerotic coronary artery disease, hyperlipidemia, and chronic hepatitis.
73	PROSTUT08	Library was constructed using RNA isolated from prostate tumor tissue removed from a 60-year-old Caucasian male during radical prostatectomy and regional lymph node excision. Pathology indicated an adenocarcinoma (Gleason grade 3+4). Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA). Patient history included a kidney cyst, and hematuria. Family history included tuberculosis, cerebrovascular disease, and arteriosclerotic coronary artery disease.
74	THYMNOT03	Library was constructed using RNA isolated from thymus tissue removed from a 21-year-old Caucasian male during a thymectomy. Pathology indicated an unremarkable thymus and a benign parathyroid adenoma in the right inferior parathyroid. Patient history included atopic dermatitis, a benign neoplasm of the parathyroid, and tobacco use. Family history included atherosclerotic coronary artery disease and benign hypertension.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
75	PENCNOT01	Library was constructed using RNA isolated from penis corpus cavernosum tissue removed from a 53-year-old male. Patient history included untreated penile carcinoma.
76	BRAUNOT01	Library was constructed using RNA isolated from caudate/putamen/nucleus accumbens tissue removed from the brain of a 35-year-old Caucasian male who died from cardiac failure. Pathology indicated moderate leptomenigeal fibrosis and multiple microinfarctions of the cerebral neocortex. Patient history included dilated cardiomyopathy, congestive heart failure, cardiomegaly and an enlarged spleen and liver.
77	HUVELPB01	This library was constructed using RNA isolated from HUV-EC-C (ATCC CRL 1730) cells stimulated with cytokine/LPS. RNA was isolated from two pools of HUV-EC-C cells that had been treated with either 4 units/ml TNF-alpha and 2 units/ml gamma IFN for 96 hours, or 1 unit/ml IL-1 beta and 100 ng/ml LPS for 5 hours.
78	HUVENOB01	This library was constructed using RNA isolated from HUV-EC-C (ATCC CRL 1730) cells.
79	HNT2RAT01	This library was constructed at Stratagene (STR937231), using RNA isolated from the HNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor). Cells were treated with retinoic acid for 24 hours.
80	BRAINOT04	This library was constructed using RNA isolated from the brain tissue of a 44-year-old Caucasian male with a cerebral hemorrhage. The tissue, which contained coagulated blood, came from the choroid plexus of the right anterior temporal lobe. Family history included coronary artery disease and myocardial infarction.
81	BRAITUT08	This library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 47-year-old Caucasian male during excision of cerebral meningeal tissue. Pathology indicated grade 4 fibrillary astrocytoma with focal tumoral radionecrosis. Patient history included cerebrovascular disease, deficiency anemia, hyperlipidemia and epilepsy. Family history included cerebrovascular disease and a malignant prostate neoplasm.
82	PROSNON01	This library was constructed from 4.4 million independent clones from a prostate library. Starting RNA was made from prostate tissue removed from a 28-year-old Caucasian male who died from a self-inflicted gunshot wound. The normalization and hybridization conditions were adapted from Soares, M.B. et al. (1994) Proc. Natl. Acad. Sci. USA 91:9228-9232, using a longer (19 hour) reannealing hybridization period.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
83	PANCTUT01	This library was constructed using RNA isolated from pancreatic tumor tissue removed from a 65-year-old Caucasian female during radical subtotal pancreatectomy. Pathology indicated an invasive grade 2 adenocarcinoma. Patient history included type II diabetes, osteoarthritis, cardiovascular disease, benign neoplasm in the large bowel, and a cataract. Previous surgeries included a total splenectomy, cholecystectomy, and abdominal hysterectomy. Family history included cardiovascular disease, type II diabetes, and stomach cancer.
84	BRAITUT13	This library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 68-year-old Caucasian male during excision of a cerebral meningeal lesion. Pathology indicated a meningioma in the left frontal lobe.
85	STOMFET01	This library was constructed using RNA isolated from the stomach tissue of a Caucasian female fetus, who died at 20 weeks' gestation.
86	PROSNOT16	This library was constructed using RNA isolated from diseased prostate tissue removed from a 68-year-old Caucasian male during a radical prostatectomy. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma (Gleason grade 3+4). The patient presented with elevated prostate specific antigen (PSA). During this hospitalization, the patient was diagnosed with myasthenia gravis. Patient history included osteoarthritis and type II diabetes. Family history included benign hypertension, acute myocardial infarction, hyperlipidemia, and arteriosclerotic coronary artery disease.
87	SINTNOT13	This library was constructed using RNA isolated from ileum tissue obtained from a 25-year-old Asian female during a partial colectomy and temporary ileostomy. Pathology indicated moderately active chronic ulcerative colitis, involving colonic mucosa from the distal margin to the ascending colon. Family history included hyperlipidemia, depressive disorder, malignant cervical neoplasm, viral hepatitis A, and depressive disorder.
88	SINTNOT13	This library was constructed using RNA isolated from ileum tissue obtained from a 25-year-old Asian female during a partial colectomy and temporary ileostomy. Pathology indicated moderately active chronic ulcerative colitis, involving colonic mucosa from the distal margin to the ascending colon. Family history included hyperlipidemia, depressive disorder, malignant cervical neoplasm, viral hepatitis A, and depressive disorder.
89	LUNGFET03	This library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation.
90	SKINBIT01	This library was constructed using RNA isolated from diseased skin tissue of the left lower leg. Patient history included erythema nodosum of the left lower leg.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
91	LUNGTUT03	This library was constructed using RNA isolated from lung tumor tissue removed from the left lower lobe of a 69-year-old Caucasian male during segmental lung resection. Pathology indicated residual grade 3 invasive squamous cell carcinoma. Patient history included acute myocardial infarction, prostatic hyperplasia, malignant skin neoplasm, and tobacco use.
92	OVARTUT01	This library was constructed using RNA isolated from ovarian tumor tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology indicated grade 2 mucinous cystadenocarcinoma involving the entire left ovary. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.
93	LUNGFET05	This library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation from anencephalus.
94	ENDANOT01	This library was constructed using RNA isolated from aortic endothelial cell tissue from an explanted heart removed from a male during a heart transplant.
95	ESOGTUT02	This library was constructed using RNA isolated from esophageal tumor tissue obtained from a 61-year-old Caucasian male during a partial esophagectomy, proximal gastrectomy, pyloromyotomy, and regional lymph node excision. Pathology indicated an invasive grade 3 adenocarcinoma in the esophagus. Family history included atherosclerotic coronary artery disease, type II diabetes, chronic liver disease, primary cardiomyopathy, benign hypertension, and cerebrovascular disease.
96	SINIUCT01	This library was constructed using RNA isolated from ileum tissue obtained from a 42-year-old Caucasian male during a total intra-abdominal colectomy and endoscopic jejunostomy. Previous surgeries included polypectomy, colonoscopy, and spinal canal exploration. Family history included cerebrovascular disease, benign hypertension, atherosclerotic coronary artery disease, and type II diabetes.
97	NPOLNOT01	This library was constructed using RNA isolated from nasal polyp tissue removed from a 78-year-old Caucasian male during a nasal polypectomy. Pathology indicated a nasal polyp and striking eosinophilia. Patient history included asthma and nasal polyps.
98	ADRENOT09	This library was constructed using RNA isolated from left adrenal gland tissue removed from a 43-year-old Caucasian male during nephroureterectomy, regional lymph node excision, and unilateral left adrenalectomy. Pathology for the associated tumor tissue indicated a grade 2 renal cell carcinoma mass in the posterior lower pole of the left kidney with invasion into the renal pelvis.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
99	BRAIUNT01	This library was constructed using RNA isolated from SK-N-MC, a neuroepithelioma cell line (ATCC HTB-10) derived from a 14-year-old Caucasian female with neuroepithelioma, with metastasis to the supra-orbital area.
100	LUNGNON03	This library was constructed from 2.56 x 1e6 independent clones from a lung tissue library. RNA was made from lung tissue removed from the left lobe a 58-year-old Caucasian male during a segmental lung resection. Pathology for the associated tumor tissue indicated a metastatic grade 3 (of 4) osteosarcoma. Patient history included soft tissue cancer, secondary cancer of the lung, prostate cancer, and an acute duodenal ulcer with hemorrhage. Patient also received radiation therapy to the retroperitoneum. Family history included prostate cancer, breast cancer, and acute leukemia. The normalization and hybridization conditions were adapted from Soares et al., PNAS (1994) 91:9228; Swaroop et al., NAR (1991) 19:1954; and Bonaldo et al., Genome Research (1996) 6:791.
101	BRADDIT02	This library was constructed using RNA isolated from diseased choroid plexus tissue of the lateral ventricle removed from the brain of a 57-year-old Caucasian male, who died from a cerebrovascular accident. Patient history included Huntington's disease, and emphysema.
102	PLACNOT05	This library was constructed using RNA isolated from placental tissue removed from a Caucasian male fetus, who died after 18 weeks' gestation from fetal demise.
103	HELATXT03	This library was constructed using RNA isolated from a treated HeLa cell line, derived from cervical adenocarcinoma removed from a 31-year-old Black female. The cells were treated with 1 microM PMA and 100 microM cycloheximide for 24 hours.
104	COLHTUT01	This library was constructed using RNA isolated from colon tumor tissue removed from the hepatic flexure of a 55-year-old Caucasian male during right hemicolectomy, incidental appendectomy, and permanent colostomy. Pathology indicated invasive grade 3 adenocarcinoma. Patient history included benign hypertension, anxiety, abnormal blood chemistry, blepharitis, heart block, osteoporosis, acne, and hyperplasia of prostate. Family history included prostate cancer, acute myocardial infarction, stroke, and atherosclerotic coronary artery disease.
105	PLACFER01	This library was constructed using RNA isolated from placental tissue removed from a Caucasian fetus who died after 16 weeks' gestation from fetal demise and hydrocephalus. Serology was positive for CMV antibody.
106	293TF2T01	This library was constructed using RNA isolated from a treated, transformed embryonal cell line (293-EBNA) derived from kidney epithelial tissue. The cells were treated with 5-aza-2'-deoxycytidine and transformed with adenovirus 5 DNA.

WO 01/07471

PCT/US00/19948

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
107	BRAENOT02	This library was constructed using RNA isolated from posterior parietal cortex tissue removed from the brain of a 35-year-old Caucasian male.
108	FTUBTUT02	This library was constructed using RNA isolated from fallopian tube tumor tissue removed from an 85-year-old Caucasian female during bilateral salpingo-oophorectomy and hysterectomy. Pathology indicated poorly differentiated mixed endometrioid and serous adenocarcinoma confined to the mucosa without mural involvement. Endometrioid carcinoma in situ was also present. Pathology for the associated uterus tumor indicated focal endometrioid adenocarcinoma in situ and moderately differentiated invasive adenocarcinoma in an endometrial polyp. Metastatic endometrioid and serous adenocarcinoma were present. The patient presented with a pelvic mass and ascites. Patient history included medullary carcinoma of the thyroid and myocardial infarction.

Table 5

Program	Description	Reference	Parameter Threshold
ABI/FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	PE Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	PE Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	PE Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and, if applicable, Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits for PFAM hits, depending on individual protein families

Table 5 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- 5 a) an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32,
 - 10 SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54,
- b) a naturally occurring amino acid sequence having at least 90% sequence identity to an
 - 15 amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33,
 - 20 SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54,
- c) a biologically active fragment of an amino acid sequence selected from the group
 - 25 consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
 - 30 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54, and
- d) an immunogenic fragment of an amino acid sequence selected from the group consisting
 - 35 of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID

NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID
 5 NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54.

2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID
 10 NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID
 15 NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54.

3. An isolated polynucleotide encoding a polypeptide of claim 1.

20 4. An isolated polynucleotide encoding a polypeptide of claim 2.

5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID
 25 NO:69, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:104, SEQ
 30 ID NO:105, SEQ ID NO:106, SEQ ID NO:107, and SEQ ID NO:108.

6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

35 7. A cell transformed with a recombinant polynucleotide of claim 6.

8. A transgenic organism comprising a recombinant polynucleotide of claim 6.

9. A method for producing a polypeptide of claim 1, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said
 5 cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide
 comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim
 1, and

b) recovering the polypeptide so expressed.

10 10. An isolated antibody which specifically binds to a polypeptide of claim 1.

11. An isolated polynucleotide comprising a polynucleotide sequence selected from the
 group consisting of:

a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:55, SEQ ID
 15 NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID
 NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID
 NO:71, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID
 NO:79, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID
 NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID
 20 NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID
 NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:105,
 SEQ ID NO:106, SEQ ID NO:107, and SEQ ID NO:108,

b) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a
 polynucleotide sequence selected from the group consisting of SEQ ID NO:55, SEQ ID NO:56, SEQ
 25 ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:64, SEQ
 ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:71, SEQ
 ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ
 ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ
 ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ
 30 ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ
 ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106,
 SEQ ID NO:107, and SEQ ID NO:108,

c) a polynucleotide sequence complementary to a),

d) a polynucleotide sequence complementary to b), and

35 e) an RNA equivalent of a)-d).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 11.

13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

16. A composition comprising an effective amount of a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

17. A composition of claim 16, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, and SEQ ID NO:54.

18. A method for treating a disease or condition associated with decreased expression of

functional CCYPR, comprising administering to a patient in need of such treatment the composition of claim 16.

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of
5 claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

20. A composition comprising an agonist compound identified by a method of claim 19 and
10 a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of
functional CCYPR, comprising administering to a patient in need of such treatment a composition of
claim 20.

15

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide
of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

20

23. A composition comprising an antagonist compound identified by a method of claim 22
and a pharmaceutically acceptable excipient.

24. A method for treating a disease or condition associated with overexpression of functional
25 CCYPR, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim
1, said method comprising the steps of:

- a) combining the polypeptide of claim 1 with at least one test compound under suitable
30 conditions, and
- b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a
compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of
35 claim 1, said method comprising:

a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,

b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and

5 c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

10 27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, and

b) detecting altered expression of the target polynucleotide.

15

28. A method for assessing toxicity of a test compound, said method comprising:

a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;

20 c) quantifying the amount of hybridization complex; and
d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

25

WO 01/07471

PCT/US00/19948

SEQUENCE LISTING

<110> INCYTE GENOMICS, INC.
HILLMAN, Jennifer L.
LAL, Preeti
TANG, Y. Tom
YUE, Henry
AU-YOUNG, Janice
BANDMAN, Olga
AZIMZAI, Yalda
YANG, Junming
LU, Dyung Aina M.
BAUGHN, Mariah R.
PATTERSON, Chandra
SHAH, Purvi

<120> CELL CYCLE AND PROLIFERATION PROTEINS

<130> PF-0722 PCT

<140> To Be Assigned

<141> Herewith

<150> 60/145,075; 60/153,129; 60/164,647

<151> 1999-07-21; 1999-09-08; 1999-11-10

<160> 108

<170> PERL Program

<210> 1

<211> 145

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 116462CD1

<400> 1

Met	Asn	Gly	Arg	Val	Asp	Tyr	Leu	Val	Thr	Glu	Glu	Glu	Ile	Asn
1				5					10					15
Leu	Thr	Arg	Gly	Pro	Ser	Gly	Leu	Gly	Phe	Asn	Ile	Val	Gly	Gly
				20					25					30
Thr	Asp	Gln	Gln	Tyr	Val	Ser	Asn	Asp	Ser	Gly	Ile	Tyr	Val	Ser
				35					40					45
Arg	Ile	Lys	Glu	Asn	Gly	Ala	Ala	Ala	Leu	Asp	Gly	Arg	Leu	Gln
				50					55					60
Glu	Gly	Asp	Lys	Ile	Leu	Ser	Val	Asn	Gly	Gln	Asp	Leu	Lys	Asn
				65					70					75
Leu	Leu	His	Gln	Asp	Ala	Val	Asp	Leu	Phe	Arg	Asn	Ala	Gly	Tyr
				80					85					90
Ala	Val	Ser	Leu	Arg	Val	Gln	His	Arg	Leu	Gln	Val	Gln	Asn	Gly
				95					100					105
Pro	Ile	Gly	His	Arg	Gly	Glu	Gly	Asp	Pro	Ser	Gly	Ile	Pro	Ile
				110					115					120
Phe	Met	Val	Leu	Val	Pro	Val	Phe	Ala	Leu	Thr	Met	Val	Ala	Ala
				125					130					135
Trp	Ala	Phe	Met	Arg	Tyr	Arg	Gln	Gln	Leu					
				140					145					

<210> 2

<211> 340

<212> PRT

WO 01/07471

PCT/US00/19948

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1210462CD1

<400> 2

```

Met Leu Thr Gln Leu Lys Ala Lys Ser Glu Gly Lys Leu Ala Lys
 1          5          10          15
Gln Ile Cys Lys Val Val Leu Asp His Phe Glu Lys Gln Tyr Ser
          20          25          30
Lys Glu Leu Gly Asp Ala Trp Asn Thr Val Arg Glu Ile Leu Thr
          35          40          45
Ser Pro Ser Cys Trp Gln Tyr Ala Val Leu Leu Asn Arg Phe Asn
          50          55          60
Tyr Pro Phe Glu Leu Glu Lys Asp Leu His Leu Lys Gly Tyr His
          65          70          75
Thr Leu Ser Gln Gly Ser Leu Pro Asn Tyr Pro Lys Ser Val Lys
          80          85          90
Cys Tyr Leu Ser Arg Thr Pro Gly Arg Ile Pro Ser Glu Arg His
          95          100          105
Gln Ile Gly Asn Leu Lys Lys Tyr Tyr Leu Leu Asn Ala Ala Ser
          110          115          120
Leu Leu Pro Val Leu Ala Leu Glu Leu Arg Asp Gly Glu Lys Val
          125          130          135
Leu Asp Leu Cys Ala Ala Pro Gly Gly Lys Ser Ile Ala Leu Leu
          140          145          150
Gln Cys Ala Cys Pro Gly Tyr Leu His Cys Asn Glu Tyr Asp Ser
          155          160          165
Leu Arg Leu Arg Trp Leu Arg Gln Thr Leu Glu Ser Phe Ile Pro
          170          175          180
Gln Pro Leu Ile Asn Val Ile Lys Val Ser Glu Leu Asp Gly Arg
          185          190          195
Lys Met Gly Asp Ala Gln Pro Glu Met Phe Asp Lys Val Leu Val
          200          205          210
Asp Ala Pro Cys Ser Asn Asp Arg Ser Trp Leu Phe Ser Ser Asp
          215          220          225
Ser Gln Lys Ala Ser Cys Arg Ile Ser Gln Arg Arg Asn Leu Pro
          230          235          240
Leu Leu Gln Ile Glu Leu Leu Arg Ser Ala Ile Lys Ala Leu Arg
          245          250          255
Pro Gly Gly Ile Leu Val Tyr Ser Thr Cys Thr Leu Ser Lys Ala
          260          265          270
Glu Asn Gln Asp Val Ile Ser Glu Ile Leu Asn Ser His Gly Asn
          275          280          285
Ile Met Pro Met Asp Ile Lys Gly Ile Ala Arg Thr Cys Ser His
          290          295          300
Asp Phe Thr Phe Ala Pro Thr Gly Gln Glu Cys Gly Leu Leu Val
          305          310          315
Ile Pro Asp Lys Gly Lys Ala Trp Gly Pro Met Tyr Val Ala Lys
          320          325          330
Leu Lys Lys Ser Trp Ser Thr Gly Lys Trp
          335          340

```

<210> 3

<211> 418

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1305252CD1

<400> 3

WO 01/07471

PCT/US00/19948

```

Met Leu Tyr Leu Glu Asp Tyr Leu Glu Met Ile Glu Gln Leu Pro
 1      5      10      15
Met Asp Leu Arg Asp Arg Phe Thr Glu Met Arg Glu Met Asp Leu
 20      25      30
Gln Val Gln Asn Ala Met Asp Gln Leu Glu Gln Arg Val Ser Glu
 35      40      45
Phe Phe Met Asn Ala Lys Lys Asn Lys Pro Glu Trp Arg Glu Glu
 50      55      60
Gln Met Ala Ser Ile Lys Lys Asp Tyr Tyr Lys Ala Leu Glu Asp
 65      70      75
Ala Asp Glu Lys Val Gln Leu Ala Asn Gln Ile Tyr Asp Leu Val
 80      85      90
Asp Arg His Leu Arg Lys Leu Asp Gln Glu Leu Ala Lys Phe Lys
 95      100      105
Met Glu Leu Glu Ala Asp Asn Ala Gly Ile Thr Glu Ile Leu Glu
110      115      120
Arg Arg Ser Leu Glu Leu Asp Thr Pro Ser Gln Pro Val Asn Asn
125      130      135
His His Ala His Ser His Thr Pro Val Glu Lys Arg Lys Tyr Asn
140      145      150
Pro Thr Ser His His Thr Thr Thr Asp His Ile Pro Glu Lys Lys
155      160      165
Phe Lys Ser Glu Ala Leu Leu Ser Thr Leu Thr Ser Asp Ala Ser
170      175      180
Lys Glu Asn Thr Leu Gly Cys Arg Asn Asn Asn Ser Thr Ala Ser
185      190      195
Ser Asn Asn Ala Tyr Asn Val Asn Ser Ser Gln Pro Leu Gly Ser
200      205      210
Tyr Asn Ile Gly Ser Leu Ser Ser Gly Thr Gly Ala Gly Ala Ile
215      220      225
Thr Met Ala Ala Ala Gln Ala Val Gln Ala Thr Ala Gln Met Lys
230      235      240
Glu Gly Arg Arg Thr Ser Ser Leu Lys Ala Ser Tyr Glu Ala Phe
245      250      255
Lys Asn Asn Asp Phe Gln Leu Gly Lys Glu Phe Ser Met Ala Arg
260      265      270
Glu Thr Val Gly Tyr Ser Ser Ser Ser Ala Leu Met Thr Thr Leu
275      280      285
Thr Gln Asn Ala Ser Ser Ser Ala Ala Asp Ser Arg Ser Gly Arg
290      295      300
Lys Ser Lys Asn Asn Asn Lys Ser Ser Ser Gln Gln Ser Ser Ser
305      310      315
Ser Ser Ser Ser Ser Ser Leu Ser Ser Cys Ser Ser Ser Ser Thr
320      325      330
Val Val Gln Glu Ile Ser Gln Gln Thr Thr Val Val Pro Glu Ser
335      340      345
Asp Ser Asn Ser Gln Val Asp Trp Thr Tyr Asp Pro Asn Glu Pro
350      355      360
Arg Tyr Cys Ile Cys Asn Gln Val Ser Tyr Gly Glu Met Val Gly
365      370      375
Cys Asp Asn Gln Asp Cys Pro Ile Glu Trp Phe His Tyr Gly Cys
380      385      390
Val Gly Leu Thr Glu Ala Pro Lys Gly Lys Trp Tyr Cys Pro Gln
395      400      405
Cys Thr Ala Ala Met Lys Arg Arg Gly Ser Arg His Lys
410      415

```

<210> 4

<211> 297

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

WO 01/07471

PCT/US00/19948

<223> Incyte ID No: 1416289CD1

<400> 4

Met	Ala	Tyr	Asn	Val	Ile	Ile	Ile	Tyr	Phe	Asn	Phe	Arg	Cys	Leu	1	5	10	15
Glu	Trp	Leu	Leu	Asn	Asn	Leu	Met	Thr	His	Gln	Asn	Val	Glu	Leu	20	25	30	35
Phe	Lys	Glu	Leu	Ser	Ile	Asn	Val	Met	Lys	Gln	Leu	Ile	Gly	Ser	40	45	50	55
Ser	Asn	Leu	Phe	Val	Met	Gln	Val	Glu	Met	Asp	Ile	Tyr	Thr	Ala	60	65	70	75
Leu	Lys	Lys	Trp	Met	Phe	Leu	Gln	Leu	Val	Pro	Ser	Trp	Asn	Gly	80	85	90	95
Ser	Leu	Lys	Gln	Leu	Leu	Thr	Glu	Thr	Asp	Val	Trp	Phe	Ser	Lys	100	105	110	115
Gln	Arg	Lys	Asp	Phe	Glu	Gly	Met	Ala	Phe	Leu	Glu	Thr	Glu	Gln	120	125	130	135
Gly	Lys	Pro	Phe	Val	Ser	Val	Phe	Arg	His	Leu	Arg	Leu	Gln	Tyr	140	145	150	155
Ile	Ile	Ser	Asp	Leu	Ala	Ser	Ala	Arg	Ile	Ile	Glu	Gln	Asp	Ala	160	165	170	175
Val	Val	Pro	Ser	Glu	Trp	Leu	Ser	Ser	Val	Tyr	Lys	Gln	Gln	Trp	180	185	190	195
Phe	Ala	Met	Leu	Arg	Ala	Glu	Gln	Asp	Ser	Glu	Val	Gly	Pro	Gln	200	205	210	215
Glu	Ile	Asn	Lys	Glu	Glu	Leu	Glu	Gly	Asn	Ser	Met	Arg	Cys	Gly	220	225	230	235
Arg	Lys	Leu	Ala	Lys	Asp	Gly	Glu	Tyr	Cys	Trp	Arg	Trp	Thr	Gly	240	245	250	255
Phe	Asn	Phe	Gly	Phe	Asp	Leu	Leu	Val	Thr	Tyr	Thr	Asn	Arg	Tyr	260	265	270	275
Ile	Ile	Phe	Lys	Arg	Asn	Thr	Leu	Asn	Gln	Pro	Cys	Ser	Gly	Ser	280	285	290	295
Val	Ser	Leu	Gln	Pro	Arg	Arg	Ser	Ile	Ala	Phe	Arg	Leu	Arg	Leu				
Ala	Ser	Phe	Asp	Ser	Ser	Gly	Lys	Leu	Ile	Cys	Ser	Arg	Thr	Thr				
Gly	Tyr	Gln	Ile	Leu	Thr	Leu	Glu	Lys	Asp	Gln	Glu	Gln	Val	Val				
Met	Asn	Leu	Asp	Ser	Arg	Leu	Leu	Ile	Phe	Pro	Leu	Tyr	Ile	Cys				
Cys	Asn	Phe	Leu	Tyr	Ile	Ser	Pro	Glu	Lys	Lys	Asn							

<210> 5

<211> 184

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1558289CD1

<400> 5

Met	Glu	Ser	Phe	Ser	Ser	Lys	Ser	Leu	Ala	Leu	Gln	Ala	Glu	Lys	1	5	10	15
Lys	Leu	Leu	Ser	Lys	Met	Ala	Gly	Arg	Ser	Val	Ala	His	Leu	Phe	20	25	30	35
Ile	Asp	Glu	Thr	Ser	Ser	Glu	Val	Leu	Asp	Glu	Leu	Tyr	Arg	Val	40	45	50	55
Ser	Lys	Glu	Tyr	Thr	His	Ser	Arg	Pro	Gln	Ala	Gln	Arg	Val	Ile	60	65	70	75
Lys	Asp	Leu	Ile	Lys	Val	Ala	Ile	Lys	Val	Ala	Val	Leu	His	Arg				

WO 01/07471

PCT/US00/19948

```

Asn Gly Ser Phe Gly Pro Ser Glu Leu Ala Leu Ala Thr Arg Phe
      80      85      90
Arg Gln Lys Leu Arg Gln Gly Ala Met Thr Ala Leu Ser Phe Gly
      95     100     105
Glu Val Asp Phe Thr Phe Glu Ala Ala Val Leu Ala Gly Leu Leu
     110     115     120
Thr Glu Cys Arg Asp Val Leu Leu Glu Leu Val Glu His His Leu
     125     130     135
Thr Pro Lys Ser His Gly Arg Ile Arg His Val Phe Asp His Phe
     140     145     150
Ser Asp Pro Gly Leu Leu Thr Ala Leu Tyr Gly Pro Asp Phe Thr
     155     160     165
Gln His Leu Gly Lys Ile Cys Asp Gly Leu Arg Lys Leu Leu Asp
     170     175     180
Glu Gly Lys Leu

```

<210> 6
 <211> 173
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1577739CD1

```

<400> 6
Met Asp Val Arg Arg Val Leu Val Lys Ala Glu Met Glu Lys Phe
  1      5      10      15
Leu Gln Asn Lys Glu Leu Phe Ser Ser Leu Lys Lys Gly Lys Ile
     20      25      30
Cys Cys Cys Cys Arg Ala Lys Phe Pro Leu Phe Ser Trp Pro Pro
     35      40      45
Ser Cys Leu Phe Cys Lys Arg Ala Val Cys Thr Ser Cys Ser Ile
     50      55      60
Lys Met Lys Met Pro Ser Lys Lys Phe Gly His Ile Pro Val Tyr
     65      70      75
Thr Leu Gly Phe Glu Ser Pro Gln Arg Val Ser Ala Ala Lys Thr
     80      85      90
Ala Pro Ile Gln Arg Arg Asp Ile Phe Gln Ser Leu Gln Gly Pro
     95     100     105
Gln Trp Gln Ser Val Glu Glu Ala Phe Pro His Ile Tyr Ser His
    110     115     120
Gly Cys Val Leu Lys Asp Val Cys Ser Glu Cys Thr Ser Phe Val
    125     130     135
Ala Asp Val Val Arg Ser Ser Arg Lys Ser Val Asp Val Leu Asn
    140     145     150
Thr Thr Pro Arg Arg Ser Arg Gln Thr Gln Ser Leu Tyr Ile Pro
    155     160     165
Asn Thr Arg Thr Leu Asp Phe Lys
    170

```

<210> 7
 <211> 591
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1752768CD1

```

<400> 7
Met Val Pro Val Ala Val Thr Ala Ala Val Ala Pro Val Leu Ser
  1      5      10      15
Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile Lys Lys Gln Leu

```


WO 01/07471

PCT/US00/19948

Glu Ile Val Glu His Leu Glu Glu Ser Thr Ala Phe Arg Tyr Leu
 500 505 510
 Ala Gln Tyr Tyr Phe Lys Cys Lys Leu Trp Asp Glu Ala Ser Thr
 515 520 525
 Cys Ala Gln Lys Cys Cys Ala Phe Asn Asp Thr Arg Glu Glu Gly
 530 535 540
 Lys Ala Leu Leu Arg Gln Ile Leu Gln Leu Arg Asn Gln Gly Glu
 545 550 555
 Thr Pro Thr Thr Glu Val Pro Ala Pro Phe Phe Leu Pro Ala Ser
 560 565 570
 Leu Ser Ala Asn Asn Thr Pro Thr Arg Arg Val Ser Pro Leu Asn
 575 580 585
 Leu Ser Ser Val Thr Pro
 590

<210> 8
 <211> 463
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1887228CD1

<400> 8
 Met Pro Leu Leu Asn Trp Val Ala Leu Lys Pro Ser Gln Ile Thr
 1 5 10 15
 Gly Thr Val Phe Thr Glu Leu Asn Asp Glu Lys Val Leu Gln Glu
 20 25 30
 Leu Asp Met Ser Asp Phe Glu Glu Gln Phe Lys Thr Lys Ser Gln
 35 40 45
 Gly Pro Ser Leu Asp Leu Ser Ala Leu Lys Ser Lys Ala Ala Gln
 50 55 60
 Lys Ala Pro Ser Lys Ala Thr Leu Ile Glu Ala Asn Arg Ala Lys
 65 70 75
 Asn Leu Ala Ile Thr Leu Arg Lys Gly Asn Leu Gly Ala Glu Arg
 80 85 90
 Ile Cys Gln Ala Ile Glu Ala Tyr Asp Leu Gln Ala Leu Gly Leu
 95 100 105
 Asp Phe Leu Glu Leu Leu Met Arg Phe Leu Pro Thr Glu Tyr Glu
 110 115 120
 Arg Ser Leu Ile Thr Arg Phe Glu Arg Glu Gln Arg Pro Met Glu
 125 130 135
 Glu Leu Ser Glu Glu Asp Arg Phe Met Leu Cys Phe Ser Arg Ile
 140 145 150
 Pro Arg Leu Pro Glu Arg Met Thr Thr Leu Thr Phe Leu Gly Asn
 155 160 165
 Phe Pro Asp Thr Ala Gln Leu Leu Met Pro Gln Leu Asn Ala Ile
 170 175 180
 Ile Ala Ala Ser Met Ser Ile Lys Ser Ser Asp Lys Leu Arg Gln
 185 190 195
 Ile Leu Glu Ile Val Leu Ala Phe Gly Asn Tyr Met Asn Ser Ser
 200 205 210
 Lys Arg Gly Ala Ala Tyr Gly Phe Arg Leu Gln Ser Leu Asp Ala
 215 220 225
 Leu Leu Glu Met Lys Ser Thr Asp Arg Lys Gln Thr Leu Leu His
 230 235 240
 Tyr Leu Val Lys Val Ile Ala Glu Lys Tyr Pro Gln Leu Thr Gly
 245 250 255
 Phe His Ser Asp Leu His Phe Leu Asp Lys Ala Gly Ser Val Ser
 260 265 270
 Leu Asp Ser Val Leu Ala Asp Val Arg Ser Leu Gln Arg Gly Leu
 275 280 285
 Glu Leu Thr Gln Arg Glu Phe Val Arg Gln Asp Asp Cys Met Val

WO 01/07471

PCT/US00/19948

Leu Lys Glu Phe	290	Leu Arg Ala Asn Ser	295	Pro Thr Met Asp Lys	300
	305		310		315
Leu Ala Asp Ser	320	Lys Thr Ala Gln Glu	325	Ala Phe Glu Ser Val	330
	335		340		345
Glu Tyr Phe Gly	350	Glu Asn Pro Lys Thr	355	Thr Ser Pro Gly Leu	360
	365		370		375
Phe Ser Leu Phe	380	Ser Arg Phe Ile Lys	385	Ala Tyr Lys Lys Ala	390
	395		400		405
Gln Glu Val Glu	410	Gln Trp Lys Lys Glu	415	Ala Ala Ala Gln Glu	420
	425		430		435
Gly Ala Asp Thr	440	Pro Gly Lys Gly Glu	445	Pro Pro Ala Pro Lys	450
	455		460		
Pro Pro Lys Ala		Arg Arg Pro Gln Met		Asp Leu Ile Ser Glu	
Lys Arg Arg Gln		Gln Lys Glu Pro Leu		Ile Tyr Glu Ser Asp	
Asp Gly Ala Ile		Glu Asp Ile Ile Thr		Asp Leu Arg Asn Gln	
Tyr Ile Arg Ala		Asp Thr Gly Arg Arg		Ser Ala Arg Arg Arg	
Pro Gly Pro Pro		Leu Gln Val Thr Ser		Asp Leu Ser Leu	

<210> 9

<211> 270

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1988468CD1

<400> 9

Met Ala Asp His	Met	Met	Ala	Met	Asn	His	Gly	Arg	Phe	Pro	Asp
1	5					10					15
Gly Thr Asn Gly	Leu	His	His	His	Pro	Ala	His	Arg	Met	Gly	Met
	20					25					30
Gly Gln Phe Pro	Ser	Pro	His	His	His	Gln	Gln	Gln	Gln	Pro	Gln
	35					40					45
His Ala Phe Asn	Ala	Leu	Met	Gly	Glu	His	Ile	His	Tyr	Gly	Ala
	50					55					60
Gly Asn Met Asn	Ala	Thr	Ser	Gly	Ile	Arg	His	Ala	Met	Gly	Pro
	65					70					75
Gly Thr Val Asn	Gly	Gly	His	Pro	Pro	Ser	Ala	Leu	Ala	Pro	Ala
	80					85					90
Ala Arg Phe Asn	Asn	Ser	Gln	Phe	Met	Gly	Pro	Pro	Val	Ala	Ser
	95					100					105
Gln Gly Gly Ser	Leu	Pro	Ala	Ser	Met	Gln	Leu	Gln	Lys	Leu	Asn
	110					115					120
Asn Gln Tyr Phe	Asn	His	His	Pro	Tyr	Pro	His	Asn	His	Tyr	Met
	125					130					135
Pro Asp Leu His	Pro	Ala	Ala	Gly	His	Gln	Met	Asn	Gly	Thr	Asn
	140					145					150
Gln His Phe Arg	Asp	Cys	Asn	Pro	Lys	His	Ser	Gly	Gly	Ser	Ser
	155					160					165
Thr Pro Gly Gly	Ser	Gly	Gly	Ser	Ser	Thr	Pro	Gly	Gly	Ser	Gly
	170					175					180
Ser Ser Ser Gly	Gly	Gly	Ala	Gly	Ser	Ser	Asn	Ser	Gly	Gly	Gly
	185					190					195
Ser Gly Ser Gly	Asn	Met	Pro	Ala	Ser	Val	Ala	His	Val	Pro	Ala
	200					205					210
Ala Met Leu Pro	Pro	Asn	Val	Ile	Asp	Thr	Asp	Phe	Ile	Asp	Glu
	215					220					225

WO 01/07471

PCT/US00/19948

Glu	Val	Leu	Met	Ser	Leu	Val	Ile	Glu	Met	Gly	Leu	Asp	Arg	Ile
				230					235					240
Lys	Glu	Leu	Pro	Glu	Leu	Trp	Leu	Gly	Gln	Asn	Glu	Phe	Asp	Phe
				245					250					255
Met	Thr	Asp	Phe	Val	Cys	Lys	Gln	Gln	Pro	Ser	Arg	Val	Ser	Cys
				260					265					270

<210> 10
 <211> 255
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2049176CD1

<400> 10	
Met Val Ser Trp Met Ile Ser Arg Ala Val Val Leu Val Phe Gly	
1 5 10 15	
Met Leu Tyr Pro Ala Tyr Tyr Ser Tyr Lys Ala Val Lys Thr Lys	
20 25 30	
Asn Val Lys Glu Tyr Val Arg Trp Met Met Tyr Trp Ile Val Phe	
35 40 45	
Ala Leu Tyr Thr Val Ile Glu Thr Val Ala Asp Gln Thr Val Ala	
50 55 60	
Trp Phe Pro Leu Tyr Tyr Glu Leu Lys Ile Ala Phe Val Ile Trp	
65 70 75	
Leu Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Ile Tyr Arg Lys	
80 85 90	
Phe Leu His Pro Leu Leu Ser Ser Lys Glu Arg Glu Ile Asp Asp	
95 100 105	
Tyr Ile Val Gln Ala Lys Glu Arg Gly Tyr Glu Thr Met Val Asn	
110 115 120	
Phe Gly Arg Gln Gly Leu Asn Leu Ala Ala Thr Ala Ala Val Thr	
125 130 135	
Ala Ala Val Lys Ser Gln Gly Ala Ile Thr Glu Arg Leu Arg Ser	
140 145 150	
Phe Ser Met His Asp Leu Thr Thr Ile Gln Gly Asp Glu Pro Val	
155 160 165	
Gly Gln Arg Pro Tyr Gln Pro Leu Pro Glu Ala Lys Lys Lys Ser	
170 175 180	
Lys Pro Ala Pro Ser Glu Ser Ala Gly Tyr Gly Ile Pro Leu Lys	
185 190 195	
Asp Gly Asp Glu Lys Thr Asp Glu Glu Ala Glu Gly Pro Tyr Ser	
200 205 210	
Asp Asn Glu Met Leu Thr His Lys Gly Leu Arg Arg Ser Gln Ser	
215 220 225	
Met Lys Ser Val Lys Thr Thr Lys Gly Arg Lys Glu Val Arg Tyr	
230 235 240	
Gly Ser Leu Lys Tyr Lys Val Lys Lys Arg Pro Gln Val Tyr Phe	
245 250 255	

<210> 11
 <211> 533
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2686765CD1

<400> 11
 Met Ser Gly Thr Leu Glu Ser Leu Ala Asp Asp Val Ser Ser Met

WO 01/07471

PCT/US00/19948

1	5	10	15
Gly Ser Asp Ser Glu	Ile Asn Gly Leu	Ala Leu Arg Lys Thr	Asp
20	25	30	
Lys Tyr Gly Phe Leu	Gly Gly Ser Gln	Tyr Ser Gly Ser Leu	Glu
35	40	45	
Ser Ser Ile Pro Val	Asp Val Ala Arg	Gln Arg Glu Leu Lys	Trp
50	55	60	
Leu Asp Met Phe Ser	Asn Trp Asp Lys	Trp Leu Ser Arg Arg	Phe
65	70	75	
Gln Lys Val Lys Leu	Arg Cys Arg Lys	Gly Ile Pro Ser Ser	Leu
80	85	90	
Arg Ala Lys Ala Trp	Gln Tyr Leu Ser	Asn Ser Lys Glu Leu	Leu
95	100	105	
Glu Gln Asn Pro Gly	Lys Phe Glu Glu	Leu Glu Arg Ala Pro	Gly
110	115	120	
Asp Pro Lys Trp Leu	Asp Val Ile Glu	Lys Asp Leu His Arg	Gln
125	130	135	
Phe Pro Phe His Glu	Met Phe Ala Ala	Arg Gly Gly His Gly	Gln
140	145	150	
Gln Asp Leu Tyr Arg	Ile Leu Lys Ala	Tyr Thr Ile Tyr Arg	Pro
155	160	165	
Asp Glu Gly Tyr Cys	Gln Ala Gln Ala	Pro Val Ala Ala Val	Leu
170	175	180	
Leu Met His Met Pro	Ala Glu Lys Pro	Phe Gly Ala Trp Val	Gln
185	190	195	
Ile Cys Asp Lys Tyr	Leu Pro Gly Tyr	Tyr Ser Ala Gly Leu	Glu
200	205	210	
Ala Ile Gln Leu Asp	Gly Glu Ile Phe	Phe Ala Leu Leu Arg	Arg
215	220	225	
Ala Ser Pro Leu Ala	His Arg His Leu	Gln Arg Gln Arg Ile	Asp
230	235	240	
Pro Val Leu Tyr Met	Thr Glu Trp Phe	Met Cys Ile Phe Ala	Arg
245	250	255	
Thr Leu Pro Trp Ala	Ser Val Leu Arg	Val Trp Asp Met Phe	Phe
260	265	270	
Cys Glu Gly Val Lys	Ile Ile Phe Arg	Val Ala Leu Val Leu	Leu
275	280	285	
Arg His Thr Leu Gly	Ser Val Glu Lys	Leu Arg Ser Cys Gln	Gly
290	295	300	
Met Tyr Glu Thr Met	Glu Gln Leu Arg	Asn Leu Pro Gln Gln	Cys
305	310	315	
Met Gln Glu Asp Phe	Leu Val His Glu	Val Thr Asn Leu Pro	Val
320	325	330	
Thr Glu Ala Leu Ile	Glu Arg Glu Asn	Ala Ala Gln Leu Lys	Lys
335	340	345	
Trp Arg Glu Thr Arg	Gly Glu Leu Gln	Tyr Arg Pro Ser Arg	Arg
350	355	360	
Leu His Gly Ser Arg	Ala Ile His Glu	Glu Arg Arg Arg Gln	Gln
365	370	375	
Pro Pro Leu Gly Pro	Ser Ser Ser Leu	Leu Ser Leu Pro Gly	Leu
380	385	390	
Lys Ser Arg Gly Ser	Arg Ala Ala Gly	Gly Ala Pro Ser Pro	Pro
395	400	405	
Pro Pro Val Arg Arg	Ala Ser Ala Gly	Pro Ala Pro Gly Pro	Val
410	415	420	
Val Thr Ala Glu Gly	Leu His Pro Ser	Leu Pro Ser Pro Thr	Gly
425	430	435	
Asn Ser Thr Pro Leu	Gly Ser Ser Lys	Glu Thr Arg Lys Gln	Glu
440	445	450	
Lys Glu Arg Gln Lys	Gln Glu Lys Glu	Arg Gln Lys Gln Glu	Lys
455	460	465	
Glu Arg Glu Lys Glu	Arg Gln Lys Gln	Glu Lys Glu Arg Glu	Lys
470	475	480	

WO 01/07471

PCT/US00/19948

Gln	Glu	Lys	Glu	Arg	Glu	Lys	Gln	Glu	Lys	Glu	Arg	Gln	Lys	Gln
				485					490					495
Glu	Lys	Lys	Ala	Gln	Gly	Arg	Lys	Leu	Ser	Leu	Arg	Arg	Lys	Ala
				500					505					510
Asp	Gly	Pro	Pro	Gly	Pro	His	Asp	Gly	Gly	Asp	Arg	Pro	Ser	Ala
				515					520					525
Glu	Ala	Arg	Gln	Asp	Ala	Tyr	Phe							
				530										

<210> 12
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3215187CD1

<400> 12	Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ser	Leu	Val
1					5					10					15
Leu	Cys	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala	
				20					25					30	
Phe	Asp	Glu	Leu	Arg	Thr	Asp	Phe	Lys	Ser	Pro	Ile	Asp	Gln	Cys	
				35					40					45	
Asn	Pro	Val	His	Ala	Arg	Glu	Arg	Leu	Arg	Asn	Ile	Glu	Arg	Ile	
				50					55					60	
Cys	Phe	Leu	Leu	Arg	Lys	Leu	Val	Leu	Pro	Glu	Tyr	Ser	Ile	His	
				65					70					75	
Ser	Leu	Phe	Cys	Ile	Met	Phe	Leu	Cys	Ala	Gln	Glu	Trp	Leu	Thr	
				80					85					90	
Leu	Gly	Leu	Asn	Val	Pro	Leu	Leu	Phe	Tyr	His	Phe	Trp	Arg	Tyr	
				95					100					105	
Phe	His	Cys	Pro	Ala	Asp	Ser	Ser	Glu	Leu	Ala	Tyr	Asp	Pro	Pro	
				110					115					120	
Val	Val	Met	Asn	Ala	Asp	Thr	Leu	Ser	Tyr	Cys	Gln	Lys	Glu	Ala	
				125					130					135	
Trp	Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ser	Phe	Phe	Tyr	Tyr	Leu	
				140					145					150	
Tyr	Cys	Met	Ile	Tyr	Thr	Leu	Val	Ser	Ser						
				155					160						

<210> 13
 <211> 531
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3500375CD1

<400> 13	Met	Ala	Asp	Val	Leu	Ser	Val	Leu	Arg	Gln	Tyr	Asn	Ile	Gln	Lys
1					5					10					15
Lys	Glu	Ile	Val	Val	Lys	Gly	Asp	Glu	Val	Ile	Phe	Gly	Glu	Phe	
				20					25					30	
Ser	Trp	Pro	Lys	Asn	Val	Lys	Thr	Asn	Tyr	Val	Val	Trp	Gly	Thr	
				35					40					45	
Gly	Lys	Glu	Gly	Gln	Pro	Arg	Glu	Tyr	Tyr	Thr	Leu	Asp	Ser	Ile	
				50					55					60	
Leu	Phe	Leu	Leu	Asn	Asn	Val	His	Leu	Ser	His	Pro	Val	Tyr	Val	
				65					70					75	
Arg	Arg	Ala	Ala	Thr	Glu	Asn	Ile	Pro	Val	Val	Arg	Arg	Pro	Asp	
				80					85					90	
Arg	Lys	Asp	Leu	Leu	Gly	Tyr	Leu	Asn	Gly	Glu	Ala	Ser	Thr	Ser	

WO 01/07471

PCT/US00/19948

	95		100		105
Ala Ser Ile Asp	Arg Ser Ala Pro Leu	Glu Ile Gly Leu Gln	Arg		
	110		115		120
Ser Thr Gln Val	Lys Arg Ala Ala Asp	Glu Val Leu Ala Glu	Ala		
	125		130		135
Lys Lys Pro Arg	Ile Glu Asp Glu Glu	Cys Val Arg Leu Asp	Lys		
	140		145		150
Glu Arg Leu Ala	Ala Arg Leu Glu Gly	His Lys Glu Gly Ile	Val		
	155		160		165
Gln Thr Glu Gln	Ile Arg Ser Leu Ser	Glu Ala Met Ser Val	Glu		
	170		175		180
Lys Ile Ala Ala	Ile Lys Ala Lys Ile	Met Ala Lys Lys Arg	Ser		
	185		190		195
Thr Ile Lys Thr	Asp Leu Asp Asp Asp	Ile Thr Ala Leu Lys	Gln		
	200		205		210
Arg Ser Phe Val	Asp Ala Glu Val Asp	Val Thr Arg Asp Ile	Val		
	215		220		225
Ser Arg Glu Arg	Val Trp Arg Thr Arg	Thr Thr Ile Leu Gln	Ser		
	230		235		240
Thr Gly Lys Asn	Phe Ser Lys Asn Ile	Phe Ala Ile Leu Gln	Ser		
	245		250		255
Val Lys Ala Arg	Glu Glu Gly Arg Ala	Pro Glu Gln Arg Pro	Ala		
	260		265		270
Pro Asn Ala Ala	Pro Val Asp Pro Thr	Leu Arg Thr Lys Gln	Pro		
	275		280		285
Ile Pro Ala Ala	Tyr Asn Arg Tyr Asp	Gln Glu Arg Phe Lys	Gly		
	290		295		300
Lys Glu Glu Thr	Glu Gly Phe Lys Ile	Asp Thr Met Gly Thr	Tyr		
	305		310		315
His Gly Met Thr	Leu Lys Ser Val Thr	Glu Gly Ala Ser Ala	Arg		
	320		325		330
Lys Thr Gln Thr	Pro Ala Ala Gln Pro	Val Pro Arg Pro Val	Ser		
	335		340		345
Gln Ala Arg Pro	Pro Pro Asn Gln Lys	Lys Gly Ser Arg Thr	Pro		
	350		355		360
Ile Ile Ile Ile	Pro Ala Ala Thr Thr	Ser Leu Ile Thr Met	Leu		
	365		370		375
Asn Ala Lys Asp	Leu Leu Gln Asp Leu	Lys Phe Val Pro Ser	Asp		
	380		385		390
Glu Lys Lys Lys	Gln Gly Cys Gln Arg	Glu Asn Glu Thr Leu	Ile		
	395		400		405
Gln Arg Arg Lys	Asp Gln Met Gln Pro	Gly Gly Thr Ala Ile	Ser		
	410		415		420
Val Thr Val Pro	Tyr Arg Val Val Asp	Gln Pro Leu Lys Leu	Met		
	425		430		435
Pro Gln Asp Trp	Asp Arg Val Val Ala	Val Phe Val Gln Gly	Pro		
	440		445		450
Ala Trp Gln Phe	Lys Gly Trp Pro Trp	Leu Leu Pro Asp Gly	Ser		
	455		460		465
Pro Val Asp Ile	Phe Ala Lys Ile Lys	Ala Phe His Leu Lys	Tyr		
	470		475		480
Asp Glu Val Arg	Leu Asp Pro Asn Val	Gln Lys Trp Asp Val	Thr		
	485		490		495
Val Leu Glu Leu	Ser Tyr His Lys Arg	His Leu Asp Arg Pro	Val		
	500		505		510
Phe Leu Arg Phe	Trp Glu Thr Leu Asp	Arg Tyr Met Val Lys	His		
	515		520		525
Lys Ser His Leu	Arg Phe				
	530				

<210> 14

<211> 165

<212> PRT

<213> Homo sapiens

WO 01/07471

PCT/US00/19948

<220>

<221> misc_feature

<223> Incyte ID No: 5080410CD1

<400> 14

Met	Ala	Ser	Met	Arg	Glu	Ser	Asp	Thr	Gly	Leu	Trp	Leu	His	Asn
1				5					10					15
Lys	Leu	Gly	Ala	Thr	Asp	Glu	Leu	Trp	Ala	Pro	Pro	Ser	Ile	Ala
				20					25					30
Ser	Leu	Leu	Thr	Ala	Ala	Val	Ile	Asp	Asn	Ile	Arg	Leu	Cys	Phe
				35					40					45
His	Gly	Leu	Ser	Ser	Ala	Val	Lys	Leu	Lys	Leu	Leu	Leu	Gly	Thr
				50					55					60
Leu	His	Leu	Pro	Arg	Arg	Thr	Val	Asp	Glu	His	Pro	Ile	Leu	Pro
				65					70					75
Met	Lys	Gly	Ala	Leu	Met	Glu	Ile	Ile	Gln	Leu	Ala	Ser	Leu	Asp
				80					85					90
Ser	Asp	Pro	Trp	Val	Leu	Met	Val	Ala	Asp	Ile	Leu	Lys	Ser	Phe
				95					100					105
Pro	Asp	Thr	Gly	Ser	Leu	Asn	Leu	Glu	Leu	Glu	Glu	Gln	Asn	Pro
				110					115					120
Asn	Val	Gln	Asp	Ile	Leu	Gly	Glu	Leu	Arg	Glu	Lys	Val	Gly	Glu
				125					130					135
Cys	Glu	Ala	Ser	Ala	Met	Leu	Pro	Leu	Glu	Cys	Gln	Tyr	Leu	Asn
				140					145					150
Lys	Asn	Ala	Ala	Asp	Asp	Pro	Arg	Gly	Thr	Pro	His	Ser	Pro	Gly
				155					160					165

<210> 15

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5218248CD1

<400> 15

Met	Ser	Asn	Met	Glu	Lys	His	Leu	Phe	Asn	Leu	Lys	Phe	Ala	Ala
1				5					10					15
Lys	Glu	Leu	Ser	Arg	Ser	Ala	Lys	Lys	Cys	Asp	Lys	Glu	Glu	Lys
				20					25					30
Ala	Glu	Lys	Ala	Lys	Ile	Lys	Lys	Ala	Ile	Gln	Lys	Gly	Asn	Met
				35					40					45
Glu	Val	Ala	Arg	Ile	His	Ala	Glu	Asn	Ala	Ile	Arg	Gln	Lys	Asn
				50					55					60
Gln	Ala	Val	Asn	Phe	Leu	Arg	Met	Ser	Ala	Arg	Val	Asp	Ala	Val
				65					70					75
Ala	Ala	Arg	Val	Gln	Thr	Ala	Val	Thr	Met	Gly	Lys	Val	Thr	Lys
				80					85					90
Ser	Met	Ala	Gly	Val	Val	Lys	Ser	Met	Asp	Ala	Thr	Leu	Lys	Thr
				95					100					105
Met	Asn	Leu	Glu	Lys	Ile	Ser	Ala	Leu	Met	Asp	Lys	Phe	Glu	His
				110					115					120
Gln	Phe	Glu	Thr	Leu	Asp	Val	Gln	Thr	Gln	Gln	Met	Glu	Asp	Thr
				125					130					135
Met	Ser	Ser	Thr	Thr	Thr	Leu	Thr	Thr	Pro	Gln	Asn	Gln	Val	Asp
				140					145					150
Met	Leu	Leu	Gln	Glu	Met	Ala	Asp	Glu	Ala	Gly	Leu	Asp	Leu	Asn
				155					160					165
Met	Glu	Leu	Pro	Gln	Gly	Gln	Thr	Gly	Ser	Val	Gly	Thr	Ser	Val
				170					175					180
Ala	Ser	Ala	Glu	Gln	Asp	Glu	Leu	Ser	Gln	Arg	Leu	Ala	Arg	Leu

WO 01/07471

PCT/US00/19948

Arg Asp Gln Val 185 190 195

<210> 16
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 058336CD1

<400> 16
Met Ala Phe Asn Asp Cys Phe Ser Leu Asn Tyr Pro Gly Asn Pro
1 5 10 15
Cys Pro Gly Asp Leu Ile Glu Val Phe Arg Pro Gly Tyr Gln His
20 25 30
Trp Ala Leu Tyr Leu Gly Asp Gly Tyr Val Ile Asn Ile Ala Pro
35 40 45
Val Asp Gly Ile Pro Ala Ser Phe Thr Ser Ala Lys Ser Val Phe
50 55 60
Ser Ser Lys Ala Leu Val Lys Met Gln Leu Leu Lys Asp Val Val
65 70 75
Gly Asn Asp Thr Tyr Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr
80 85 90
Pro Pro Leu Pro Val Glu Glu Ile Ile Lys Arg Ser Glu Phe Val
95 100 105
Ile Gly Gln Glu Val Ala Tyr Asn Leu Leu Val Asn Asn Cys Glu
110 115 120
His Phe Val Thr Leu Leu Arg Tyr Gly Glu Gly Val Ser Glu Gln
125 130 135
Ala Asn Arg Ala Ile Ser Thr Val Glu Phe Val Thr Ala Ala Val
140 145 150
Gly Val Phe Ser Phe Leu Gly Leu Phe Pro Lys Gly Gln Arg Ala
155 160 165
Lys Tyr Tyr

<210> 17
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1511488CD1

<400> 17
Met Leu Arg Ala Val Gly Ser Leu Leu Arg Leu Gly Arg Gly Leu
1 5 10 15
Thr Val Arg Cys Gly Pro Gly Ala Pro Leu Glu Ala Thr Arg Arg
20 25 30
Pro Ala Pro Ala Leu Pro Pro Arg Gly Leu Pro Cys Tyr Ser Ser
35 40 45
Gly Gly Ala Pro Ser Asn Ser Gly Pro Gln Gly His Gly Glu Ile
50 55 60
His Arg Val Pro Thr Gln Arg Arg Pro Ser Gln Phe Asp Lys Lys
65 70 75
Ile Leu Leu Trp Thr Gly Arg Phe Lys Ser Met Glu Glu Ile Pro
80 85 90
Pro Arg Ile Pro Pro Glu Met Ile Asp Thr Ala Arg Asn Lys Ala
95 100 105
Arg Val Lys Ala Cys Tyr Ile Met Ile Gly Leu Thr Ile Ile Ala
110 115 120

WO 01/07471

PCT/US00/19948

Cys Phe Ala Val Ile Val Ser Ala Lys Arg Ala Val Glu Arg His
 125 130 135
 Glu Ser Leu Thr Ser Trp Asn Leu Ala Lys Lys Ala Lys Trp Arg
 140 145 150
 Glu Glu Ala Ala Leu Ala Ala Gln Ala Lys Ala Lys
 155 160

<210> 18
 <211> 246
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1638819CD1

<400> 18
 Met Ala Gly Tyr Leu Lys Leu Val Cys Val Ser Phe Gln Arg Gln
 1 5 10 15
 Gly Phe His Thr Val Gly Ser Arg Cys Lys Asn Arg Thr Gly Ala
 20 25 30
 Glu His Leu Trp Leu Thr Arg His Leu Arg Asp Pro Phe Val Lys
 35 40 45
 Ala Ala Lys Val Glu Ser Tyr Arg Cys Arg Ser Ala Phe Lys Leu
 50 55 60
 Leu Glu Val Asn Glu Arg His Gln Ile Leu Arg Pro Gly Leu Arg
 65 70 75
 Val Leu Asp Cys Gly Ala Ala Pro Gly Ala Trp Ser Gln Val Ala
 80 85 90
 Val Gln Lys Val Asn Ala Ala Gly Thr Asp Pro Ser Ser Pro Val
 95 100 105
 Gly Phe Val Leu Gly Val Asp Leu Leu His Ile Phe Pro Leu Glu
 110 115 120
 Gly Ala Thr Phe Leu Cys Pro Ala Asp Val Thr Asp Pro Arg Thr
 125 130 135
 Ser Gln Arg Ile Leu Glu Val Leu Pro Gly Arg Arg Ala Asp Val
 140 145 150
 Ile Leu Ser Asp Met Ala Pro Asn Ala Thr Gly Phe Arg Asp Leu
 155 160 165
 Asp His Asp Arg Leu Ile Ser Leu Cys Leu Thr Leu Leu Ser Val
 170 175 180
 Thr Pro Asp Ile Leu Gln Pro Gly Gly Thr Phe Leu Cys Lys Thr
 185 190 195
 Trp Ala Gly Ser Gln Ser Arg Arg Leu Gln Arg Arg Leu Thr Glu
 200 205 210
 Glu Phe Gln Asn Val Arg Ile Ile Lys Pro Glu Ala Ser Arg Lys
 215 220 225
 Glu Ser Ser Glu Val Tyr Phe Leu Ala Thr Gln Tyr His Gly Arg
 230 235 240
 Lys Gly Thr Val Lys Gln
 245

<210> 19
 <211> 483
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1655123CD1

<400> 19
 Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly
 1 5 10 15
 Pro Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly

WO 01/07471

PCT/US00/19948

	20		25		30
Gly Arg Ala Leu Pro	Gln Leu Ser Asp	Asp Ile Pro Phe Arg Val			
35	40	45			
Asn Trp Pro Gly Thr	Glu Phe Ser Leu Pro	Thr Thr Gly Val Leu			
50	55	60			
Tyr Lys Glu Asp Asn	Tyr Val Ile Met Thr	Thr Ala His Lys Glu			
65	70	75			
Lys Tyr Lys Cys Ile	Leu Pro Leu Val Thr	Ser Gly Asp Glu Glu			
80	85	90			
Glu Glu Lys Asp Tyr	Lys Gly Pro Asn Pro	Arg Glu Leu Leu Glu			
95	100	105			
Pro Leu Phe Lys Gln	Ser Ser Cys Ser Tyr	Arg Ile Glu Ser Tyr			
110	115	120			
Trp Thr Tyr Glu Val	Cys His Gly Lys His	Ile Arg Gln Tyr His			
125	130	135			
Glu Glu Lys Glu Thr	Gly Gln Lys Ile Asn	Ile His Glu Tyr Tyr			
140	145	150			
Leu Gly Asn Met Leu	Ala Lys Asn Leu Leu	Phe Glu Lys Glu Arg			
155	160	165			
Glu Ala Glu Glu Lys	Glu Lys Ser Asn Glu	Ile Pro Thr Lys Asn			
170	175	180			
Ile Glu Gly Gln Met	Thr Pro Tyr Tyr Pro	Val Gly Met Gly Asn			
185	190	195			
Gly Thr Pro Cys Ser	Leu Lys Gln Asn Arg	Pro Arg Ser Ser Thr			
200	205	210			
Val Met Tyr Ile Cys	His Pro Glu Ser Lys	His Glu Ile Leu Ser			
215	220	225			
Val Ala Glu Val Thr	Thr Cys Glu Tyr Glu	Val Val Ile Leu Thr			
230	235	240			
Pro Leu Leu Cys Ser	His Pro Lys Tyr Arg	Phe Arg Ala Ser Pro			
245	250	255			
Val Asn Asp Ile Phe	Cys Gln Ser Leu Pro	Gly Ser Pro Phe Lys			
260	265	270			
Pro Leu Thr Leu Arg	Gln Leu Glu Gln Gln	Glu Glu Ile Leu Arg			
275	280	285			
Val Pro Phe Arg Arg	Asn Lys Glu Glu Asp	Leu Gln Ser Thr Lys			
290	295	300			
Glu Glu Arg Phe Pro	Ala Ile His Lys Ser	Ile Ala Ile Gly Ser			
305	310	315			
Gln Pro Val Leu Thr	Val Gly Thr Thr His	Ile Ser Lys Leu Thr			
320	325	330			
Asp Asp Gln Leu Ile	Lys Glu Phe Leu Ser	Gly Ser Tyr Cys Phe			
335	340	345			
Arg Gly Gly Val Gly	Trp Trp Lys Tyr Glu	Phe Cys Tyr Gly Lys			
350	355	360			
His Val His Gln Tyr	His Glu Asp Lys Asp	Ser Gly Lys Thr Ser			
365	370	375			
Val Val Val Gly Thr	Trp Asn Gln Glu Glu	His Ile Glu Trp Ala			
380	385	390			
Lys Lys Asn Thr Ala	Arg Ala Tyr His Leu	Gln Asp Asp Gly Thr			
395	400	405			
Gln Thr Val Arg Met	Val Ser His Phe Tyr	Gly Asn Gly Asp Ile			
410	415	420			
Cys Asp Ile Thr Asp	Lys Pro Arg Gln Val	Thr Val Lys Leu Lys			
425	430	435			
Cys Lys Glu Ser Asp	Ser Pro His Ala Val	Thr Val Tyr Met Leu			
440	445	450			
Glu Pro His Ser Cys	Gln Tyr Ile Leu Gly	Val Glu Ser Pro Val			
455	460	465			
Ile Cys Lys Ile Leu	Asp Thr Ala Asp Glu	Asn Gly Leu Leu Ser			
470	475	480			
Leu Pro Asn					

WO 01/07471

PCT/US00/19948

<210> 20
<211> 280
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 2553926CD1

<400> 20
Met Glu Ala Ala Glu Thr Glu Ala Glu Ala Ala Ala Leu Glu Val
1 5 10 15
Leu Ala Glu Val Ala Gly Ile Leu Glu Pro Val Gly Leu Gln Glu
20 25 30
Glu Ala Glu Leu Pro Ala Lys Ile Leu Val Glu Phe Val Val Asp
35 40 45
Ser Gln Lys Lys Asp Lys Leu Leu Cys Ser Gln Leu Gln Val Ala
50 55 60
Asp Phe Leu Gln Asn Ile Leu Ala Gln Glu Asp Thr Ala Lys Gly
65 70 75
Leu Asp Pro Leu Ala Ser Glu Asp Thr Ser Arg Gln Lys Ala Ile
80 85 90
Ala Ala Lys Glu Gln Trp Lys Glu Leu Lys Ala Thr Tyr Arg Glu
95 100 105
His Val Glu Ala Ile Lys Ile Gly Leu Thr Lys Ala Leu Thr Gln
110 115 120
Met Glu Glu Ala Gln Arg Lys Arg Thr Gln Leu Arg Glu Ala Phe
125 130 135
Glu Gln Leu Gln Ala Lys Lys Gln Met Ala Met Glu Lys Arg Arg
140 145 150
Ala Val Gln Asn Gln Trp Gln Leu Gln Gln Glu Lys His Leu Gln
155 160 165
His Leu Ala Glu Val Ser Ala Glu Val Arg Glu Arg Lys Thr Gly
170 175 180
Thr Gln Gln Glu Leu Asp Gly Val Phe Gln Lys Leu Gly Asn Leu
185 190 195
Lys Gln Gln Ala Glu Gln Glu Arg Asp Lys Leu Gln Arg Tyr Gln
200 205 210
Thr Phe Leu Gln Leu Leu Tyr Thr Leu Gln Gly Lys Leu Leu Phe
215 220 225
Pro Glu Ala Glu Ala Glu Ala Glu Asn Leu Pro Asp Asp Lys Pro
230 235 240
Gln Gln Pro Thr Arg Pro Gln Glu Gln Ser Thr Gly Asp Thr Met
245 250 255
Gly Arg Asp Pro Gly Val Ser Phe Lys Phe Ser Lys Ala Val Gly
260 265 270
Leu Gln Pro Ala Gly Asp Val Asn Leu Pro
275 280

<210> 21
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 2800717CD1

<400> 21
Met Gly Glu Asp Ala Ala Gln Ala Glu Lys Phe Gln His Pro Gly
1 5 10 15
Ser Asp Met Arg Gln Glu Lys Pro Ser Ser Pro Ser Pro Met Pro
20 25 30
Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly Asn Thr Glu Glu


```

35      40      45
Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr Val Leu Thr
50      55      60
Leu Leu Asp Lys Leu Val Asn Met Leu Asp Ala Val Gln Glu Asn
65      70      75
Gln His Lys Met Glu Gln Arg Gln Ile Ser Leu Glu Gly Ser Val
80      85      90
Lys Gly Ile Gln Asn Asp Leu Thr Lys Leu Ser Lys Tyr Gln Ala
95      100     105
Ser Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Ser Arg Lys
110     115     120
Val Ser Ala His Thr Arg Ala Val Lys Glu Arg Met Asp Arg Gln
125     130     135
Cys Ala Gln Val Lys Arg Leu Glu Asn Asn His Ala Gln Leu Leu
140     145     150
Arg Arg Asn His Phe Lys Val Leu Ile Phe Gln Glu Glu Asn Glu
155     160     165
Ile Pro Ala Ser Val Phe Val Lys Gln Pro Val Ser Gly Ala Val
170     175     180
Glu Gly Lys Glu Glu Leu Pro Asp Glu Asn Lys Ser Leu Glu Glu
185     190     195
Thr Leu His Thr Val Asp Leu Ser Ser Asp Asp Asp Leu Pro His
200     205     210
Asp Glu Glu Ala Leu Glu Asp Ser Ala Glu Glu Lys Val Glu Glu
215     220     225
Ser Arg Ala Glu Lys Ile Lys Arg Ser Ser Leu Lys Lys Val Asp
230     235     240
Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met
245     250     255
Asn Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys
260     265     270
Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly
275     280     285
Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys
290     295     300
Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser
305     310     315
Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu Glu
320     325     330
Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala
335     340     345
Leu Val Glu Gly Glu Ile Ala Glu Glu Ala Ala Glu Lys Ala Thr
350     355     360
Ser Arg Gly Ser Asn Ser Gly Met Asp Ser Asn Ile Asp Leu Thr
365     370     375
Ile Val Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala
380     385     390
Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu
395     400     405
Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln
410     415     420
Val His Gln Thr Ser
425

```

<210> 22

<211> 128

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5664154CD1

<400> 22

WO 01/07471

PCT/US00/19948

```

Met Glu Ser Lys Glu Glu Arg Ala Leu Asn Asn Leu Ile Val Glu
 1          5          10          15
Asn Val Asn Gln Glu Asn Asp Glu Lys Asp Glu Lys Glu Gln Val
          20          25          30
Ala Asn Lys Gly Glu Pro Leu Ala Leu Pro Leu Asn Val Ser Glu
          35          40          45
Tyr Cys Val Pro Arg Gly Asn Arg Arg Phe Arg Val Arg Gln
          50          55          60
Pro Ile Leu Gln Tyr Arg Trp Asp Ile Met His Arg Leu Gly Glu
          65          70          75
Pro Gln Ala Arg Met Arg Glu Glu Asn Met Glu Arg Ile Gly Glu
          80          85          90
Glu Val Arg Gln Leu Met Glu Lys Leu Arg Glu Lys Gln Leu Ser
          95          100          105
His Ser Leu Arg Ala Val Ser Thr Asp Pro Pro His His Asp His
          110          115          120
His Asp Glu Phe Cys Leu Met Pro
          125

```

```

<210> 23
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 017900CD1

```

```

<400> 23
Met Asp Gly Arg Val Gln Leu Ile Lys Ala Leu Leu Ala Leu Pro
 1          5          10          15
Ile Arg Pro Ala Thr Arg Arg Trp Arg Asn Pro Ile Pro Phe Pro
          20          25          30
Glu Thr Phe Asp Gly Asp Thr Asp Arg Leu Pro Glu Phe Ile Val
          35          40          45
Gln Thr Gly Ser Tyr Met Phe Val Asp Glu Asn Thr Phe Ser Ser
          50          55          60
Asp Ala Leu Lys Val Thr Phe Leu Ile Thr Arg Leu Thr Gly Pro
          65          70          75
Ala Leu Gln Trp Val Ile Pro Tyr Ile Lys Lys Glu Ser Pro Leu
          80          85          90
Leu Asn Asp Tyr Arg Gly Phe Leu Ala Glu Met Lys Arg Val Phe
          95          100          105
Gly Trp Glu Glu Asp Glu Asp Phe
          110

```

```

<210> 24
<211> 308
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Incyte ID No: 035102CD1

```

```

<400> 24
Met Leu Gln Thr Pro Glu Ser Arg Gly Leu Pro Val Pro Gln Ala
 1          5          10          15
Glu Gly Glu Lys Asp Gly Gly His Asp Gly Glu Thr Arg Ala Pro
          20          25          30
Thr Ala Ser Gln Glu Arg Pro Lys Glu Glu Leu Gly Ala Gly Arg
          35          40          45
Glu Glu Gly Ala Ala Glu Pro Ala Leu Thr Arg Lys Gly Ala Arg
          50          55          60
Ala Leu Ala Ala Lys Ser Leu Ala Arg Arg Arg Ala Tyr Arg Arg

```

WO 01/07471

PCT/US00/19948

	65		70		75
Leu Asn Arg Thr	Val Ala Glu Leu Val	Gln Phe Leu Leu Val	Lys		
	80		85		90
Asp Lys Lys Lys	Ser Pro Ile Thr Arg	Ser Glu Met Val Lys	Tyr		
	95		100		105
Val Ile Gly Asp	Leu Lys Ile Leu Phe	Pro Asp Ile Ile Ala	Arg		
	110		115		120
Ala Ala Glu His	Leu Arg Tyr Val Phe	Gly Phe Glu Leu Lys	Gln		
	125		130		135
Phe Asp Arg Lys	His His Thr Tyr Ile	Leu Ile Asn Lys Leu	Lys		
	140		145		150
Pro Leu Glu Glu	Glu Glu Glu Glu	Asp Leu Gly Gly Asp	Gly		
	155		160		165
Pro Arg Leu Gly	Leu Leu Met Met Ile	Leu Gly Leu Ile Tyr	Met		
	170		175		180
Arg Gly Asn Ser	Ala Arg Glu Ala Gln	Val Trp Glu Met Leu	Arg		
	185		190		195
Arg Leu Gly Val	Gln Pro Ser Lys Tyr	His Phe Leu Phe Gly	Tyr		
	200		205		210
Pro Lys Arg Leu	Ile Met Glu Asp Phe	Val Gln Gln Arg Tyr	Leu		
	215		220		225
Ser Tyr Arg Arg	Val Pro His Thr Asn	Pro Pro Ala Tyr Glu	Phe		
	230		235		240
Ser Trp Gly Pro	Arg Ser Asn Leu Glu	Ile Ser Lys Met Glu	Val		
	245		250		255
Leu Gly Phe Val	Ala Lys Leu His Lys	Lys Glu Pro Gln His	Trp		
	260		265		270
Pro Val Gln Tyr	Arg Glu Ala Leu Ala	Asp Glu Ala Asp Arg	Ala		
	275		280		285
Arg Ala Lys Ala	Arg Ala Glu Ala Ser	Met Arg Ala Arg Ala	Ser		
	290		295		300
Ala Arg Ala Gly	Ile His Leu Trp				
	305				

<210> 25

<211> 221

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 259983CD1

<400> 25

Met Phe Gly Phe	His Lys Pro Lys Met	Tyr Arg Ser Ile Glu Gly
1	5	10
Cys Cys Ile Cys	Arg Ala Lys Ser Ser	Ser Ser Arg Phe Thr Asp
	20	25
Ser Lys Arg Tyr	Glu Lys Asp Phe Gln	Ser Cys Phe Gly Leu His
	35	40
Glu Thr Arg Ser	Gly Asp Ile Cys Asn	Ala Cys Val Leu Leu Val
	50	55
Lys Arg Trp Lys	Lys Leu Pro Ala Gly	Ser Lys Lys Asn Trp Asn
	65	70
His Val Val Asp	Ala Arg Ala Gly Pro	Ser Leu Lys Thr Thr Leu
	80	85
Lys Pro Lys Lys	Val Lys Thr Leu Ser	Gly Asn Arg Ile Lys Ser
	95	100
Asn Gln Ile Ser	Lys Leu Gln Lys Glu	Phe Lys Arg His Asn Ser
	110	115
Asp Ala His Ser	Thr Thr Ser Ser Ala	Ser Pro Ala Gln Ser Pro
	125	130
Cys Tyr Ser Asn	Gln Ser Asp Asp Gly	Ser Asp Thr Glu Met Ala
	140	145
		150

WO 01/07471

PCT/US00/19948

Ser	Gly	Ser	Asn	Arg	Thr	Pro	Val	Phe	Ser	Phe	Leu	Asp	Leu	Thr
				155					160					165
Tyr	Trp	Lys	Arg	Gln	Lys	Ile	Cys	Cys	Gly	Ile	Ile	Tyr	Lys	Gly
				170					175					180
Arg	Phe	Gly	Glu	Val	Leu	Ile	Asp	Thr	His	Leu	Phe	Lys	Pro	Cys
				185					190					195
Cys	Ser	Asn	Lys	Lys	Ala	Ala	Ala	Glu	Lys	Pro	Glu	Glu	Gln	Gly
				200					205					210
Pro	Glu	Pro	Leu	Pro	Ile	Ser	Thr	Gln	Glu	Trp				
				215					220					

<210> 26

<211> 402

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 926810CD1

<400> 26

Met	Ala	Ser	Ile	Ile	Ala	Arg	Val	Gly	Asn	Ser	Arg	Arg	Leu	Asn
1				5					10					15
Ala	Pro	Leu	Pro	Pro	Trp	Ala	His	Ser	Met	Leu	Arg	Ser	Leu	Gly
				20					25					30
Arg	Ser	Leu	Gly	Pro	Ile	Met	Ala	Ser	Met	Ala	Asp	Arg	Asn	Met
				35					40					45
Lys	Leu	Phe	Ser	Gly	Arg	Val	Val	Pro	Ala	Gln	Gly	Glu	Glu	Thr
				50					55					60
Phe	Glu	Asn	Trp	Leu	Thr	Gln	Val	Asn	Gly	Val	Leu	Pro	Asp	Trp
				65					70					75
Asn	Met	Ser	Glu	Glu	Glu	Lys	Leu	Lys	Arg	Leu	Met	Lys	Thr	Leu
				80					85					90
Arg	Gly	Pro	Ala	Arg	Glu	Val	Met	Arg	Val	Leu	Gln	Ala	Thr	Asn
				95					100					105
Pro	Asn	Leu	Ser	Val	Ala	Asp	Phe	Leu	Arg	Ala	Met	Lys	Leu	Val
				110					115					120
Phe	Gly	Glu	Ser	Glu	Ser	Ser	Val	Thr	Ala	His	Gly	Lys	Phe	Phe
				125					130					135
Asn	Thr	Leu	Gln	Ala	Gln	Gly	Glu	Lys	Ala	Ser	Leu	Tyr	Val	Ile
				140					145					150
Arg	Leu	Glu	Val	Gln	Leu	Gln	Asn	Ala	Ile	Gln	Ala	Gly	Ile	Ile
				155					160					165
Ala	Glu	Lys	Asp	Ala	Asn	Arg	Thr	Arg	Leu	Gln	Gln	Leu	Leu	Leu
				170					175					180
Gly	Gly	Glu	Leu	Ser	Arg	Asp	Leu	Arg	Leu	Arg	Leu	Lys	Asp	Phe
				185					190					195
Leu	Arg	Met	Tyr	Ala	Asn	Glu	Gln	Glu	Arg	Leu	Pro	Asn	Phe	Leu
				200					205					210
Glu	Leu	Ile	Arg	Met	Val	Arg	Glu	Glu	Glu	Asp	Trp	Asp	Asp	Ala
				215					220					225
Phe	Ile	Lys	Arg	Lys	Arg	Pro	Lys	Arg	Ser	Glu	Ser	Met	Val	Glu
				230					235					240
Arg	Ala	Val	Ser	Pro	Val	Ala	Phe	Gln	Gly	Ser	Pro	Pro	Ile	Val
				245					250					255
Ile	Gly	Ser	Ala	Asp	Cys	Asn	Val	Ile	Glu	Ile	Asp	Asp	Thr	Leu
				260					265					270
Asp	Asp	Ser	Asp	Glu	Asp	Val	Ile	Leu	Val	Glu	Ser	Gln	Asp	Pro
				275					280					285
Pro	Leu	Pro	Ser	Trp	Gly	Ala	Pro	Pro	Leu	Arg	Asp	Arg	Ala	Arg
				290					295					300
Pro	Gln	Asp	Glu	Val	Leu	Val	Ile	Asp	Ser	Pro	His	Asn	Ser	Arg
				305					310					315
Ala	Gln	Phe	Pro	Ser	Thr	Ser	Gly	Gly	Ser	Gly	Tyr	Lys	Asn	Asn

22/93

WO 01/07471

PCT/US00/19948

Asp Asp Lys Gly	215	Ala Gln Ala Ala Arg	220	Gly Ser Ser Asn Ala	225
	230		235		240
Leu Lys Glu Glu	245	Glu Cys Lys Glu Pro	250	Leu Leu Phe His Ser	255
Asp His Tyr Pro	260	Leu Ser Asp Gly Asp	265	Trp Ser Pro Leu Glu	270
Thr Tyr Pro Gln	275	Thr Ala Cys Pro Lys	280	Ser Asp Ser Glu Leu	285
Val Lys Pro Ala	290	Glu Ser Leu Leu Arg	295	Ser Glu Tyr His Met	300
Trp Thr Trp Gly	305	Gly Phe Pro Glu Ser	310	Thr Lys Val Ser Lys	315
Glu Arg Ser Asp	320	His His Pro Arg Thr	325	Ala Thr Ile Thr Pro	330
Glu Asn Thr His	335	Phe Arg Val Ile Pro	340	Ser Glu Asp Asn Leu	345
Ser Glu Val Glu	350	Lys Asp Ala Ser Met	355	Glu Asp Thr Val Cys	360
Ile Val Lys Pro	365	Lys Pro Arg Ala Leu	370	Gly Thr Gln Met Ser	375
Pro Thr Ser Val	380	Ala Glu Leu Leu Glu	385	Pro Pro Leu Glu Ser	390
Gln Ile Ser Ser	395	Met Leu Asp Ala Asp	400	His Leu Pro Asn Ala	405
Leu Ala Glu Ala	410	Pro Ser Glu Ser Lys	415	Pro Ala Ala Lys Val	420
Ser Pro Ser Lys	425	Lys Lys Gly Val His	430	Lys Arg Ile Gln His	435
Gly Pro Asp Asp	440	Ile Tyr Leu Asp Asp	445	Leu Lys Gly Leu Glu	450
Glu Val Ala Ala	455	Leu Tyr Phe Pro Lys	460	Ser Glu Ser Glu Pro	465
Ser Arg Gln Trp	470	Pro Glu Ser Asp Thr	475	Leu Ser Gly Ser Gln	480
Pro Gln Ser Val	485	Gly Ser Ala Ala Ala	490	Asp Ser Gly Thr Glu	495
Leu Ser Asp Ser	500	Ala Met Asp Leu Pro	505	Asp Val Thr Leu Ser	510
Cys Gly Gly Leu	515	Ser Glu Asn Gly Lys	520	Ile Ser Lys Glu Lys	525
Met Glu His Ile	530	Ile Thr Tyr His Glu	535	Phe Ala Glu Asn Pro	540
Leu Ile Asp Asn	545	Pro Asn Leu Val Ile	550	Arg Ile Tyr Asn Arg	555
Tyr Asn Trp Ala	560	Leu Ala Ala Pro Met	565	Ile Leu Ser Leu Gln	570
Phe Gln Lys Ser	575	Leu Pro Lys Ala Thr	580	Val Glu Ser Trp Val	585
Asp Lys Met Pro	590	Lys Lys Ser Gly Arg	595	Trp Trp Phe Trp Arg	600
Arg Glu Ser Met	605	Thr Lys Gln Leu Pro	610	Glu Ser Lys Glu Gly	615
Ser Glu Ala Pro	620	Pro Ala Ser Asp Leu	625	Pro Ser Ser Ser Lys	630
Pro Ala Gly Ala	635	Arg Pro Ala Glu Asn	640	Asp Ser Ser Ser Asp	645
Gly Ser Gln Glu	650	Leu Glu Glu Ser Ile	655	Thr Val Asp Pro Ile	660
Thr Glu Pro Leu	665	Ser His Gly Ser Thr	670	Thr Ser Tyr Lys Lys	675
Leu Arg Leu Ser	680	Ser Asp Gln Ile Ala	685	Lys Leu Lys Leu His	690

WO 01/07471

PCT/US00/19948

Gly	Pro	Asn	Asp	Val	Val	Phe	Ser	Ile	Thr	Thr	Gln	Tyr	Gln	Gly
				695					700					705
Thr	Cys	Arg	Cys	Ala	Gly	Thr	Ile	Tyr	Leu	Trp	Asn	Trp	Asn	Asp
				710					715					720
Lys	Ile	Ile	Ile	Ser	Asp	Ile	Asp	Gly	Thr	Ile	Thr	Lys	Ser	Asp
				725					730					735
Ala	Leu	Gly	Gln	Ile	Leu	Pro	Gln	Leu	Gly	Lys	Asp	Trp	Thr	His
				740					745					750
Gln	Gly	Ile	Ala	Lys	Leu	Tyr	His	Ser	Ile	Asn	Glu	Asn	Gly	Tyr
				755					760					765
Lys	Phe	Leu	Tyr	Cys	Ser	Ala	Arg	Ala	Ile	Gly	Met	Ala	Asp	Met
				770					775					780
Thr	Arg	Gly	Tyr	Leu	His	Trp	Val	Asn	Asp	Lys	Gly	Thr	Ile	Leu
				785					790					795
Pro	Arg	Gly	Pro	Leu	Met	Leu	Ser	Pro	Ser	Ser	Leu	Phe	Ser	Ala
				800					805					810
Phe	His	Arg	Glu	Val	Ile	Glu	Lys	Lys	Pro	Glu	Lys	Phe	Lys	Ile
				815					820					825
Glu	Cys	Leu	Asn	Asp	Ile	Lys	Asn	Leu	Phe	Ala	Pro	Ser	Lys	Gln
				830					835					840
Pro	Phe	Tyr	Ala	Ala	Phe	Gly	Asn	Arg	Pro	Asn	Asp	Val	Tyr	Ala
				845					850					855
Tyr	Thr	Gln	Val	Gly	Val	Pro	Asp	Cys	Arg	Ile	Phe	Thr	Val	Asn
				860					865					870
Pro	Lys	Gly	Glu	Leu	Ile	Gln	Glu	Arg	Thr	Lys	Gly	Asn	Lys	Ser
				875					880					885
Ser	Tyr	His	Arg	Leu	Ser	Glu	Leu	Val	Glu	His	Val	Phe	Pro	Leu
				890					895					900
Leu	Ser	Lys	Glu	Gln	Asn	Ser	Ala	Phe	Pro	Cys	Pro	Glu	Phe	Ser
				905					910					915
Ser	Phe	Cys	Tyr	Trp	Arg	Asp	Pro	Ile	Pro	Glu	Val	Asp	Leu	Asp
				920					925					930

Asp Leu Ser

<210> 32

<211> 268

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1708229CD1

<400> 32

Met	Leu	Gly	Asp	His	Cys	Ser	Leu	Pro	Glu	Asp	Gln	Ala	Arg	Pro
1				5					10					15
Gly	Gln	Ser	Leu	Gln	Ser	Gly	Leu	Cys	Cys	Lys	Met	Val	Leu	Gln
				20					25					30
Ala	Val	Ser	Lys	Val	Leu	Arg	Lys	Ser	Lys	Ala	Lys	Pro	Asn	Gly
				35					40					45
Lys	Lys	Pro	Ala	Ala	Glu	Glu	Arg	Lys	Ala	Tyr	Leu	Glu	Pro	Glu
				50					55					60
His	Thr	Lys	Ala	Arg	Ile	Thr	Asp	Phe	Gln	Phe	Lys	Glu	Leu	Val
				65					70					75
Val	Leu	Pro	Arg	Glu	Ile	Asp	Leu	Asn	Glu	Trp	Leu	Ala	Ser	Asn
				80					85					90
Thr	Thr	Thr	Phe	Phe	His	His	Ile	Asn	Leu	Gln	Tyr	Ser	Thr	Ile
				95					100					105
Ser	Glu	Phe	Cys	Thr	Gly	Glu	Thr	Cys	Gln	Thr	Met	Ala	Val	Cys
				110					115					120
Asn	Thr	Gln	Tyr	Tyr	Trp	Tyr	Asp	Glu	Arg	Gly	Lys	Lys	Val	Lys
				125					130					135
Cys	Thr	Ala	Pro	Gln	Tyr	Val	Asp	Phe	Val	Met	Ser	Ser	Val	Gln

WO 01/07471

PCT/US00/19948

	140		145		150
Lys Leu Val Thr	Asp Glu Asp Val Phe	Pro Thr Lys Tyr Gly	Arg		
	155		160		165
Glu Phe Pro Ser	Ser Phe Glu Ser Leu	Val Arg Lys Ile Cys	Arg		
	170		175		180
His Leu Phe His	Val Leu Ala His Ile	Tyr Trp Ala His Phe	Lys		
	185		190		195
Glu Thr Leu Ala	Leu Glu Leu His Gly	His Leu Asn Thr Leu	Tyr		
	200		205		210
Val His Phe Ile	Leu Phe Ala Arg Glu	Phe Asn Leu Leu Asp	Pro		
	215		220		225
Lys Glu Thr Ala	Ile Met Asp Asp Leu	Thr Glu Val Leu Cys	Ser		
	230		235		240
Gly Ala Gly Gly	Val His Ser Gly Gly	Ser Gly Asp Gly Ala	Gly		
	245		250		255
Ser Gly Gly Pro	Gly Ala Gln Asn His	Val Lys Glu Arg			
	260		265		

<210> 33'

<211> 337

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1806454CD1

<400> 33

Met Leu Leu Gly Leu	Ala Ala Met Glu Leu	Lys Val Trp Val Asp	
1	5	10	15
Gly Ile Gln Arg Val	Val Cys Gly Val Ser	Glu Gln Thr Thr Cys	
	20	25	30
Gln Glu Val Val Ile	Ala Leu Ala Gln Ala	Ile Gly Gln Thr Gly	
	35	40	45
Arg Phe Val Leu Val	Gln Arg Leu Arg Glu	Lys Glu Arg Gln Leu	
	50	55	60
Leu Pro Gln Glu Cys	Pro Val Gly Ala Gln	Ala Thr Cys Gly Gln	
	65	70	75
Phe Ala Ser Asp Val	Gln Phe Val Leu Arg	Arg Thr Gly Pro Ser	
	80	85	90
Leu Ala Gly Arg Pro	Ser Ser Asp Ser Cys	Pro Pro Pro Glu Arg	
	95	100	105
Cys Leu Ile Arg Ala	Ser Leu Pro Val Lys	Pro Arg Ala Ala Leu	
	110	115	120
Gly Cys Glu Pro Arg	Lys Thr Leu Thr Pro	Glu Pro Ala Pro Ser	
	125	130	135
Leu Ser Arg Pro Gly	Pro Ala Ala Pro Val	Thr Pro Thr Pro Gly	
	140	145	150
Cys Cys Thr Asp Leu	Arg Gly Leu Glu Leu	Arg Val Gln Arg Asn	
	155	160	165
Ala Glu Glu Leu Gly	His Glu Ala Phe Trp	Glu Gln Glu Leu Arg	
	170	175	180
Arg Glu Gln Ala Arg	Glu Arg Glu Gly Gln	Ala Arg Leu Gln Ala	
	185	190	195
Leu Ser Ala Ala Thr	Ala Glu His Ala Ala	Arg Leu Gln Ala Leu	
	200	205	210
Asp Ala Gln Ala Arg	Ala Leu Glu Ala Glu	Leu Gln Leu Ala Ala	
	215	220	225
Glu Ala Pro Gly Pro	Pro Ser Pro Met Ala	Ser Ala Thr Glu Arg	
	230	235	240
Leu His Gln Asp Leu	Ala Val Gln Glu Arg	Gln Ser Ala Glu Val	
	245	250	255
Gln Gly Ser Leu Ala	Leu Val Ser Arg Ala	Leu Glu Ala Ala Glu	
	260	265	270

WO 01/07471

PCT/US00/19948

Arg	Ala	Leu	Gln	Ala	Gln	Ala	Gln	Glu	Leu	Glu	Glu	Leu	Asn	Arg
				275					280					285
Glu	Leu	Arg	Gln	Cys	Asn	Leu	Gln	Gln	Phe	Ile	Gln	Gln	Thr	Gly
				290					295					300
Ala	Ala	Leu	Pro	Pro	Pro	Pro	Arg	Pro	Asp	Arg	Gly	Pro	Pro	Gly
				305					310					315
Thr	Gln	Val	Gly	Val	Val	Leu	Gly	Gly	Gly	Trp	Glu	Val	Arg	Thr
				320					325					330
Trp	Pro	Ser	Pro	Thr	Pro	Ser								
				335										

<210> 34

<211> 565

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1806850CD1

<400> 34

Met	Lys	Glu	Glu	Glu	Glu	Val	Phe	Gln	Pro	Met	Leu	Met	Glu	Tyr
1				5					10					15
Phe	Thr	Tyr	Glu	Glu	Leu	Lys	Tyr	Ile	Lys	Lys	Lys	Val	Ile	Ala
				20					25					30
Gln	His	Cys	Ser	Gln	Lys	Asp	Thr	Ala	Glu	Leu	Leu	Arg	Gly	Leu
				35					40					45
Ser	Leu	Trp	Asn	His	Ala	Glu	Glu	Arg	Gln	Lys	Phe	Phe	Lys	Tyr
				50					55					60
Ser	Val	Asp	Glu	Lys	Ser	Asp	Lys	Glu	Ala	Glu	Val	Ser	Glu	His
				65					70					75
Ser	Thr	Gly	Ile	Thr	His	Leu	Pro	Pro	Glu	Val	Met	Leu	Ser	Ile
				80					85					90
Phe	Ser	Tyr	Leu	Asn	Pro	Gln	Glu	Leu	Cys	Arg	Cys	Ser	Gln	Val
				95					100					105
Ser	Met	Lys	Trp	Ser	Gln	Leu	Thr	Lys	Thr	Gly	Ser	Leu	Trp	Lys
				110					115					120
His	Leu	Tyr	Pro	Val	His	Trp	Ala	Arg	Gly	Asp	Trp	Tyr	Ser	Gly
				125					130					135
Pro	Ala	Thr	Glu	Leu	Asp	Thr	Glu	Pro	Asp	Asp	Glu	Trp	Val	Lys
				140					145					150
Asn	Arg	Lys	Asp	Glu	Ser	Arg	Ala	Phe	His	Glu	Trp	Asp	Glu	Asp
				155					160					165
Ala	Asp	Ile	Asp	Glu	Ser	Glu	Glu	Ser	Ala	Glu	Glu	Ser	Ile	Ala
				170					175					180
Ile	Ser	Ile	Ala	Gln	Met	Glu	Lys	Arg	Leu	Leu	His	Gly	Leu	Ile
				185					190					195
His	Asn	Val	Leu	Pro	Tyr	Val	Gly	Thr	Ser	Val	Lys	Thr	Leu	Val
				200					205					210
Leu	Ala	Tyr	Ser	Ser	Ala	Val	Ser	Ser	Lys	Met	Val	Arg	Gln	Ile
				215					220					225
Leu	Glu	Leu	Cys	Pro	Asn	Leu	Glu	His	Leu	Asp	Leu	Thr	Gln	Thr
				230					235					240
Asp	Ile	Ser	Asp	Ser	Ala	Phe	Asp	Ser	Trp	Ser	Trp	Leu	Gly	Cys
				245					250					255
Cys	Gln	Ser	Leu	Arg	His	Leu	Asp	Leu	Ser	Gly	Cys	Glu	Lys	Ile
				260					265					270
Thr	Asp	Val	Ala	Leu	Glu	Lys	Ile	Ser	Arg	Ala	Leu	Gly	Ile	Leu
				275					280					285
Thr	Ser	His	Gln	Ser	Gly	Phe	Leu	Lys	Thr	Ser	Thr	Ser	Lys	Ile
				290					295					300
Thr	Ser	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Ile	Thr	Met	Gln	Ser	Thr
				305					310					315
Lys	Gln	Tyr	Ala	Cys	Leu	His	Asp	Leu	Thr	Asn	Lys	Gly	Ile	Gly

WO 01/07471

PCT/US00/19948

	320		325		330
Glu Glu Ile Asp	Asn Glu His Pro Trp	Thr Lys Pro Val Ser	Ser		
	335		340		345
Glu Asn Phe Thr	Ser Pro Tyr Val Trp	Met Leu Asp Ala Glu	Asp		
	350		355		360
Leu Ala Asp Ile	Glu Asp Thr Val Glu	Trp Arg His Arg Asn	Val		
	365		370		375
Glu Ser Leu Cys	Val Met Glu Thr Ala	Ser Asn Phe Ser Cys	Ser		
	380		385		390
Thr Ser Gly Cys	Phe Ser Lys Asp Ile	Val Gly Leu Arg Thr	Ser		
	395		400		405
Val Cys Trp Gln	Gln His Cys Ala Ser	Pro Ala Phe Ala Tyr	Cys		
	410		415		420
Gly His Ser Phe	Cys Cys Thr Gly Thr	Ala Leu Arg Thr Met	Ser		
	425		430		435
Ser Leu Pro Glu	Ser Ser Ala Met Cys	Arg Lys Ala Ala Arg	Thr		
	440		445		450
Arg Leu Pro Arg	Gly Lys Asp Leu Ile	Tyr Phe Gly Ser Glu	Lys		
	455		460		465
Ser Asp Gln Glu	Thr Gly Arg Val Leu	Leu Phe Leu Ser Leu	Ser		
	470		475		480
Gly Cys Tyr Gln	Ile Thr Asp His Gly	Leu Arg Val Leu Thr	Leu		
	485		490		495
Gly Gly Gly Leu	Pro Tyr Leu Glu His	Leu Asn Leu Ser Gly	Cys		
	500		505		510
Leu Thr Ile Thr	Gly Ala Gly Leu Gln	Asp Leu Val Ser Ala	Cys		
	515		520		525
Pro Ser Leu Asn	Asp Glu Tyr Phe Tyr	Tyr Cys Asp Asn Ile	Asn		
	530		535		540
Gly Pro His Ala	Asp Thr Ala Ser Gly	Cys Gln Asn Leu Gln	Cys		
	545		550		555
Gly Phe Arg Ala	Cys Cys Arg Ser Gly	Glu			
	560		565		

<210> 35

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1851534CD1

<400> 35

Met Asp Phe Ser	Phe Ser Phe Met Gln	Gly Ile Met Gly Asn	Thr
1	5	10	15
Ile Gln Gln Pro	Pro Gln Leu Ile Asp	Ser Ala Asn Ile Arg	Gln
	20	25	30
Glu Asp Ala Phe	Asp Asn Asn Ser Asp	Ile Ala Glu Asp Gly	Gly
	35	40	45
Gln Thr Pro Tyr	Glu Ala Thr Leu Gln	Gln Gly Phe Gln Tyr	Pro
	50	55	60
Ala Thr Thr Glu	Asp Leu Pro Pro Leu	Thr Asn Gly Tyr Pro	Ser
	65	70	75
Ser Ile Ser Val	Tyr Glu Thr Gln Thr	Lys Tyr Gln Ser Tyr	Asn
	80	85	90
Gln Tyr Pro Asn	Gly Ser Ala Asn Gly	Phe Gly Ala Val Arg	Asn
	95	100	105
Phe Ser Pro Thr	Asp Tyr Tyr His Ser	Glu Ile Pro Asn Thr	Arg
	110	115	120
Pro His Glu Ile	Leu Glu Lys Pro Ser	Pro Pro Gln Pro Pro	Pro
	125	130	135
Pro Pro Ser Val	Pro Gln Thr Val Ile	Pro Lys Lys Thr Gly	Ser
	140	145	150

WO 01/07471

PCT/US00/19948

Pro Glu Ile Lys Leu Lys Ile Thr Lys Thr Ile Gln Asn Gly Arg
 155 160 165
 Glu Leu Phe Glu Ser Leu Cys Gly Asp Leu Leu Asn Glu Val
 170 175 180
 Gln Ala Ser Glu His Thr Lys Ser Lys His Glu Ser Arg Lys Glu
 185 190 195
 Lys Arg Lys Lys Ser Asn Lys His Asp Ser Ser Arg Ser Glu Glu
 200 205 210
 Arg Lys Ser His Lys Ile Pro Lys Leu Glu Pro Glu Glu Gln Asn
 215 220 225
 Met Thr Lys

<210> 36
 <211> 495
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1868749CD1

<400> 36
 Met Lys Gly Met Lys Val Glu Val Leu Asn Ser Asp Ala Val Leu
 1 5 10 15
 Pro Ser Arg Val Tyr Trp Ile Ala Ser Val Ile Gln Thr Ala Gly
 20 25 30
 Tyr Arg Val Leu Leu Arg Tyr Glu Gly Phe Glu Asn Asp Ala Ser
 35 40 45
 His Asp Phe Trp Cys Asn Leu Gly Thr Val Asp Val His Pro Ile
 50 55 60
 Gly Trp Cys Ala Ile Asn Ser Lys Ile Leu Val Pro Pro Arg Thr
 65 70 75
 Ile His Ala Lys Phe Thr Asp Trp Lys Gly Tyr Leu Met Lys Arg
 80 85 90
 Leu Val Gly Ser Arg Thr Leu Pro Val Asp Phe His Ile Lys Met
 95 100 105
 Val Glu Ser Met Lys Tyr Pro Phe Arg Gln Gly Met Arg Leu Glu
 110 115 120
 Val Val Asp Lys Ser Gln Val Ser Arg Thr Arg Met Ala Val Val
 125 130 135
 Asp Thr Val Ile Gly Gly Arg Leu Arg Leu Leu Tyr Glu Asp Gly
 140 145 150
 Asp Ser Asp Asp Asp Phe Trp Cys His Met Trp Ser Pro Leu Ile
 155 160 165
 His Pro Val Gly Trp Ser Arg Arg Val Gly His Gly Ile Lys Met
 170 175 180
 Ser Glu Arg Arg Ser Asp Met Ala His His Pro Thr Phe Arg Lys
 185 190 195
 Ile Tyr Cys Asp Ala Val Pro Tyr Leu Phe Lys Lys Val Arg Ala
 200 205 210
 Val Tyr Thr Glu Gly Gly Trp Phe Glu Glu Gly Met Lys Leu Glu
 215 220 225
 Ala Ile Asp Pro Leu Asn Leu Gly Asn Ile Cys Val Ala Thr Val
 230 235 240
 Cys Lys Val Leu Leu Asp Gly Tyr Leu Met Ile Cys Val Asp Gly
 245 250 255
 Gly Pro Ser Thr Asp Gly Leu Asp Trp Phe Cys Tyr His Ala Ser
 260 265 270
 Ser His Ala Ile Phe Pro Ala Thr Phe Cys Gln Lys Asn Asp Ile
 275 280 285
 Glu Leu Thr Pro Pro Lys Gly Tyr Glu Ala Gln Thr Phe Asn Trp
 290 295 300
 Glu Asn Tyr Leu Glu Lys Thr Lys Ser Lys Ala Ala Pro Ser Arg

WO 01/07471

PCT/US00/19948

Leu Phe Asn Met	305	Asp Cys Pro Asn His	310	Gly Phe Lys Val Gly	315
	320		325		330
Lys Leu Glu Ala	335	Val Asp Leu Met Glu	340	Pro Arg Leu Ile Cys	345
	350		355		360
Ala Thr Val Lys	365	Arg Val Val His Arg	370	Leu Leu Ser Ile His	375
	380		385		390
Asp Gly Trp Asp	395	Ser Glu Tyr Asp Gln	400	Trp Val Asp Cys Glu	405
	410		415		420
Pro Asp Ile Tyr	425	Pro Val Gly Trp Cys	430	Glu Leu Thr Gly Tyr	435
	440		445		450
Leu Gln Pro Pro	455	Val Ala Ala Glu Pro	460	Ala Thr Pro Leu Lys	465
	470		475		480
Lys Glu Ala Thr	485	Lys Lys Lys Lys Lys	490	Gln Phe Gly Lys Lys	495
Lys Arg Ile Pro		Pro Thr Lys Thr Arg		Pro Leu Arg Gln Gly	
Lys Lys Pro Leu		Leu Glu Asp Asp Pro		Gln Gly Ala Arg Lys	
Ser Ser Glu Pro		Val Pro Gly Glu Ile		Ile Ala Val Arg Val	
Glu Glu His Leu		Asp Val Ala Ser Pro		Asp Lys Ala Ser Ser	
Glu Leu Pro Val		Ser Val Glu Asn Ile		Lys Gln Glu Thr Asp	

<210> 37

<211> 1336

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1980010CD1

<400> 37

Met Val Asp Gln	Leu Glu Gln Ile	Leu Ser Val	Ser Glu Leu Leu
1	5	10	15
Glu Lys His Gly	Leu Glu Lys Pro	Ile Ser Phe	Val Lys Asn Thr
20	25		30
Gln Ser Ser Ser	Glu Glu Ala Arg	Lys Leu Met	Val Arg Leu Thr
35	40		45
Arg His Thr Gly	Arg Lys Gln Pro	Pro Val Ser	Glu Ser His Trp
50	55		60
Arg Thr Leu Leu	Gln Asp Met Leu	Thr Met Gln	Gln Asn Val Tyr
65	70		75
Thr Cys Leu Asp	Ser Asp Ala Cys	Tyr Glu Ile	Phe Thr Glu Ser
80	85		90
Leu Leu Cys Ser	Ser Arg Leu Glu	Asn Ile His	Leu Ala Gly Gln
95	100		105
Met Met His Cys	Ser Ala Cys Ser	Glu Asn Pro	Pro Ala Gly Ile
110	115		120
Ala His Lys Gly	Asn Pro His Tyr	Arg Val Ser	Tyr Glu Lys Ser
125	130		135
Ile Asp Leu Val	Leu Ala Ala Ser	Arg Glu Tyr	Phe Asn Ser Ser
140	145		150
Thr Asn Leu Thr	Asp Ser Cys Met	Asp Leu Ala	Arg Cys Cys Leu
155	160		165
Gln Leu Ile Thr	Asp Arg Pro Pro	Ala Ile Gln	Glu Glu Leu Asp
170	175		180
Leu Ile Gln Ala	Val Gly Cys Leu	Glu Phe Gly	Val Lys Ile
185	190		195
Leu Pro Leu Gln	Val Arg Leu Cys	Pro Asp Arg	Ile Ser Leu Ile

WO 01/07471

PCT/US00/19948

Lys Glu Cys Ile	200	Ser Gln Ser Pro Thr	205	Cys Tyr Lys Gln Ser Thr	210
Lys Leu Leu Gly	215	Leu Ala Glu Leu Leu	220	Arg Val Ala Gly Glu Asn	225
Pro Glu Glu Arg	230	Arg Gly Gln Val Leu	235	Ile Leu Leu Val Glu Gln	240
Ala Leu Arg Phe	245	His Asp Tyr Lys Ala	250	Ala Ser Met His Cys Gln	255
Glu Leu Met Ala	260	Thr Gly Tyr Pro Lys	265	Ser Trp Asp Val Cys Ser	270
Gln Leu Gly Gln	275	Ser Glu Gly Tyr Gln	280	Leu Ala Thr Arg Gln	285
Glu Leu Met Ala	290	Phe Ala Leu Thr His	295	Cys Pro Pro Ser Ser Ile	300
Glu Leu Leu Leu	305	Ala Ala Ser Ser Ser	310	Leu Gln Thr Glu Ile Leu	315
Tyr Gln Arg Val	320	Asn Phe Gln Ile His	325	His Glu Gly Gly Glu Asn	330
Ile Ser Ala Ser	335	Pro Leu Thr Ser Lys	340	Ala Val Gln Glu Asp Glu	345
Val Gly Val Pro	350	Gly Ser Asn Ser Ala	355	Asp Leu Leu Arg Trp Thr	360
Thr Ala Thr Thr	365	Met Lys Val Leu Ser	370	Asn Thr Thr Thr Thr	375
Lys Ala Val Leu	380	Gln Ala Val Ser Asp	385	Gly Gln Trp Trp Lys Lys	390
Ser Leu Thr Tyr	395	Leu Arg Pro Leu Gln	400	Gly Gln Lys Cys Gly Gly	405
Ala Tyr Gln Ile	410	Gly Thr Thr Ala Asn	415	Glu Asp Leu Glu Lys Gln	420
Gly Cys His Pro	425	Phe Tyr Glu Ser Val	430	Ile Ser Asn Pro Phe Val	435
Ala Glu Ser Glu	440	Gly Thr Tyr Asp Thr	445	Tyr Gln His Val Pro Val	450
Glu Ser Phe Ala	455	Glu Val Leu Leu Arg	460	Thr Gly Lys Leu Ala Glu	465
Ala Lys Asn Lys	470	Gly Glu Val Phe Pro	475	Thr Thr Glu Val Leu Leu	480
Gln Leu Ala Ser	485	Glu Ala Leu Pro Asn	490	Asp Met Thr Leu Ala Leu	495
Ala Tyr Leu Leu	500	Ala Leu Pro Gln Val	505	Leu Asp Ala Asn Arg Cys	510
Phe Glu Lys Gln	515	Ser Pro Ser Ala Leu	520	Ser Leu Gln Leu Ala Ala	525
Tyr Tyr Tyr Ser	530	Leu Gln Ile Tyr Ala	535	Arg Leu Ala Pro Cys Phe	540
Arg Asp Lys Cys	545	His Pro Leu Tyr Arg	550	Ala Asp Pro Lys Glu Leu	555
Ile Lys Met Val	560	Thr Arg His Val Thr	565	Arg His Glu His Glu Ala	570
Trp Pro Glu Asp	575	Leu Ile Ser Leu Thr	580	Lys Gln Leu His Cys Tyr	585
Asn Glu Arg Leu	590	Leu Asp Phe Thr Gln	595	Ala Gln Ile Leu Gln Gly	600
Leu Arg Lys Gly	605	Val Asp Val Gln Arg	610	Phe Thr Ala Asp Asp Gln	615
Tyr Lys Arg Glu	620	Thr Ile Leu Gly Leu	625	Ala Glu Thr Leu Glu Glu	630
Ser Val Tyr Ser	635	Ile Ala Ile Ser Leu	640	Ala Gln Arg Tyr Ser Val	645
Ser Arg Trp Glu	650	Val Phe Met Thr His	655	Leu Glu Phe Leu Phe Thr	660
	665		670		675

33/93

WO 01/07471

PCT/US00/19948

1145	1150	1155
Val Ile Thr Asn Asn Pro Trp Val Arg Leu Ala Thr Val Met Leu		
1160	1165	1170
Thr Arg Cys Thr Met Glu Asn Lys Glu Gly Leu Gly Asn Glu Val		
1175	1180	1185
Leu Lys Met Cys Arg Ser Leu Tyr Asn Thr Lys Gln Met Leu Pro		
1190	1195	1200
Ala Glu Gly Val Lys Glu Leu Cys Leu Leu Leu Leu Asn Gln Ser		
1205	1210	1215
Leu Leu Leu Pro Ser Leu Lys Leu Leu Leu Glu Ser Arg Asp Glu		
1220	1225	1230
His Leu His Glu Met Ala Leu Glu Gln Ile Thr Ala Val Thr Thr		
1235	1240	1245
Val Asn Asp Ser Asn Cys Asp Gln Glu Leu Leu Ser Leu Leu Leu		
1250	1255	1260
Asp Ala Lys Leu Leu Val Lys Cys Val Ser Thr Pro Phe Tyr Pro		
1265	1270	1275
Arg Ile Val Asp His Leu Leu Ala Ser Leu Gln Gln Gly Arg Trp		
1280	1285	1290
Asp Ala Glu Glu Leu Gly Arg His Leu Arg Glu Ala Gly His Glu		
1295	1300	1305
Ala Glu Ala Gly Ser Leu Leu Leu Ala Val Arg Gly Thr His Gln		
1310	1315	1320
Ala Phe Arg Thr Phe Ser Thr Ala Leu Arg Ala Ala Gln His Trp		
1325	1330	1335
Val		

<210> 38

<211> 934

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2259032CD1

<400> 38

Met Phe Trp Lys Phe Asp Leu Asn Thr Thr Ser His Val Asp Lys		
1	5	10
Leu Leu Asp Lys Glu His Val Thr Leu Gln Glu Leu Met Asp Glu		
	20	25
Asp Asp Ile Leu Gln Glu Cys Lys Ala Gln Asn Gln Lys Leu Leu		
	35	40
Asp Phe Leu Cys Arg Gln Gln Cys Met Glu Glu Leu Val Ser Leu		
	50	55
Ile Thr Gln Asp Pro Pro Leu Asp Met Glu Glu Lys Val Arg Phe		
	65	70
Lys Tyr Pro Asn Thr Ala Cys Glu Leu Leu Thr Cys Asp Val Pro		
	80	85
Gln Ile Ser Asp Arg Leu Gly Gly Asp Glu Ser Leu Leu Ser Leu		
	95	100
Leu Tyr Asp Phe Leu Asp His Glu Pro Pro Leu Asn Pro Leu Leu		
	110	115
Ala Ser Phe Phe Ser Lys Thr Ile Gly Asn Leu Ile Ala Arg Lys		
	125	130
Thr Glu Gln Val Ile Thr Phe Leu Lys Lys Lys Asp Lys Phe Ile		
	140	145
Ser Leu Val Leu Lys His Ile Gly Thr Ser Ala Leu Met Asp Leu		
	155	160
Leu Leu Arg Leu Val Ser Cys Val Glu Pro Ala Gly Leu Arg Gln		
	170	175
Asp Val Leu His Trp Leu Asn Glu Glu Lys Val Ile Gln Arg Leu		
	185	190

PCT/US00/19948

35/93

WO 01/07471

PCT/US00/19948

Pro Pro Val Glu	665	Gly Asp Ser Glu Ala	670	Gly Ala Met Trp Thr	675
Val Phe Asp Glu	680	Pro Ala Asn Ser Thr	685	Pro Thr Ala Pro Gly	690
Val Arg Asp Val	695	Gly Ser Ser Val Trp	700	Ala Ala Gly Thr Ser	705
Pro Glu Glu Lys	710	Gly Trp Ala Lys Phe	715	Thr Asp Phe Gln Pro	720
Cys Cys Ser Glu	725	Ser Gly Pro Arg Cys	730	Ser Ser Pro Val Asp	735
Glu Cys Ser His	740	Ala Glu Gly Ser Arg	745	Ser Gln Gly Pro Glu	750
Ala Phe Ser Pro	755	Ala Ser Pro Cys Ala	760	Thr Asn Val Cys Val	765
Arg Lys Ala Pro	770	Leu Leu Ala Ser Asp	775	Ser Ser Ser Ser Gly	780
Ser His Ser Glu	785	Asp Gly Asp Gln Lys	790	Ala Ala Ser Ala Met	795
Ala Val Ser Arg	800	Gly Pro Gly Arg Glu	805	Ala Pro Pro Leu Pro	810
Val Ala Arg Thr	815	Glu Glu Ala Val Gly	820	Arg Val Gly Cys Ala	825
Ser Arg Leu Leu	830	Ser Pro Ala Cys Pro	835	Ala Pro Lys Glu Val	840
Ala Ala Pro Ala	845	Val Ala Val Pro Pro	850	Glu Ala Thr Val Ala	855
Thr Thr Ala Leu	860	Ser Lys Ala Gly Pro	865	Ala Ile Pro Thr Pro	870
Val Ser Ser Ala	875	Leu Ala Val Ala Val	880	Pro Leu Gly Pro Ile	885
Ala Val Thr Ala	890	Ala Pro Ala Met Val	895	Ala Thr Leu Gly Thr	900
Thr Lys Asp Gly	905	Lys Thr Asp Ala Pro	910	Pro Glu Gly Ala Ala	915
Asn Gly Pro Val	920		925		930

<210> 39

<211> 515

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2359526CD1

<400> 39

Met Ala Ala Asn	Met	Tyr Arg Val Gly	Asp	Tyr Val Tyr Phe	Glu
1	5		10		15
Asn Ser Ser Ser	Asn	Pro Tyr Leu Ile	Arg	Arg Ile Glu Glu	Leu
20	20		25		30
Asn Lys Thr Ala	Ser	Gly Asn Val Glu	Ala	Lys Val Val Cys	Phe
35	35		40		45
Tyr Arg Arg Arg	Asp	Ile Ser Asn Thr	Leu	Ile Met Leu Ala	Asp
50	50		55		60
Lys His Ala Lys	Glu	Ile Glu Glu Glu	Ser	Glu Thr Thr Val	Glu
65	65		70		75
Ala Asp Leu Thr	Asp	Lys Gln Lys His	Gln	Leu Lys His Arg	Glu
80	80		85		90
Leu Phe Leu Ser	Arg	Gln Tyr Glu Ser	Leu	Pro Ala Thr His	Ile
95	95		100		105
Arg Gly Lys Cys	Ser	Val Ala Leu Leu	Asn	Glu Thr Glu Ser	Val
110	110		115		120

WO 01/07471

PCT/US00/19948

Leu	Ser	Tyr	Leu	Asp	Lys	Glu	Asp	Thr	Phe	Phe	Tyr	Ser	Leu	Val
				125					130					135
Tyr	Asp	Pro	Ser	Leu	Lys	Thr	Leu	Leu	Ala	Asp	Lys	Gly	Glu	Ile
				140					145					150
Arg	Val	Gly	Pro	Arg	Tyr	Gln	Ala	Asp	Ile	Pro	Glu	Met	Leu	Leu
				155					160					165
Glu	Gly	Glu	Ser	Asp	Glu	Arg	Glu	Gln	Ser	Lys	Leu	Glu	Val	Lys
				170					175					180
Val	Trp	Asp	Pro	Asn	Ser	Pro	Leu	Thr	Asp	Arg	Gln	Ile	Asp	Gln
				185					190					195
Phe	Leu	Val	Val	Ala	Arg	Ala	Val	Gly	Thr	Phe	Ala	Arg	Ala	Leu
				200					205					210
Asp	Cys	Ser	Ser	Ser	Val	Arg	Gln	Pro	Ser	Leu	His	Met	Ser	Ala
				215					220					225
Ala	Ala	Ala	Ser	Arg	Asp	Ile	Thr	Leu	Phe	His	Ala	Met	Asp	Thr
				230					235					240
Leu	Tyr	Arg	His	Ser	Tyr	Asp	Leu	Ser	Ser	Ala	Ile	Ser	Val	Leu
				245					250					255
Val	Pro	Leu	Gly	Gly	Pro	Val	Leu	Cys	Arg	Asp	Glu	Met	Glu	Glu
				260					265					270
Trp	Ser	Ala	Ser	Glu	Ala	Ser	Leu	Phe	Glu	Glu	Ala	Leu	Glu	Lys
				275					280					285
Tyr	Gly	Lys	Asp	Phe	Asn	Asp	Ile	Arg	Gln	Asp	Phe	Leu	Pro	Trp
				290					295					300
Lys	Ser	Leu	Thr	Ser	Ile	Ile	Glu	Tyr	Tyr	Tyr	Met	Trp	Lys	Thr
				305					310					315
Thr	Asp	Arg	Tyr	Val	Gln	Gln	Lys	Arg	Leu	Lys	Ala	Ala	Glu	Ala
				320					325					330
Glu	Ser	Lys	Leu	Lys	Gln	Val	Tyr	Ile	Pro	Thr	Tyr	Ser	Lys	Pro
				335					340					345
Asn	Pro	Asn	Gln	Ile	Ser	Thr	Ser	Asn	Gly	Lys	Pro	Gly	Ala	Val
				350					355					360
Asn	Gly	Ala	Val	Gly	Thr	Thr	Phe	Gln	Pro	Gln	Asn	Pro	Leu	Leu
				365					370					375
Gly	Arg	Ala	Cys	Glu	Ser	Cys	Tyr	Ala	Thr	Gln	Ser	His	Gln	Trp
				380					385					390
Tyr	Ser	Trp	Gly	Pro	Pro	Asn	Met	Gln	Cys	Arg	Leu	Cys	Ala	Ile
				395					400					405
Cys	Trp	Leu	Tyr	Trp	Lys	Lys	Tyr	Gly	Gly	Leu	Lys	Met	Pro	Thr
				410					415					420
Gln	Ser	Glu	Glu	Glu	Lys	Leu	Ser	Pro	Ser	Pro	Thr	Thr	Glu	Asp
				425					430					435
Pro	Arg	Val	Arg	Ser	His	Val	Ser	Arg	Gln	Ala	Met	Gln	Gly	Met
				440					445					450
Pro	Val	Arg	Asn	Thr	Gly	Ser	Pro	Lys	Ser	Ala	Val	Lys	Thr	Arg
				455					460					465
Gln	Ala	Phe	Phe	Leu	His	Thr	Thr	Tyr	Phe	Thr	Lys	Phe	Ala	Arg
				470					475					480
Gln	Val	Cys	Lys	Asn	Thr	Leu	Arg	Leu	Arg	Gln	Ala	Ala	Arg	Arg
				485					490					495
Pro	Phe	Val	Ala	Ile	Asn	Tyr	Ala	Ala	Ile	Arg	Ala	Glu	Cys	Lys
				500					505					510
Met	Leu	Leu	Asn	Ser										
				515										

<210> 40

<211> 146

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2456494CD1

WO 01/07471

PCT/US00/19948

<400> 40
 Met Val Asp Glu Leu Val Leu Leu Leu His Ala Leu Leu Met Arg
 1 5 10 15
 His Arg Ala Leu Ser Ile Glu Asn Ser Gln Leu Met Glu Gln Leu
 20 25 30
 Arg Leu Leu Val Cys Glu Arg Ala Ser Leu Leu Arg Gln Val Arg
 35 40 45
 Pro Pro Ser Cys Pro Val Pro Phe Pro Glu Thr Phe Asn Gly Glu
 50 55 60
 Ser Ser Arg Leu Pro Glu Phe Ile Val Gln Thr Ala Ser Tyr Met
 65 70 75
 Leu Val Asn Glu Asn Arg Phe Cys Asn Asp Ala Met Lys Val Ala
 80 85 90
 Phe Leu Ile Ser Leu Leu Thr Gly Glu Ala Glu Glu Trp Val Val
 95 100 105
 Pro Tyr Ile Glu Met Asp Ser Pro Ile Leu Gly Asp Tyr Arg Ala
 110 115 120
 Phe Leu Asp Glu Met Lys Gln Cys Phe Gly Trp Asp Asp Asp Glu
 125 130 135
 Asp Asp Asp Asp Glu Glu Glu Asp Asp Tyr
 140 145

<210> 41
 <211> 580
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2668536CD1

<400> 41
 Met Lys Glu Asn Lys Glu Asn Ser Ser Pro Ser Val Thr Ser Ala
 1 5 10 15
 Asn Leu Asp His Thr Lys Pro Cys Trp Tyr Trp Asp Lys Lys Asp
 20 25 30
 Leu Ala His Thr Pro Ser Gln Leu Glu Gly Leu Asp Pro Ala Thr
 35 40 45
 Glu Ala Arg Tyr Arg Arg Glu Gly Ala Arg Phe Ile Phe Asp Val
 50 55 60
 Gly Thr Arg Leu Gly Leu His Tyr Asp Thr Leu Ala Thr Gly Ile
 65 70 75
 Ile Tyr Phe His Arg Phe Tyr Met Phe His Ser Phe Lys Gln Phe
 80 85 90
 Pro Arg Tyr Val Thr Gly Ala Cys Cys Leu Phe Leu Ala Gly Lys
 95 100 105
 Val Glu Glu Thr Pro Lys Lys Cys Lys Asp Ile Ile Lys Thr Ala
 110 115 120
 Arg Ser Leu Leu Asn Asp Val Gln Phe Gly Gln Phe Gly Asp Asp
 125 130 135
 Pro Lys Glu Glu Val Met Val Leu Glu Arg Ile Leu Leu Gln Thr
 140 145 150
 Ile Lys Phe Asp Leu Gln Val Glu His Pro Tyr Gln Phe Leu Leu
 155 160 165
 Lys Tyr Ala Lys Gln Leu Lys Gly Asp Lys Asn Lys Ile Gln Lys
 170 175 180
 Leu Val Gln Met Ala Trp Thr Phe Val Asn Asp Ser Leu Cys Thr
 185 190 195
 Thr Leu Ser Leu Gln Trp Glu Pro Glu Ile Ile Ala Val Ala Val
 200 205 210
 Met Tyr Leu Ala Gly Arg Leu Cys Lys Phe Glu Ile Gln Glu Trp
 215 220 225
 Thr Ser Lys Pro Met Tyr Arg Arg Trp Trp Glu Gln Phe Val Gln
 230 235 240

WO 01/07471

PCT/US00/19948

Asp Val Pro Val	Asp Val Leu Glu Asp	Ile Cys His Gln Ile Leu	
245	250	255	
Asp Leu Tyr Ser	Gln Gly Lys Gln Gln Met	Pro His His Thr Pro	
260	265	270	
His Gln Leu Gln	Gln Pro Pro Ser Leu Gln	Pro Thr Pro Gln Val	
275	280	285	
Pro Gln Val Gln	Gln Ser Gln Pro Ser Gln	Ser Ser Glu Pro Ser	
290	295	300	
Gln Pro Gln Gln	Lys Asp Pro Gln Gln Pro	Ala Gln Gln Gln Gln	
305	310	315	
Pro Ala Gln Gln	Pro Lys Lys Pro Ser Pro	Gln Pro Ser Ser Pro	
320	325	330	
Arg Gln Val Lys	Arg Ala Val Val Val Ser	Pro Lys Glu Glu Asn	
335	340	345	
Lys Ala Ala Glu	Pro Pro Pro Pro Lys Ile	Pro Lys Ile Glu Thr	
350	355	360	
Thr His Pro Pro	Leu Pro Pro Ala His Pro	Pro Pro Asp Arg Lys	
365	370	375	
Pro Pro Leu Ala	Ala Ala Leu Gly Glu Ala	Glu Pro Pro Gly Pro	
380	385	390	
Val Asp Ala Thr	Asp Leu Pro Lys Val Gln	Ile Pro Pro Pro Ala	
395	400	405	
His Pro Ala Pro	Val His Gln Pro Pro Pro	Leu Pro His Arg Pro	
410	415	420	
Pro Pro Pro Pro	Pro Ser Ser Tyr Met Thr	Gly Met Ser Thr Thr	
425	430	435	
Ser Ser Tyr Met	Ser Gly Glu Gly Tyr Gln	Ser Leu Gln Ser Met	
440	445	450	
Met Lys Thr Glu	Gly Pro Ser Tyr Gly Ala	Leu Pro Pro Ala Tyr	
455	460	465	
Gly Pro Pro Ala	His Leu Pro Tyr His Pro	His Val Tyr Pro Pro	
470	475	480	
Asn Pro Pro Pro	Pro Pro Val Pro Pro Pro	Pro Ala Ser Phe Pro	
485	490	495	
His Leu Pro Ser	His Pro Leu Leu Leu Ala	Thr Pro Asn Pro His	
500	505	510	
Pro Pro Thr Thr	Pro Thr Ser His Pro His	Pro His Ala Ser Arg	
515	520	525	
Leu Pro Thr Gln	Ser Pro Leu Ile Leu Leu	Gln Gly Trp Ala Cys	
530	535	540	
Arg Gln Pro Ala	Thr His Leu Leu Pro Ser	Pro Leu Glu Asp Ser	
545	550	555	
Leu Leu Cys Pro	Arg Pro Phe Pro His Pro	Ala Cys Leu Gln Leu	
560	565	570	
Glu Gly Leu Gly	Arg Ala Ala Trp Met Arg		
575	580		

<210> 42
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2683225CD1

<400> 42	
Met Ala Glu Pro Asp Tyr Ile Glu Asp Asp	Asn Pro Glu Leu Ile
1 5 10	15
Arg Pro Gln Lys Leu Ile Asn Pro Val Lys Thr Ser Arg Asn His	
20 25 30	
Gln Asp Leu His Arg Glu Leu Leu Met Asn Gln Lys Arg Gly Leu	
35 40 45	
Ala Pro Gln Asn Lys Pro Glu Leu Gln Lys Val Met Glu Lys Arg	

WO 01/07471

PCT/US00/19948

	50		55		60
Lys Arg Asp Gln Val Ile Lys Gln Lys Glu Glu Glu Ala Gln Lys					
	65		70		75
Lys Lys Ser Asp Leu Glu Ile Glu Leu Leu Lys Arg Gln Gln Lys					
	80		85		90
Leu Glu Gln Leu Glu Leu Glu Lys Gln Lys Leu Gln Glu Glu Gln					
	95		100		105
Glu Asn Ala Pro Glu Phe Val Lys Val Lys Gly Asn Leu Arg Arg					
	110		115		120
Thr Gly Gln Glu Val Ala Gln Ala Gln Glu Ser					
	125		130		

<210> 43

<211> 812

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2797839CD1

<400> 43

Met Gly Arg Lys Leu Asp Pro Thr Lys Glu Lys Arg Gly Pro Gly					
1	5		10		15
Arg Lys Ala Arg Lys Gln Lys Gly Ala Glu Thr Glu Leu Val Arg					
	20		25		30
Phe Leu Pro Ala Val Ser Asp Glu Asn Ser Lys Arg Leu Ser Ser					
	35		40		45
Arg Ala Arg Lys Arg Ala Ala Lys Arg Arg Leu Gly Ser Val Glu					
	50		55		60
Ala Pro Lys Thr Asn Lys Ser Pro Glu Ala Lys Pro Leu Pro Gly					
	65		70		75
Lys Leu Pro Lys Gly Ile Ser Ala Gly Ala Val Gln Thr Ala Gly					
	80		85		90
Lys Lys Gly Pro Gln Ser Leu Phe Asn Ala Pro Arg Gly Lys Lys					
	95		100		105
Arg Pro Ala Pro Gly Ser Asp Glu Glu Glu Glu Glu Asp Ser					
	110		115		120
Glu Glu Asp Gly Met Val Asn His Gly Asp Leu Trp Gly Ser Glu					
	125		130		135
Asp Asp Ala Asp Thr Val Asp Asp Tyr Gly Ala Asp Ser Asn Ser					
	140		145		150
Glu Asp Glu Glu Glu Gly Glu Ala Leu Leu Pro Ile Glu Arg Ala					
	155		160		165
Ala Arg Lys Gln Lys Ala Arg Glu Ala Ala Ala Gly Ile Gln Trp					
	170		175		180
Ser Glu Glu Glu Thr Glu Asp Glu Glu Glu Lys Glu Val Thr					
	185		190		195
Pro Glu Ser Gly Pro Pro Lys Val Glu Glu Ala Asp Gly Gly Leu					
	200		205		210
Gln Ile Asn Val Asp Glu Glu Pro Phe Val Leu Pro Pro Ala Gly					
	215		220		225
Glu Met Glu Gln Asp Ala Gln Ala Pro Asp Leu Gln Arg Val His					
	230		235		240
Lys Arg Ile Gln Asp Ile Val Gly Ile Leu Arg Asp Phe Gly Ala					
	245		250		255
Gln Arg Glu Glu Gly Arg Ser Arg Ser Glu Tyr Leu Asn Arg Leu					
	260		265		270
Lys Lys Asp Leu Ala Ile Tyr Tyr Ser Tyr Gly Asp Phe Leu Leu					
	275		280		285
Gly Lys Leu Met Asp Leu Phe Pro Leu Ser Glu Leu Val Glu Phe					
	290		295		300
Leu Glu Ala Asn Glu Val Pro Arg Pro Val Thr Leu Arg Thr Asn					
	305		310		315

WO 01/07471

PCT/US00/19948

Thr	Leu	Lys	Thr	Arg	Arg	Arg	Asp	Leu	Ala	Gln	Ala	Leu	Ile	Asn
				320					325					330
Arg	Gly	Val	Asn	Leu	Asp	Pro	Leu	Gly	Lys	Trp	Ser	Lys	Thr	Gly
				335					340					345
Leu	Val	Val	Tyr	Asp	Ser	Ser	Val	Pro	Ile	Gly	Ala	Thr	Pro	Glu
				350					355					360
Tyr	Leu	Ala	Gly	His	Tyr	Met	Leu	Gln	Gly	Ala	Ser	Ser	Met	Leu
				365					370					375
Pro	Val	Met	Ala	Leu	Ala	Pro	Gln	Glu	His	Glu	Arg	Ile	Leu	Asp
				380					385					390
Met	Cys	Cys	Ala	Pro	Gly	Gly	Lys	Thr	Ser	Tyr	Met	Ala	Gln	Leu
				395					400					405
Met	Lys	Asn	Thr	Gly	Val	Ile	Leu	Ala	Asn	Asp	Ala	Asn	Ala	Glu
				410					415					420
Arg	Leu	Lys	Ser	Val	Val	Gly	Asn	Leu	His	Arg	Leu	Gly	Val	Thr
				425					430					435
Asn	Thr	Ile	Ile	Ser	His	Tyr	Asp	Gly	Arg	Gln	Phe	Pro	Lys	Val
				440					445					450
Val	Gly	Gly	Phe	Asp	Arg	Val	Leu	Leu	Asp	Ala	Pro	Cys	Ser	Gly
				455					460					465
Thr	Gly	Val	Ile	Ser	Lys	Asp	Pro	Ala	Val	Lys	Thr	Asn	Lys	Asp
				470					475					480
Glu	Lys	Asp	Ile	Leu	Arg	Cys	Ala	His	Leu	Gln	Lys	Glu	Leu	Leu
				485					490					495
Leu	Ser	Ala	Ile	Asp	Ser	Val	Asn	Ala	Thr	Ser	Lys	Thr	Gly	Gly
				500					505					510
Tyr	Leu	Val	Tyr	Cys	Thr	Cys	Ser	Ile	Thr	Val	Glu	Glu	Asn	Glu
				515					520					525
Trp	Val	Val	Asp	Tyr	Ala	Leu	Lys	Lys	Arg	Asn	Val	Arg	Leu	Val
				530					535					540
Pro	Thr	Gly	Leu	Asp	Phe	Gly	Gln	Glu	Gly	Phe	Thr	Arg	Phe	Arg
				545					550					555
Glu	Arg	Arg	Phe	His	Pro	Ser	Leu	Arg	Ser	Thr	Arg	Arg	Phe	Tyr
				560					565					570
Pro	His	Thr	His	Asn	Met	Asp	Gly	Phe	Phe	Ile	Ala	Lys	Phe	Lys
				575					580					585
Lys	Phe	Ser	Asn	Ser	Ile	Pro	Gln	Ser	Gln	Thr	Gly	Asn	Ser	Glu
				590					595					600
Thr	Ala	Thr	Pro	Thr	Asn	Val	Asp	Leu	Pro	Gln	Val	Ile	Pro	Lys
				605					610					615
Ser	Glu	Asn	Ser	Ser	Gln	Pro	Ala	Lys	Lys	Ala	Lys	Gly	Ala	Ala
				620					625					630
Lys	Thr	Lys	Gln	Gln	Leu	Gln	Lys	Gln	Gln	His	Pro	Lys	Lys	Ala
				635					640					645
Ser	Phe	Gln	Lys	Leu	Asn	Gly	Ile	Ser	Lys	Gly	Ala	Asp	Ser	Glu
				650					655					660
Leu	Ser	Thr	Val	Pro	Ser	Val	Thr	Lys	Thr	Gln	Ala	Ser	Ser	Ser
				665					670					675
Phe	Gln	Asp	Ser	Ser	Gln	Pro	Ala	Gly	Lys	Ala	Glu	Gly	Ile	Arg
				680					685					690
Glu	Pro	Lys	Val	Thr	Gly	Lys	Leu	Lys	Gln	Arg	Ser	Pro	Lys	Leu
				695					700					705
Gln	Ser	Ser	Lys	Lys	Val	Ala	Phe	Leu	Arg	Gln	Asn	Ala	Pro	Pro
				710					715					720
Lys	Gly	Thr	Asp	Thr	Gln	Thr	Pro	Ala	Val	Leu	Ser	Pro	Ser	Lys
				725					730					735
Thr	Gln	Ala	Thr	Leu	Lys	Pro	Lys	Asp	His	His	Gln	Pro	Leu	Gly
				740					745					750
Arg	Ala	Lys	Gly	Val	Glu	Lys	Gln	Gln	Leu	Pro	Glu	Gln	Pro	Phe
				755					760					765
Glu	Lys	Ala	Ala	Phe	Gln	Lys	Gln	Asn	Asp	Thr	Pro	Lys	Gly	Pro
				770					775					780
Gln	Pro	Pro	Thr	Val	Ser	Pro	Ile	Arg	Ser	Ser	Arg	Pro	Pro	Pro

WO 01/07471

PCT/US00/19948

	785		790		795
Ala Lys Arg Lys	Lys Ser Gln Ser Arg	Gly Asn Ser Gln Leu	Leu		
	800		805		810
Leu Ser					

<210> 44

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2959521CD1

<400> 44

Met Arg Gly Val Gly	Ala Arg Val Tyr	Ala Asp Ala Pro Ala Lys	
1	5	10	15
Leu Leu Leu Pro Pro	Pro Ala Ala Trp Asp	Leu Ala Val Arg Leu	
	20	25	30
Arg Gly Ala Glu Ala	Ala Ser Glu Arg Gln	Val Tyr Ser Val Thr	
	35	40	45
Met Lys Leu Leu Leu	Leu His Pro Ala Phe	Gln Ser Cys Leu Leu	
	50	55	60
Leu Thr Leu Leu Gly	Leu Trp Arg Thr Thr	Pro Glu Ala His Ala	
	65	70	75
Ser Ser Leu Gly Ala	Pro Ala Ile Ser Ala	Ala Ser Phe Leu Gln	
	80	85	90
Asp Leu Ile His Arg	Tyr Gly Glu Gly Asp	Ser Leu Thr Leu Gln	
	95	100	105
Gln Leu Lys Ala Leu	Leu Asn His Leu Asp	Val Gly Val Gly Arg	
	110	115	120
Gly Asn Val Thr Gln	His Val Gln Gly His	Arg Asn Leu Ser Thr	
	125	130	135
Cys Phe Ser Ser Gly	Asp Leu Phe Thr Ala	His Asn Phe Ser Glu	
	140	145	150
Gln Ser Arg Ile Gly	Ser Ser Glu Leu Gln	Glu Phe Cys Pro Thr	
	155	160	165
Ile Leu Gln Gln Leu	Asp Ser Arg Ala Cys	Thr Ser Glu Asn Gln	
	170	175	180
Glu Asn Glu Glu Asn	Glu Gln Thr Glu Gly	Arg Pro Ser Ala	
	185	190	195
Val Glu Val Trp Gly	Tyr Gly Leu Leu Cys	Val Thr Val Ile Ser	
	200	205	210
Leu Cys Ser Leu Leu	Gly Ala Ser Val Val	Pro Phe Met Lys Lys	
	215	220	225
Thr Phe Tyr Lys Arg	Leu Leu Leu Tyr Phe	Ile Ala Leu Ala Ile	
	230	235	240
Gly Thr Leu Tyr Ser	Asn Ala Leu Phe Gln	Leu Ile Pro Glu Ala	
	245	250	255
Phe Gly Phe Asn Pro	Leu Glu Asp Tyr Tyr	Val Ser Lys Ser Ala	
	260	265	270
Val Val Phe Gly Gly	Phe Tyr Leu Phe Phe	Phe Thr Glu Lys Ile	
	275	280	285
Leu Lys Ile Leu Leu	Lys Gln Lys Asn Glu	His His His Gly His	
	290	295	300
Ser His Tyr Ala Ser	Glu Ser Leu Pro Ser	Lys Lys Asp Gln Glu	
	305	310	315
Glu Gly Val Met Glu	Lys Leu Gln Asn Gly	Asp Leu Asp His Met	
	320	325	330
Ile Pro Gln His Cys	Ser Ser Glu Leu Asp	Gly Lys Ala Pro Met	
	335	340	345
Val Asp Glu Lys Val	Ile Val Gly Ser Leu	Ser Val Gln Asp Leu	
	350	355	360

WO 01/07471

PCT/US00/19948

Trp Lys Thr Thr	215	220	225
Asp Arg Tyr Ile Gln		Gln Lys Arg Leu Lys	Ala
230		235	240
Ala Glu Ala Asp	Ser Lys Leu Lys Gln	Val Tyr Ile Pro Thr	Tyr
245		250	255
Thr Lys Pro Asn	Pro Asn Gln Ile Ile	Ser Val Gly Ser Lys	Pro
260		265	270
Gly Met Asn Gly	Ala Gly Phe Gln Lys	Gly Leu Thr Cys Glu	Ser
275		280	285
Cys His Thr Thr	Gln Ser Ala Gln Trp	Tyr Ala Trp Gly Pro	Pro
290		295	300
Asn Met Gln Cys	Arg Leu Cys Ala Ser	Cys Trp Ile Tyr Trp	Lys
305		310	315
Lys Tyr Gly Gly	Leu Lys Thr Pro Thr	Gln Leu Glu Gly Ala	Thr
320		325	330
Arg Gly Thr Thr	Glu Pro His Ser Arg	Gly His Leu Ser Arg	Pro
335		340	345
Glu Ala Gln Ser	Leu Ser Pro Tyr Thr	Thr Ser Ala Asn Arg	Ala
350		355	360
Lys Leu Leu Ala	Lys Asn Arg Gln Thr	Phe Leu Leu Gln Thr	Thr
365		370	375
Lys Leu Thr Arg	Leu Ala Arg Arg Met	Cys Arg Asp Leu Leu	Gln
380		385	390
Pro Arg Arg Ala	Ala Arg Arg Pro Tyr	Ala Pro Ile Asn Ala	Asn
395		400	405
Ala Ile Lys Ala	Glu Cys Ser Ile Arg	Leu Pro Lys Ala Ala	Lys
410		415	420
Thr Pro Leu Lys	Ile His Pro Leu Val	Arg Leu Pro Leu Ala	Thr
425		430	435
Ile Val Lys Asp	Leu Val Ala Gln Ala	Pro Leu Lys Pro Lys	Thr
440		445	450
Pro Arg Gly Thr	Lys Thr Pro Ile Asn	Arg Asn Gln Leu Ser	Gln
455		460	465
Asn Arg Gly Leu	Gly Gly Ile Met Val	Lys Arg Ala Tyr Glu	Thr
470		475	480
Met Ala Gly Ala	Gly Val Pro Phe Ser	Ala Asn Gly Arg Pro	Leu
485		490	495
Ala Ser Gly Ile	Arg Ser Ser Ser Gln	Pro Ala Ala Lys Arg	Gln
500		505	510
Lys Leu Asn Pro	Ala Asp Ala Pro Asn	Pro Val Val Phe Val	Ala
515		520	525
Thr Lys Asp Thr	Arg Ala Leu Arg Lys	Ala Leu Thr His Leu	Glu
530		535	540
Met Arg Arg Ala	Ala Arg Arg Pro Asn	Leu Pro Leu Lys Val	Lys
545		550	555
Pro Thr Leu Ile	Ala Val Arg Pro Pro	Val Pro Leu Pro Ala	Pro
560		565	570
Ser His Pro Ala	Ser Thr Asn Glu Pro	Ile Val Leu Glu Asp	
575		580	

<210> 46

<211> 425

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3520701CD1

<400> 46

Met Ala Gly Ala Glu Gly Ala Ala Gly Arg	Gln Ser Glu Leu Glu
1	5
Pro Val Val Ser Leu Val Asp Val Leu Glu	Glu Asp Glu Glu Leu
20	25
	30

WO 01/07471

PCT/US00/19948

Glu	Asn	Glu	Ala	Cys	Ala	Val	Leu	Gly	Gly	Ser	Asp	Ser	Glu	Lys
				35					40					45
Cys	Ser	Tyr	Ser	Gln	Gly	Ser	Val	Lys	Arg	Gln	Ala	Leu	Tyr	Ala
				50					55					60
Cys	Ser	Thr	Cys	Thr	Pro	Glu	Gly	Glu	Glu	Pro	Ala	Gly	Ile	Cys
				65					70					75
Leu	Ala	Cys	Ser	Tyr	Glu	Cys	His	Gly	Ser	His	Lys	Leu	Phe	Glu
				80					85					90
Leu	Tyr	Thr	Lys	Arg	Asn	Phe	Arg	Cys	Asp	Cys	Gly	Asn	Ser	Lys
				95					100					105
Phe	Lys	Asn	Leu	Glu	Cys	Lys	Leu	Leu	Pro	Asp	Lys	Ala	Lys	Val
				110					115					120
Asn	Ser	Gly	Asn	Lys	Tyr	Asn	Asp	Asn	Phe	Phe	Gly	Leu	Tyr	Cys
				125					130					135
Ile	Cys	Lys	Arg	Pro	Tyr	Pro	Asp	Pro	Glu	Asp	Glu	Ile	Pro	Asp
				140					145					150
Glu	Met	Ile	Gln	Cys	Val	Val	Cys	Glu	Asp	Trp	Phe	His	Gly	Arg
				155					160					165
His	Leu	Gly	Ala	Ile	Pro	Pro	Glu	Ser	Gly	Asp	Phe	Gln	Glu	Met
				170					175					180
Val	Cys	Gln	Ala	Cys	Met	Lys	Arg	Cys	Ser	Phe	Leu	Trp	Ala	Tyr
				185					190					195
Ala	Ala	Gln	Leu	Ala	Val	Thr	Lys	Ile	Ser	Thr	Glu	Asp	Asp	Gly
				200					205					210
Leu	Val	Arg	Asn	Ile	Asp	Gly	Ile	Gly	Asp	Gln	Glu	Val	Ile	Lys
				215					220					225
Pro	Glu	Asn	Gly	Glu	His	Gln	Asp	Ser	Thr	Leu	Lys	Glu	Asp	Val
				230					235					240
Pro	Glu	Gln	Gly	Lys	Asp	Asp	Val	Arg	Glu	Val	Lys	Val	Glu	Gln
				245					250					255
Asn	Ser	Glu	Pro	Cys	Ala	Gly	Ser	Ser	Ser	Glu	Ser	Asp	Leu	Gln
				260					265					270
Thr	Val	Phe	Lys	Asn	Glu	Ser	Leu	Asn	Ala	Glu	Ser	Lys	Ser	Gly
				275					280					285
Cys	Lys	Leu	Gln	Glu	Leu	Lys	Ala	Lys	Gln	Leu	Ile	Lys	Lys	Asp
				290					295					300
Thr	Ala	Thr	Tyr	Trp	Pro	Leu	Asn	Trp	Arg	Ser	Lys	Leu	Cys	Thr
				305					310					315
Cys	Gln	Asp	Cys	Met	Lys	Met	Tyr	Gly	Asp	Leu	Asp	Val	Leu	Phe
				320					325					330
Leu	Thr	Asp	Glu	Tyr	Asp	Thr	Val	Leu	Ala	Tyr	Glu	Asn	Lys	Gly
				335					340					345
Lys	Ile	Ala	Gln	Ala	Thr	Asp	Arg	Ser	Asp	Pro	Leu	Met	Asp	Thr
				350					355					360
Leu	Ser	Ser	Met	Asn	Arg	Val	Gln	Gln	Val	Glu	Leu	Ile	Cys	Glu
				365					370					375
Tyr	Asn	Asp	Leu	Lys	Thr	Glu	Leu	Lys	Asp	Tyr	Leu	Lys	Arg	Phe
				380					385					390
Ala	Asp	Glu	Gly	Thr	Val	Val	Lys	Arg	Glu	Asp	Ile	Gln	Gln	Phe
				395					400					405
Phe	Glu	Glu	Phe	Gln	Ser	Lys	Lys	Arg	Arg	Arg	Val	Asp	Gly	Met
				410					415					420
Gln	Tyr	Tyr	Cys	Ser										
				425										

<210> 47

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4184320CD1

WO 01/07471

PCT/US00/19948

<400> 47

Met	Tyr	Val	Arg	Val	Ser	Phe	Asp	Thr	Lys	Pro	Asp	Leu	Leu	Leu
1				5					10					15
His	Leu	Met	Thr	Lys	Glu	Trp	Gln	Leu	Glu	Leu	Pro	Lys	Leu	Leu
				20					25					30
Ile	Ser	Val	His	Gly	Gly	Leu	Gln	Asn	Phe	Glu	Leu	Gln	Pro	Lys
				35					40					45
Leu	Lys	Gln	Val	Phe	Gly	Lys	Gly	Leu	Ile	Lys	Ala	Ala	Met	Thr
				50					55					60
Thr	Gly	Ala	Trp	Ile	Phe	Thr	Gly	Gly	Val	Asn	Thr	Gly	Val	Ile
				65					70					75
Arg	His	Val	Gly	Asp	Ala	Leu	Lys	Asp	His	Ala	Ser	Lys	Ser	Arg
				80					85					90
Gly	Lys	Ile	Cys	Thr	Ile	Gly	Ile	Ala	Pro	Trp	Gly	Ile	Val	Glu
				95					100					105
Asn	Gln	Glu	Asp	Leu	Ile	Gly	Arg	Asp	Val	Val	Arg	Pro	Tyr	Gln
				110					115					120
Thr	Met	Ser	Asn	Pro	Met	Ser	Lys	Leu	Thr	Val	Leu	Asn	Ser	Met
				125					130					135
His	Ser	His	Phe	Ile	Leu	Ala	Asp	Asn	Gly	Thr	Thr	Gly	Lys	Tyr
				140					145					150
Gly	Ala	Glu	Val	Lys	Leu	Arg	Arg	Gln	Leu	Glu	Lys	His	Ile	Ser
				155					160					165
Leu	Gln	Lys	Ile	Asn	Thr	Arg	Cys	Leu	Pro	Phe	Phe	Ser	Leu	Asp
				170					175					180
Ser	Arg	Leu	Phe	Tyr	Ser	Phe	Trp	Gly	Ser	Cys	Gln	Leu	Asp	Ser
				185					190					195
Val	Gly	Ile	Gly	Gln	Gly	Val	Pro	Val	Val	Ala	Leu	Ile	Val	Glu
				200					205					210
Gly	Gly	Pro	Asn	Val	Ile	Ser	Ile	Val	Leu	Glu	Tyr	Leu	Arg	Asp
				215					220					225
Thr	Pro	Pro	Val	Pro	Val	Val	Val	Cys	Asp	Gly	Ser	Gly	Arg	Ala
				230					235					240
Ser	Asp	Ile	Leu	Ala	Phe	Gly	His	Lys	Tyr	Ser	Glu	Glu	Gly	Gly
				245					250					255

<210> 48

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4764233CD1

<400> 48

Met	Ser	Trp	Arg	Gly	Arg	Ser	Thr	Tyr	Arg	Pro	Arg	Pro	Arg	Arg
1				5					10					15
Ser	Leu	Gln	Pro	Pro	Glu	Leu	Ile	Gly	Ala	Met	Leu	Glu	Pro	Thr
				20					25					30
Asp	Glu	Glu	Pro	Lys	Glu	Glu	Lys	Pro	Pro	Thr	Lys	Ser	Arg	Asn
				35					40					45
Pro	Thr	Pro	Asp	Gln	Lys	Arg	Glu	Asp	Asp	Gln	Gly	Ala	Ala	Glu
				50					55					60
Ile	Gln	Val	Pro	Asp	Leu	Glu	Ala	Asp	Leu	Gln	Glu	Leu	Cys	Gln
				65					70					75
Thr	Lys	Thr	Gly	Asp	Gly	Cys	Glu	Gly	Gly	Thr	Asp	Val	Lys	Gly
				80					85					90
Lys	Ile	Leu	Pro	Lys	Ala	Glu	His	Phe	Lys	Met	Pro	Glu	Ala	Gly
				95					100					105
Glu	Gly	Lys	Ser	Gln	Val									
				110										

<210> 49

WO 01/07471

PCT/US00/19948

Arg Asp Arg Arg Pro Leu Leu Thr Ala Pro Asp His Cys Ser Asp
410 415 420

Asp Ala

<210> 50

<211> 397

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5040573CD1

<400> 50

Met	Ala	Met	Ile	Glu	Leu	Gly	Phe	Gly	Arg	Gln	Asn	Phe	His	Pro
1				5					10					15
Leu	Lys	Arg	Lys	Ser	Ser	Leu	Leu	Leu	Lys	Leu	Ile	Ala	Val	Val
				20					25					30
Phe	Ala	Val	Leu	Leu	Phe	Cys	Glu	Phe	Leu	Ile	Tyr	Tyr	Leu	Ala
				35					40					45
Ile	Phe	Gln	Cys	Asn	Trp	Pro	Glu	Val	Lys	Thr	Thr	Ala	Ser	Asp
				50					55					60
Gly	Glu	Gln	Thr	Thr	Arg	Glu	Pro	Val	Leu	Lys	Ala	Met	Phe	Leu
				65					70					75
Ala	Asp	Thr	His	Leu	Leu	Gly	Glu	Phe	Leu	Gly	His	Trp	Leu	Asp
				80					85					90
Lys	Leu	Arg	Arg	Glu	Trp	Gln	Met	Glu	Arg	Ala	Phe	Gln	Thr	Ala
				95					100					105
Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val	Val	Phe	Ile	Leu	Gly	Asp	Ile
				110					115					120
Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro	Glu	Ala	Trp	Ala	Asp	Asp
				125					130					135
Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His	Pro	Ser	His	Val	Gln
				140					145					150
Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly	Phe	His	Tyr	Glu
				155					160					165
Met	Asn	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Glu	Lys	Val	Phe	Ser	Ser
				170					175					180
Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met	Val	Asn
				185					190					195
Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu	Thr
				200					205					210
Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg
				215					220					225
Glu	Gln	Ala	Arg	Gly	Ser	Ser	Arg	Cys	Gly	Pro	Gly	Pro	Leu	Leu
				230					235					240
Pro	Thr	Ser	Ala	Pro	Val	Leu	Leu	Gln	His	Tyr	Pro	Leu	Tyr	Arg
				245					250					255
Arg	Ser	Asp	Ala	Asn	Cys	Ser	Gly	Glu	Asp	Ala	Ala	Pro	Pro	Glu
				260					265					270
Glu	Arg	Asp	Ile	Pro	Phe	Lys	Glu	Asn	Tyr	Asp	Val	Leu	Ser	Arg
				275					280					285
Glu	Ala	Ser	Gln	Lys	Leu	Leu	Trp	Trp	Leu	Gln	Pro	Arg	Leu	Val
				290					295					300
Leu	Ser	Gly	His	Thr	His	Ser	Ala	Cys	Glu	Val	His	His	Gly	Gly
				305					310					315
Arg	Val	Pro	Glu	Leu	Ser	Val	Pro	Ser	Phe	Ser	Trp	Arg	Asn	Arg
				320					325					330
Asn	Asn	Pro	Ser	Phe	Ile	Met	Gly	Ser	Ile	Thr	Pro	Thr	Asp	Tyr
				335					340					345
Thr	Leu	Ser	Lys	Cys	Tyr	Leu	Pro	Arg	Glu	Asp	Val	Val	Leu	Ile
				350					355					360
Ile	Tyr	Cys	Gly	Val	Val	Gly	Phe	Leu	Val	Val	Leu	Thr	Leu	Thr

WO 01/07471

PCT/US00/19948

	365		370	375
His Phe Gly Leu	Leu Ala Ser Pro Phe	Leu Ser Gly Leu Asn	Leu	
	380	385	390	
Leu Gly Lys Arg	Lys Thr Arg			
	395			

<210> 51

<211> 800

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5627029CD1

<400> 51

Met Gly Ser Ser Lys	Lys His Arg Gly Glu	Lys Glu Ala Ala Gly
1	5	10
Thr Thr Ala Ala Ala	Gly Thr Gly Gly Ala	Thr Glu Gln Pro Pro
	20	25
Arg His Arg Glu His	Lys Lys His Lys His	Arg Ser Gly Gly Ser
	35	40
Gly Gly Ser Gly Gly	Glu Arg Arg Lys Arg	Ser Arg Glu Arg Gly
	50	55
Gly Glu Arg Gly Ser	Gly Arg Arg Gly Ala	Glu Ala Glu Ala Arg
	65	70
Ser Ser Thr His Gly	Arg Glu Arg Ser Gln	Ala Glu Pro Ser Glu
	80	85
Arg Arg Val Lys Arg	Glu Lys Arg Asp Asp	Gly Tyr Glu Ala Ala
	95	100
Ala Ser Ser Lys Thr	Ser Ser Gly Asp Ala	Ser Ser Leu Ser Ile
	110	115
Glu Glu Thr Asn Lys	Leu Arg Ala Lys Leu	Gly Leu Lys Pro Leu
	125	130
Glu Val Asn Ala Ile	Lys Lys Glu Ala Gly	Thr Lys Glu Glu Pro
	140	145
Val Thr Ala Asp Val	Ile Asn Pro Met Ala	Leu Arg Gln Arg Glu
	155	160
Glu Leu Arg Glu Lys	Leu Ala Ala Ala Lys	Glu Lys Arg Leu Leu
	170	175
Asn Gln Lys Leu Gly	Lys Ile Lys Thr Leu	Gly Glu Asp Asp Pro
	185	190
Trp Leu Asp Asp Thr	Ala Ala Trp Ile Glu	Arg Ser Arg Gln Leu
	200	205
Gln Lys Glu Lys Asp	Leu Ala Glu Lys Arg	Ala Lys Leu Leu Glu
	215	220
Glu Met Asp Gln Glu	Phe Gly Val Ser Thr	Leu Val Glu Glu Glu
	230	235
Phe Gly Gln Arg Arg	Gln Asp Leu Tyr Ser	Ala Arg Asp Leu Gln
	245	250
Gly Leu Thr Val Glu	His Ala Ile Asp Ser	Phe Arg Glu Gly Glu
	260	265
Thr Met Ile Leu Thr	Leu Lys Asp Lys Gly	Val Leu Gln Glu Glu
	275	280
Glu Asp Val Leu Val	Asn Val Asn Leu Val	Asp Lys Glu Arg Ala
	290	295
Glu Lys Asn Val Glu	Leu Arg Lys Lys Lys	Pro Asp Tyr Leu Pro
	305	310
Tyr Ala Glu Asp Glu	Ser Val Asp Asp Leu	Ala Gln Gln Lys Pro
	320	325
Arg Ser Ile Leu Ser	Lys Tyr Asp Glu Glu	Leu Glu Gly Glu Arg
	335	340
Pro His Ser Phe Arg	Leu Glu Gln Gly Gly	Thr Ala Asp Gly Leu
	350	355

WO 01/07471

PCT/US00/19948

Arg	Glu	Arg	Glu	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Leu	Arg	Leu	Gln
				365					370					375
Ala	Gln	Ser	Leu	Ser	Thr	Val	Gly	Pro	Arg	Leu	Ala	Ser	Glu	Tyr
				380					385					390
Leu	Thr	Pro	Glu	Glu	Met	Val	Thr	Phe	Lys	Lys	Thr	Lys	Arg	Arg
				395					400					405
Val	Lys	Lys	Ile	Arg	Lys	Lys	Glu	Lys	Glu	Val	Val	Val	Arg	Ala
				410					415					420
Asp	Asp	Leu	Leu	Pro	Leu	Gly	Asp	Gln	Thr	Gln	Asp	Gly	Asp	Phe
				425					430					435
Gly	Ser	Arg	Leu	Arg	Gly	Arg	Gly	Arg	Arg	Arg	Val	Ser	Glu	Val
				440					445					450
Glu	Glu	Glu	Lys	Glu	Pro	Val	Pro	Gln	Pro	Leu	Pro	Ser	Asp	Asp
				455					460					465
Thr	Arg	Val	Glu	Asn	Met	Asp	Ile	Ser	Asp	Glu	Glu	Glu	Gly	Gly
				470					475					480
Ala	Pro	Pro	Pro	Ala	Ser	Pro	Gln	Val	Leu	Glu	Glu	Asp	Glu	Ala
				485					490					495
Glu	Leu	Glu	Leu	Gln	Lys	Gln	Leu	Glu	Lys	Gly	Arg	Arg	Leu	Arg
				500					505					510
Gln	Leu	Gln	Gln	Leu	Gln	Gln	Leu	Arg	Asp	Ser	Gly	Glu	Lys	Val
				515					520					525
Val	Glu	Ile	Val	Lys	Lys	Leu	Glu	Ser	Arg	Gln	Arg	Gly	Trp	Glu
				530					535					540
Glu	Asp	Glu	Asp	Pro	Glu	Arg	Lys	Gly	Ala	Ile	Val	Phe	Asn	Ala
				545					550					555
Thr	Ser	Glu	Phe	Cys	Arg	Thr	Leu	Gly	Glu	Ile	Pro	Thr	Tyr	Gly
				560					565					570
Leu	Ala	Gly	Asn	Arg	Glu	Glu	Gln	Glu	Glu	Leu	Met	Asp	Phe	Glu
				575					580					585
Arg	Asp	Glu	Glu	Arg	Ser	Ala	Asn	Gly	Gly	Ser	Glu	Ser	Asp	Gly
				590					595					600
Glu	Glu	Asn	Ile	Gly	Trp	Ser	Thr	Val	Asn	Leu	Asp	Glu	Glu	Lys
				605					610					615
Gln	Gln	Gln	Asp	Phe	Ser	Ala	Ser	Ser	Thr	Thr	Ile	Leu	Asp	Glu
				620					625					630
Glu	Pro	Ile	Val	Asn	Arg	Gly	Leu	Ala	Ala	Ala	Leu	Leu	Leu	Cys
				635					640					645
Gln	Asn	Lys	Gly	Leu	Leu	Glu	Thr	Thr	Val	Gln	Lys	Val	Ala	Arg
				650					655					660
Val	Lys	Ala	Pro	Asn	Lys	Ser	Leu	Pro	Ser	Ala	Val	Tyr	Cys	Ile
				665					670					675
Glu	Asp	Lys	Met	Ala	Ile	Asp	Asp	Lys	Tyr	Ser	Arg	Arg	Glu	Glu
				680					685					690
Tyr	Arg	Gly	Phe	Thr	Gln	Asp	Phe	Lys	Glu	Lys	Asp	Gly	Tyr	Lys
				695					700					705
Pro	Asp	Val	Lys	Ile	Glu	Tyr	Val	Asp	Glu	Thr	Gly	Arg	Lys	Leu
				710					715					720
Thr	Pro	Lys	Glu	Ala	Phe	Arg	Gln	Leu	Ser	His	Arg	Phe	His	Gly
				725					730					735
Lys	Gly	Ser	Gly	Lys	Met	Lys	Thr	Glu	Arg	Arg	Met	Lys	Lys	Leu
				740					745					750
Asp	Glu	Glu	Ala	Leu	Leu	Lys	Lys	Met	Ser	Ser	Ser	Asp	Thr	Pro
				755					760					765
Leu	Gly	Thr	Val	Ala	Leu	Leu	Gln	Glu	Lys	Gln	Lys	Ala	Gln	Lys
				770					775					780
Thr	Pro	Tyr	Ile	Val	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Met	Asn	Ala
				785					790					795
Asn	Thr	Ile	Thr	Lys										
				800										

<210> 52
 <211> 713
 <212> PRT

WO 01/07471

PCT/US00/19948

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5678487CD1

<400> 52

Met	Ala	Lys	Ser	Pro	Glu	Asn	Ser	Thr	Leu	Glu	Glu	Ile	Leu	Gly	1	5	10	15
Gln	Tyr	Gln	Arg	Ser	Leu	Arg	Glu	His	Ala	Ser	Arg	Ser	Ile	His	20	25	30	35
Gln	Leu	Thr	Cys	Ala	Leu	Lys	Glu	Gly	Asp	Val	Thr	Ile	Gly	Glu	40	45	50	55
Asp	Ala	Pro	Asn	Leu	Ser	Phe	Ser	Thr	Ser	Val	Gly	Asn	Glu	Asp	60	65	70	75
Ala	Arg	Thr	Ala	Trp	Pro	Glu	Leu	Gln	Gln	Ser	His	Ala	Val	Asn	80	85	90	95
Gln	Leu	Lys	Asp	Leu	Leu	Arg	Gln	Gln	Ala	Asp	Lys	Glu	Ser	Glu	100	105	110	115
Val	Ser	Pro	Ser	Arg	Arg	Arg	Lys	Met	Ser	Pro	Leu	Arg	Ser	Leu	120	125	130	135
Glu	His	Glu	Glu	Thr	Asn	Met	Pro	Thr	Met	His	Asp	Leu	Val	His	140	145	150	155
Thr	Ile	Asn	Asp	Gln	Ser	Gln	Tyr	Ile	His	His	Leu	Glu	Ala	Glu	160	165	170	175
Val	Lys	Phe	Cys	Lys	Glu	Glu	Leu	Ser	Gly	Met	Lys	Asn	Lys	Ile	180	185	190	195
Gln	Val	Val	Val	Leu	Glu	Asn	Glu	Gly	Leu	Gln	Gln	Gln	Leu	Lys	200	205	210	215
Ser	Gln	Arg	Gln	Glu	Glu	Thr	Leu	Arg	Gln	Thr	Leu	Leu	Asp		220	225	230	235
Ala	Ser	Gly	Asn	Met	His	Asn	Ser	Trp	Ile	Thr	Thr	Gly	Glu	Asp	240	245	250	255
Ser	Gly	Val	Gly	Glu	Thr	Ser	Lys	Arg	Pro	Phe	Ser	His	Asp	Asn	260	265	270	275
Ala	Asp	Phe	Gly	Lys	Ala	Ala	Ser	Ala	Gly	Glu	Gln	Leu	Glu	Leu	280	285	290	295
Glu	Lys	Leu	Lys	Leu	Thr	Tyr	Glu	Glu	Lys	Cys	Glu	Ile	Glu	Glu	300	305	310	315
Ser	Gln	Leu	Lys	Phe	Leu	Arg	Asn	Asp	Leu	Ala	Glu	Tyr	Gln	Arg	320	325	330	335
Thr	Cys	Glu	Asp	Leu	Lys	Glu	Gln	Leu	Lys	His	Lys	Glu	Phe	Leu	340	345	350	355
Leu	Ala	Ala	Asn	Thr	Cys	Asn	Arg	Val	Gly	Gly	Leu	Cys	Leu	Lys	360	365	370	375
Cys	Ala	Gln	His	Glu	Ala	Val	Leu	Ser	Gln	Thr	His	Thr	Asn	Val	380	385	390	395
His	Met	Gln	Thr	Ile	Glu	Arg	Leu	Val	Lys	Glu	Arg	Asp	Asp	Leu	400	405	410	415
Met	Ser	Ala	Leu	Val	Ser	Val	Arg	Ser	Ser	Leu	Ala	Asp	Thr	Gln				
Gln	Arg	Glu	Ala	Ser	Ala	Tyr	Glu	Gln	Val	Lys	Gln	Val	Leu	Gln				
Ile	Ser	Glu	Glu	Ala	Asn	Phe	Glu	Lys	Thr	Lys	Ala	Leu	Ile	Gln				
Cys	Asp	Gln	Leu	Arg	Lys	Glu	Leu	Glu	Arg	Gln	Ala	Glu	Arg	Leu				
Glu	Lys	Asp	Leu	Ala	Ser	Gln	Gln	Glu	Lys	Arg	Ala	Ile	Glu	Lys				
Asp	Met	Met	Lys	Lys	Glu	Ile	Thr	Lys	Glu	Arg	Glu	Tyr	Met	Gly				
Ser	Lys	Met	Leu	Ile	Leu	Ser	Gln	Asn	Ile	Ala	Gln	Leu	Glu	Ala				

WO 01/07471

PCT/US00/19948

Gln Val Glu Lys Val Thr Lys Glu Lys Ile Ser Ala Ile Asn Gln
 425 430 435
 Leu Glu Glu Ile Gln Ser Gln Leu Ala Ser Arg Glu Met Asp Val
 440 445 450
 Thr Lys Val Cys Gly Glu Met Arg Tyr Gln Leu Asn Lys Thr Asn
 455 460 465
 Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg Glu Phe Arg Ala
 470 475 480
 Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu Ile Glu Lys
 485 490 495
 Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu Gln Glu
 500 505 510
 Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu Thr
 515 520 525
 Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Gln
 530 535 540
 Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala
 545 550 555
 Gln Ala Leu Gln Ala Gln Gln Arg Glu Gln Glu Leu Thr Gln Lys
 560 565 570
 Ile Gln Gln Met Glu Ala Gln His Asp Lys Thr Glu Asn Glu Gln
 575 580 585
 Tyr Leu Leu Leu Thr Ser Gln Asn Thr Phe Leu Thr Lys Leu Lys
 590 595 600
 Glu Glu Cys Cys Thr Leu Ala Lys Lys Leu Glu Gln Ile Ser Gln
 605 610 615
 Lys Thr Arg Ser Glu Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr
 620 625 630
 Thr Tyr Asp Lys Leu Gly Lys Leu Gln Arg Arg Asn Glu Glu Leu
 635 640 645
 Glu Glu Gln Cys Val Gln His Gly Arg Val His Glu Thr Met Lys
 650 655 660
 Gln Arg Leu Arg Gln Leu Asp Lys His Ser Gln Ala Thr Ala Gln
 665 670 675
 Gln Leu Val Gln Leu Leu Ser Lys Gln Asn Gln Leu Leu Leu Glu
 680 685 690
 Arg Gln Ser Leu Ser Glu Glu Val Asp Arg Leu Arg Thr Gln Leu
 695 700 705
 Pro Ser Met Pro Gln Ser Asp Cys
 710

<210> 53

<211> 880

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5682976CD1

<400> 53

Met Ser Arg Gly Gly Ser Cys Pro His Leu Leu Trp Asp Val Arg
 1 5 10 15
 Lys Arg Ser Leu Gly Leu Glu Asp Pro Ser Arg Leu Arg Ser Arg
 20 25 30
 Tyr Leu Gly Arg Arg Glu Phe Ile Gln Arg Leu Lys Leu Glu Ala
 35 40 45
 Thr Leu Asn Val His Asp Gly Cys Val Asn Thr Ile Cys Trp Asn
 50 55 60
 Asp Thr Gly Glu Tyr Ile Leu Ser Gly Ser Asp Asp Thr Lys Leu
 65 70 75
 Val Ile Ser Asn Pro Tyr Ser Arg Lys Val Leu Thr Thr Ile Arg
 80 85 90
 Ser Gly His Arg Ala Asn Ile Phe Ser Ala Lys Phe Leu Pro Cys

WO 01/07471

PCT/US00/19948

	95		100		105
Thr Asn Asp Lys	Gln Ile Val Ser Cys	Ser Gly Asp Gly Val	Ile		
	110		115		120
Phe Tyr Thr Asn	Val Glu Gln Asp Ala	Glu Thr Asn Arg Gln	Cys		
	125		130		135
Gln Phe Thr Cys	His Tyr Gly Thr Thr	Tyr Glu Ile Met Thr	Val		
	140		145		150
Pro Asn Asp Pro	Tyr Thr Phe Leu Ser	Cys Gly Glu Asp Gly	Thr		
	155		160		165
Val Arg Trp Phe	Asp Thr Arg Ile Lys	Thr Ser Cys Thr Lys	Glu		
	170		175		180
Asp Cys Lys Asp	Asp Ile Leu Ile Asn	Cys Arg Arg Ala Ala	Thr		
	185		190		195
Ser Val Ala Ile	Cys Pro Pro Ile Pro	Tyr Tyr Leu Ala Val	Gly		
	200		205		210
Cys Ser Asp Ser	Ser Val Arg Ile Tyr	Asp Arg Arg Met Leu	Gly		
	215		220		225
Thr Arg Ala Thr	Gly Asn Tyr Ala Gly	Arg Gly Thr Thr Gly	Met		
	230		235		240
Val Ala Arg Phe	Ile Pro Ser His Leu	Asn Asn Lys Ser Cys	Arg		
	245		250		255
Val Thr Ser Leu	Cys Tyr Ser Glu Asp	Gly Gln Glu Ile Leu	Val		
	260		265		270
Ser Tyr Ser Ser	Asp Tyr Ile Tyr Leu	Phe Asp Pro Lys Asp	Asp		
	275		280		285
Thr Ala Arg Glu	Leu Lys Thr Pro Ser	Ala Glu Glu Arg Arg	Glu		
	290		295		300
Glu Leu Arg Gln	Pro Pro Val Lys Arg	Leu Arg Leu Arg Gly	Asp		
	305		310		315
Trp Ser Asp Thr	Gly Pro Arg Ala Arg	Pro Glu Ser Glu Arg	Glu		
	320		325		330
Arg Asp Gly Glu	Gln Ser Pro Asn Val	Ser Leu Met Gln Arg	Met		
	335		340		345
Ser Asp Met Leu	Ser Arg Trp Phe Glu	Glu Ala Ser Glu Val	Ala		
	350		355		360
Gln Ser Asn Arg	Gly Arg Gly Arg Ser	Arg Pro Arg Gly Gly	Thr		
	365		370		375
Ser Gln Ser Asp	Ile Ser Thr Leu Pro	Thr Val Pro Ser Ser	Pro		
	380		385		390
Asp Leu Glu Val	Ser Glu Thr Ala Met	Glu Val Asp Thr Pro	Ala		
	395		400		405
Glu Gln Phe Leu	Gln Pro Ser Thr Ser	Ser Thr Met Ser Ala	Gln		
	410		415		420
Ala His Ser Thr	Ser Ser Pro Thr Glu	Ser Pro His Ser Thr	Pro		
	425		430		435
Leu Leu Ser Ser	Pro Asp Ser Glu Gln	Arg Gln Ser Val Glu	Ala		
	440		445		450
Ser Gly His His	Thr His His Gln Ser	Asp Ser Pro Ser Ser	Val		
	455		460		465
Val Asn Lys Gln	Leu Gly Ser Met Ser	Leu Asp Glu Gln Gln	Asp		
	470		475		480
Asn Asn Asn Glu	Lys Leu Ser Pro Lys	Pro Gly Thr Gly Glu	Pro		
	485		490		495
Val Leu Ser Leu	His Tyr Ser Thr Glu	Gly Thr Thr Thr Ser	Thr		
	500		505		510
Ile Lys Leu Asn	Phe Thr Asp Glu Trp	Ser Ser Ile Ala Ser	Ser		
	515		520		525
Ser Arg Gly Ile	Gly Ser His Cys Lys	Ser Glu Gly Gln Glu	Glu		
	530		535		540
Ser Phe Val Pro	Gln Ser Ser Val Gln	Pro Pro Glu Gly Asp	Ser		
	545		550		555
Glu Thr Lys Ala	Pro Glu Glu Ser Ser	Glu Asp Val Thr Lys	Tyr		
	560		565		570

WO 01/07471

PCT/US00/19948

Gln	Glu	Gly	Val	Ser	Ala	Glu	Asn	Pro	Val	Glu	Asn	His	Ile	Asn	
				575					580					585	
Ile	Thr	Gln	Ser	Asp	Lys	Phe	Thr	Ala	Lys	Pro	Leu	Asp	Ser	Asn	
				590					595					600	
Ser	Gly	Glu	Arg	Asn	Asp	Leu	Asn	Leu	Asp	Arg	Ser	Cys	Gly	Val	
				605					610					615	
Pro	Glu	Glu	Ser	Ala	Ser	Ser	Glu	Lys	Ala	Lys	Glu	Pro	Glu	Thr	
				620					625					630	
Ser	Asp	Gln	Thr	Ser	Thr	Glu	Ser	Ala	Thr	Asn	Glu	Asn	Asn	Thr	
				635					640					645	
Asn	Pro	Glu	Pro	Gln	Phe	Gln	Thr	Glu	Ala	Thr	Gly	Pro	Ser	Ala	
				650					655					660	
His	Glu	Glu	Thr	Ser	Thr	Arg	Asp	Ser	Ala	Leu	Gln	Asp	Thr	Asp	
				665					670					675	
Asp	Ser	Asp	Asp	Asp	Pro	Val	Leu	Ile	Pro	Gly	Ala	Arg	Tyr	Arg	
				680					685					690	
Ala	Gly	Pro	Gly	Asp	Arg	Arg	Ser	Ala	Val	Ala	Arg	Ile	Gln	Glu	
				695					700					705	
Phe	Phe	Arg	Arg	Arg	Lys	Glu	Arg	Lys	Glu	Met	Glu	Glu	Leu	Asp	
				710					715					720	
Thr	Leu	Asn	Ile	Arg	Arg	Pro	Leu	Val	Lys	Met	Val	Tyr	Lys	Gly	
				725					730					735	
His	Arg	Asn	Ser	Arg	Thr	Met	Ile	Lys	Glu	Ala	Asn	Phe	Trp	Gly	
				740					745					750	
Ala	Asn	Phe	Val	Met	Ser	Gly	Ser	Asp	Cys	Gly	His	Ile	Phe	Ile	
				755					760					765	
Trp	Asp	Arg	His	Thr	Ala	Glu	His	Leu	Met	Leu	Leu	Glu	Ala	Asp	
				770					775					780	
Asn	His	Val	Val	Asn	Cys	Leu	Gln	Pro	His	Pro	Phe	Asp	Pro	Ile	
				785					790					795	
Leu	Ala	Ser	Ser	Gly	Ile	Asp	Tyr	Asp	Ile	Lys	Ile	Trp	Ser	Pro	
				800					805					810	
Leu	Glu	Glu	Ser	Arg	Ile	Phe	Asn	Arg	Lys	Leu	Ala	Asp	Glu	Val	
				815					820					825	
Ile	Thr	Arg	Asn	Glu	Leu	Met	Leu	Glu	Glu	Thr	Arg	Asn	Thr	Ile	
				830					835					840	
Thr	Val	Pro	Ala	Ser	Phe	Met	Leu	Arg	Met	Leu	Ala	Ser	Leu	Asn	
				845					850					855	
His	Ile	Arg	Ala	Asp	Arg	Leu	Glu	Gly	Asp	Arg	Ser	Glu	Gly	Ser	
				860					865					870	
Gly	Gln	Glu	Asn	Glu	Asn	Glu	Asp	Glu	Glu						
				875					880						

<210> 54

<211> 855

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5992432CD1

<400> 54

Met	Val	Val	Met	Ala	Arg	Leu	Ser	Arg	Pro	Glu	Arg	Pro	Asp	Leu	
1				5					10					15	
Val	Phe	Glu	Glu	Glu	Asp	Leu	Pro	Tyr	Glu	Glu	Glu	Ile	Met	Arg	
				20					25					30	
Asn	Gln	Phe	Ser	Val	Lys	Cys	Trp	Leu	Arg	Tyr	Ile	Glu	Phe	Lys	
				35					40					45	
Gln	Gly	Ala	Pro	Lys	Pro	Arg	Leu	Asn	Gln	Leu	Tyr	Glu	Arg	Ala	
				50					55					60	
Leu	Lys	Leu	Leu	Pro	Cys	Ser	Tyr	Lys	Leu	Trp	Tyr	Arg	Tyr	Leu	
				65					70					75	
Lys	Ala	Arg	Arg	Ala	Gln	Val	Lys	His	Arg	Cys	Val	Thr	Asp	Pro	

55/93

WO 01/07471

PCT/US00/19948

```

ggctttcatg agataccggc aacaactttg aaaaacttgc tctctttcaa tactcccaat 780
gaagatacat ttctactcacc ctccacccct gctattctgc catgtctttc cctctctctg 840
catagccaga ttggaagtga ctgataccca ccccaaacct tgctgttcac agtctccaat 900
tcttcatatt ctaatgggaa agtaaaggta ttgtttgaag gaaaactgaa gaaaagactt 960
ggcttagaac aaatgaggag ttatatattt tactaggact tttgatagaa attcagctac 1020
aacccaaaga gagaaagatt gagtcttcct gtcaccatag gcaatacctt ttttcttagc 1080
tggcatgcc taaaggccag ctatgtgata ttagaggaag aaaggatttt tctttttaat 1140
gatcttccct gggaaattat tgtggccttt atttaatttc taactacgta cctgggtgcc 1200
tatatcgaca aagagtgaga agagcatttt tactttttta aaaaagcaaa tacatatata 1260
cacatacgta tgcaaatatt atagtataat agtgatccct atggagaatt aaagggtgaga 1320
aagctacttt gtggtgtcta ggtttctgat aaaagggatg atcttaactg aagaatttaa 1380
agagatactt aaacagagca aatgtagtag gaacaaggga gtgagcctta taagaggacg 1440
ttcagtctca tttattaaaa taataactga gactgggaga ggtggctcat gcctgtaaat 1500
cccagcactt tggtagcctg aagtgggaga ttgcttgagt ccaggagacc agcctgggca 1560
acatagcaaa acctcatctc tatttaaaaa aaaaaaaa 1598

```

```

<210> 56
<211> 1432
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1210462CB1

```

```

<400> 56
tgagaatgaa agtggatgcc cgcgaatccc ggaagtcaga ctgttttttt cagttccctg 60
gaggcttttt gatactgatt cgcgtacacc tgttggttga aagctctcag cgggacaatg 120
ctgaccacgc tgaaaagcaaa atcagagggg aagcttgcaa aacagatttg caaagttgtg 180
ttggatcatt ttgaaaaaca gtattccaaa gaactcggag atgcctggaa tacagtaagg 240
gagatactaa catctccatc atgtctggcaa tatgctgtcc tgcttaaccg attcaattat 300
ccttttgaac tggaaaagga tttacatttg aagggtatc acacactctc tcagggatct 360
ttacccaact atcctaaatc agtgaagtgt taccttagca gaactccggg ccgaatccct 420
tcagaaagac accaaattgg aaacctgaaa aaatattatc tcctaaatgc tgcttctctt 480
ctcccagtgt tggctctgga attaagggat ggggagaagg ttctggatct ctgtgctgct 540
cctggaggga aatcaatagc tctgctgcag tgtgctgtc caggttatct tcattgtaat 600
gaatatgata gtctgagatt gaggtggcta aggcagacgt tggaatcttt catcccacag 660
cctttgataa atgtaattaa agtgtctgaa ttggatggca gaaaaatggg agatgcacag 720
cctgaaatgt ttgacaaggt gtagtggtat gctccgtgtt caaatgatcg aagctgggtg 780
ttttctcttg actctcagaa ggcacccctg aggataagtc aaaggaggaa tttgcctctt 840
ctacagatag agctgttaag gtctgcaatt aaggccttac gtccctggagg gatacttgta 900
tactctacat gcacgctttc caaggcagaa aatcaagatg tgatcagtga aatttttaaac 960
tcccacggta acatcatgcc tatggacatt aaagggaatg caaggacttg ctcccacgac 1020
ttcacatttg ctcccactgg ccaggaatgt gggctcttag tgattccaga taaggggcaaa 1080
gcctggggcc caatgtatgt agccaaattg aagaaatcat ggagcacagg aaaatggtga 1140
catgaatttg taaactgtgt ttatgtgtta ttatatttat atttctgaac tcagtacatg 1200
ttaatattta aataattatg cagtaacttt ctctgggtct gtttggaatc ctatttagtt 1260
aatactttag catcttagaa tctaggcttg agaattgttc aggtgtattt ttttcttaga 1320
aatatatctg taacaatgat ttaagggtgt gcagatgggt tttgttctat attataaatc 1380
tgctgtcttt gcttggcatt ttatagttaa attaattaga atatgtggtt tt 1432

```

```

<210> 57
<211> 2317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1305252CB1

```

```

<400> 57
gcgggtgctg ctagcggagg cgccatattg gaggggacaa aactccggcg acacgagtga 60
cacaaataaa cccctggacc ccttgtttcc ctcagctcta agggccgcga tgtgtacct 120

```


WO 01/07471

PCT/US00/19948

```

agaagactat ctggaaatga ttgagcagct tcctatggat ctgcgggacc gcttcacgga 180
aatgcgcgag atggacctgc aggtgcagaa tgcaatggat caactagaac aaagagtcag 240
tgaattcttt atgaatgcaa agaaaaataa acctgagtg agggaagagc aaatggcatc 300
catcaaaaaa gactactata aagcttttga agatgcagat gagaagggtc agttggcaaa 360
ccagatatat gacttggtag atcgacactt gagaaagctg gatcaggaac tggctaagtt 420
taaaatggag ctggaagctg ataatgctgg aattacagaa atattagaga ggcgatcttt 480
ggaattagac actccttcac agccagtga caatcaccat gctcattcac atactccagt 540
ggaaaaaagg aatatataat caacttctca ccatacgaca acagatcata ttctgaaaa 600
gaaatttaaa tctgaagctc ttctatccac ccttacgtca gatgcctcta aggaaaatac 660
actaggttgt cgaataata attccacagc ctcttctaac aatgcctaca atgtgaattc 720
ctcccaacct ctgggactct ataacattgg ctctgttatc tcaggaactg gtgcaggggc 780
aattaccatg gcagctgctc aagcagttca ggctacagct cagatgaagg agggacgaag 840
aacatcaagt ttaaaagcca gttatgaagc atttaagaat aatgactttc agttgggaaa 900
agaattttca atggccaggg aaacagttgg ctattcatca tcttcggcac ttatgacaac 960
attaacacag aatgccagtt catcagcagc cgactcacgg agtggtcgaa agagcaaaaa 1020
caacaacaag tcttcaagcc agcagtcac atcttctctc tctcttctt ccttatcatc 1080
gtgttcttca tcatcaactg ttgtacaaga aatctctcaa caacaactg tagtgccaga 1140
atctgattca aatagtcagg ttgattggac ttacgaccca aatgaacctc gatactgcat 1200
ttgtaatcag gtatcttatg gtgagatggg gggatgtgat aaccaagatt gccctataga 1260
atggttccat tatggctgcg ttggattgac agaggcacca aaaggcaaat ggtactgtcc 1320
acagtgcact gctgcaatga agagaagagg cagcagacac aaataaagggt ggtccttttg 1380
tttgatgaag aaataaactt cagctgaaga ttttatatag gactttaaaa agaagagaag 1440
agaaagaaga aacaatgcat ttccaggcaa ccacttaaag gatttacata gacaatccta 1500
taagatcttg aacttgaatt ttatgggttg tattttaata atgtaagtaa attatttatg 1560
cactctgggt gtgctatgaa tattattcca gttagccttg gattatttca gtggccaaca 1620
tatgcagaca tttgtactcc tcaaccattt tctcaaagta atgggcattc tatgatttag 1680
acttcaagga attccaatga tgaagatttt aaggaaagta ttttatattc aacagggtata 1740
ttctgctgca tgtactgtac tccagagctg ttatgtaaca ctgtatataa atggttgcaa 1800
aaaaaaaaaa aaagtcagtg cttctaaaaa gaatttaaga taatggtttt taaaatgcct 1860
ttataataag ctttgtttct ttgtgaaact aattcagcag gctgaaggaa atggttctatg 1920
tgataatgtg ggtggtatc ctctagagta cctgggtaca taaacagaaa ctctcttagg 1980
taaaaagtaa tttgtgcat tagtctttct atgtttctgc atccagatag agtgcagttc 2040
atgacgcgag gggccggggg actgaaaggg gaaagggcgt taaagtgata catttttata 2100
cccaaagtgt tttatttttt tttggtgcca agtaaacctt ttaaaaattg gccaatgtga 2160
attaaggggg gttaaaaaata aaaggttttt ttaaaaaaaa tttaaaacaa aacaaaagaa 2220
gaaaaaaaaa aaggggccgg gcccccgcga tcttaagttg aagcctcccg ttggaacccc 2280
gcggggggaat tttaaatttt ccgggggacc cggttga 2317

```

<210> 58

<211> 1774

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1416289CB1

<400> 58

```

tgtaagcta aaagttttga gcatgttctg gcaagattaa tctgatttta ttttaactat 60
aagtcctact taataaattg taaatacatg gcatataatg taataattat atattttaat 120
ttcaggtgcc ttgaatggct tctaaacaat ttgatgactc accagaatgt tgaacttttt 180
aaagaactca gtataaatgt catgaaacag ctcatgggt catctaactt atttgtgatg 240
caagtggaga tggatatata cactgctcta aaaaagtggg tgttccttca acttgtgctc 300
tcttggaaat gatcttttaa acagcttttg acagaaacag atgtctggtt ttctaaacag 360
aggaaagatt ttgaaggtat ggcctttctt gaaactgaac aaggaaaacc atttgtgtca 420
gtattcagac atttaagggtt acaatatatt atcagtgatc tggcttctgc aagaattatt 480
gaacaagatg ctgtagtacc ttcagaatgg ctctcttctg tgataaaca gcagtggttt 540
gctatgctgc gggcagaaac ggacagttag gtggggcctc aagaaatcaa taaagaagaa 600
ctagagggaa acagcatgag gtgtggtaga aagcttgcca aagatggtga atactgctgg 660
cgttggacag gttttaactt cggcttcgac ctacttgtaa cttacaccaa tcgatacatc 720
attttcaaac gcaatacact gaatcagcca tgtagcggat ctgtcagttt acagcctcga 780
aggagcatag catttagatt acgtttggct tcttttgata gtagtgaaa actaatatgt 840
agtagaacia ctggctatca aatacttaca cttgaaaagg atcaggaaca agtgggtgatg 900

```


WO 01/07471

PCT/US00/19948

```

ctgtctcttc tgcaagagag cegtctgcac ttctgttagc ataaagatga agatgccttc 300
taagaaatth ggacacatcc ctgtctacac actgggcttt gagagtcctc agaggggtatc 360
agctgccaac accgcgcca tccagagaag agacatcttt cagtctctgc aagggccaca 420
gtggcagagc gtggaggagg cgttccccc catctactcc cacggctgtg tectgaagga 480
tgtctgcagt gagtgcacca gctttgtggc agacgtggtg cgttccagcc gcaagagcgt 540
ggacgtcctc aacactacgc cagcagcag tcgccagacc caatccctct acatccctaa 600
caccaggact cttgacttca agtgacagcc ccagggtggc aggcctccag gaggcaccag 660
gcaggccctg tatcaggcta ggacgtctg agctgtgcat gtacatatat acatatatag 720
atacatttat aatatataca cacagtctat atatttatat acactgtttc ctggcccccag 780
agctcatttg ggttcaggcg cacttcaaaa cctccctgg gggaggctgt ttcttctcag 840
gattccttgc cagggaggaa ggggaggaa cagggtgggt tttctcactg aagagagaaa 900
gcagaagggt ctagatcctg gcacagactg catcccatgt tcccatgtct ttctccgtcc 960
ccaggaatgc gaacggcagt tcccttccc cagtggacgt ctaggtgggg acaggggtatc 1020
ttggctccca gctggaccag agtgcctgc ttgctctgc tctccctttg tggggactca 1080
ggcagcagag gcattctggga agtctctgag taggcagggt cctcctggga ggcaccccca 1140
cctgtttgaa aggtctggcc aggcgtggtg gttcaggcct gtaattccag cactttggga 1200
ggccgaggag ggaggatcac ctgaggtcag gagtttgaga ccagcctggc caacatgatg 1260
aatgtttgtc tctactgaaa atgcaaaaat tagccaggta tagtggcagg aacctgtaat 1320
cccagctaca g

```

<210> 61

<211> 3227

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1752768CB1

<400> 61

```

tgcaggtacc tccatggctc cgggtggctgt gacggcggca gtggcgccctg tctgtgccat 60
aaacagcgat ttctcagatt tgcgggaaat taaaaagcaa ctgctgctta ttgcgggcct 120
taccggggag cggggcctac tacacagtag caaatggctg gcggagttgg ctttctctct 180
ccctgcattg cctctggccg agctgcaacc gcctccgcct attacagagg aagatgcccc 240
ggatatggat gcctataccc tggccaaggc ctactttgac gttaaagagt atgatcgggc 300
agcacatttc ctgcatggct gcaatagcaa gaaagcctat tttctgtata tgtattccag 360
atatctgtct ggagaaaaaa agaaggacga tgaacagtt gatagcttag gccccctgga 420
aaaaggacaa gtgaaaaatg aggcgcttag agaattgaga gtggagctca gcaaaaaaca 480
ccaagctcga gaacttgatg gatttggact ttatctgtat ggtgtgggtg ttcgaaaact 540
ggacttgggt aaagaggcca ttgatgtgtt tgtggaagct actcatgttt tgcctttgca 600
ttggggagcc tggttagaac tctgtaacct gatcacagac aaagagatgc tgaagttcct 660
gtctttgcca gacacctgga tgaaagagtt ttttctggct catatataca cagagttgca 720
gttgatagag gaggccctgc aaaagtatca gaatctcatt gatgtgggct tctctaagag 780
ctcgtatatt gtttcccaaa ttgcagttgc ctatcacaat atcagagata ttgacaaagc 840
cctctccatt tttaatgagc taaggaaaca agacccttac aggattgaaa atatggacac 900
attctccaac cttctttatg tcaggagcat gaaatcggag ttgagttatc tggctcataa 960
cctctgtgag attgataaat atcgtgtaga aacgtgctgt gtaattggca attattacag 1020
tttacgttct cagcatgaga aagcagcctt atatttccag agagccctga aattaaatcc 1080
tcggtatctt ggtgcctgga cactaatggg acatgagtac atggagatga agaacacgtc 1140
tgctgctatc caggcttata gacatgccat tgaggatcac aaacgggact acagagcttg 1200
gtatggcctc gggcagacct atgaaatcct taagatgcca ttttactgcc ttattattg 1260
tagacgggce caccagcttc gacccaatga ttctcgcatg ctggttgctt taggagaatg 1320
ttacgagaaa ctcaatcaac tagtggaagc caaaaagtgt tattggagag cttacgccgt 1380
gggagatgtg gagaaaatgg ctctggtgaa actggcaaag cttcatgaac agttgactga 1440
gtcagaacag gctgcccagt gttacatcaa atatatccaa gatatctatt cctgtgggga 1500
aatagtagaa cacttggagg aaagcactgc ctttcgctat ctggcccagt actattttaa 1560
gtgcaaacct tgggaatgaa cttcaacttg tgcacaaaag tgttgtgcat ttaatgtac 1620
ccgggaagaa ggtaaggcct tactccggca aatcctacag cttcggaacc aaggcgagac 1680
tcctaccacc gaggtgcctg ctcccttttt cctacctgct tcaactctct ctaacaatac 1740
ccccacacgc agagttttct cactcaactt gtcttctgtc acgccatagt tggctactct 1800
caagccagca cattgttaga cccatcttaa ttaagcctta cctccatgta aagaacagca 1860
cgtctgttcc aaggacctca gctcttcttg tttctacaga tggcaacagc tccataggga 1920
cagcttgat aattacctc agaggccaac tgacagaatc ctggcaggaa cagacattat 1980

```

WO 01/07471

PCT/US00/19948

```

cttgccagtt agaagtactt ctgtctcact tatgtccaaa gagtggctat agatcttggc 2040
cttcttccct gaatgctttt ttttttttgg cccccaagaa agtccctttt atagcacttt 2100
agcacaggca atgctacagg aacaaagttt caatgctgct gagagtgaag gaaaggagga 2160
aagctcgcca ctctaccctg agctggcagt agggcactga gtaccctagg aagaagtcag 2220
agcaatggat acaaatgacc ttgctcttgg atttgctgag catgatccct attctgatgt 2280
cagagattag gtttaaattg aatagagcta tccatttggt cttactctct agggagacaa 2340
tcttccaaaa cagttttggg ggggtcttct aaagctttca aattggaagt aactttattc 2400
acctagagtt gaataaaaaga agggcaaaaa taatctcaca gagcttggaa ctgctgatag 2460
cccttactga gggcaaaaaga tggctatatatt gttagctata ctccctacca agcaagcaag 2520
gagataggat tatagataat ttcacggaca tttggaaata acattggtga ttatacagac 2580
aagaataaac tcacttcaag ctggtctgtt ttaataaatt ttcaacgtaa ttgtctatct 2640
tttccctcc catctgcaac agaatacatt ttttccagcc tttatctaga tgaggtaaag 2700
ggaatcattc ttatggtgct cttggagagt ttcaggcctg tgcattgtgtg tacagcagga 2760
ggtaatatgc tataatgtct gctgtaatat atttgcacag tagatgctat ggatcattct 2820
gagctcaggg tccagacttt attcttattc ccagaatttt gtgttacgtt ttacctcct 2880
aacatatgac acttcatctt atattaagga aggtttagaa tatctaatac gacttgaatt 2940
catttggtac taagccttct caggcaagct gtatactagt tactggtctc cactgccatg 3000
ccttttcaag gtccccatgg tccagaatga tgtttgattc ttaatttttc tgtccctttt 3060
ataattttgt ttaatgattt tgctacattt ggaattcaat aaaaaatgtg aacaataata 3120
tctttaatat aactgttttt gtgtgcatag aaatcatata agtaataaaa aaaaaacaa 3180
aacatgagat tacataggtg gttataatac aaaagtgaga aaaaagc 3227

```

<210> 62

<211> 1865

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1887228CB1

<400> 62

```

gttctagatc gcgagcggcc gcctcccgga ggtcctcctg atgccctagg aagacgcgac 60
tcagaatttg gccaggagt gaaggccaag aagcccatcc agactaagtt ccgaatgcc 120
ctcttgaact ggggtggcatt gaaaccagc cagatcaccg gcactgtctt cacagagctc 180
aatgatgaga aggtgctgca ggagctagac atgagtgatt ttgaggaaca gttcaagacc 240
aagtcccaag gcccagcct ggacctcagc gctctcaaga gtaaggcagc ccagaaggcc 300
cccagcaagg cgacactcat tgaggccaac cgggccaaga acttgcccat caccctgcg 360
aagggcaacc tgggggcccga gcgcattctg caagccattg aggcgtacga cctgcaggct 420
ctgggccttg acttcttgga gctgctgat cgttctctgc ccacagagta tgagcgcagc 480
ctcatcacc gctttgagcg ggagcagcg ccaatggagg agctgtcaga ggaggaccgc 540
ttcatgctat gcttcagccg catcccgcg cgtccggagc gcatgaccac actcaccttc 600
ctgggcaact tcccggacac agcccagctg ctcatgccg aactgaatgc catcattgca 660
gcctcaatgt ccatcaagtc ctctgacaaa ctccgccaga tcttgagat tgtcctggcc 720
tttggaact acatgaacag tagcaagcgt ggggcagcct atggcttccg gctccagagc 780
ctggatgcgc tgttgagat gaagtcgact gatcgcaagc agacgctgct gcactacctg 840
gtgaagggtca ttgctgagaa gtaccgcgaa ctcacaggct tccacagcga cctgcacttc 900
ctggacaagg cgggctcagt gtccctggac agtgtcctgg cggacgtgcg ctccctgcag 960
cgaggcctag agttgacaca gagagagttt gtgcggcagg atgactgcat ggtgctcaag 1020
gagttcctga gggccaactc gccaccatg gacaagctgc tggcagacag caagacggct 1080
caggaggcct ttgagctgtt ggtggagtac ttcggagaga accccaagac cacatcccca 1140
ggcctgttct tctccctctt tagcgccttc attaaggcct acaagaaagc tgagcaggag 1200
gtggaacagt ggaaaaaaga agccgctgcc caggaggcag gcgctgatac cccgggcaaa 1260
ggggagcccc cagcacccaa gtcaccgcca aaggcccggc ggccacagat ggacctcatc 1320
tctgagctga aacggaggca gcagaaggag ccactcattt atgagagcga ccgtgatggg 1380
gccattgaag acatcatcac agatctgcgg aaccagccct acatccgcgc agacacaggc 1440
cgccgcagt cccgtcgcg tccccggc aggtcacctc cgacctctcg 1500
ctgtagccgc tatttctgca ggtggattct gcagggtgtg ggggccgtgg acaggctgag 1560
gctcaaggaa ggtggtctc agctcggtg gccgggcagc ccctcctccg ctgtggcccg 1620
cctcaaacgg gctggtgcat cctcctcttg gccacagagg gcagcatcgc ccgccccttc 1680
ccccaaatgc tgcttgagc acccacccta aagccccctc caaatagcca tacttagcct 1740
cagcaggagc ctggcctgta acttataaag tgcacctcgc ccccgcaagc cccagcccg 1800
aggaccgtcc atggacctta tttttatatg agattaataa agatgtttgc aaaaaaaaa 1860

```

WO 01/07471

PCT/US00/19948

aaaaa

1865

<210> 63
<211> 1924
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1988468CB1

<400> 63
agctgccggg cggctcctgcc gagctgtgag ggcaacggag gggaaataaa agggaaacggc 60
tccgaatctg cccagcggc cgctgcgaga cctcggcgcc gacatcgca cagagcgctt 120
tgcacgccag gaaggtcccc tctatgtgct gctgagccgg tcctggacgc gacgagcccg 180
ccctcggtct tcggagcaga aatcgcaaaa acggaaggac tggaaatggc agaccatatg 240
atggccatga accacgggcg cttccccgac ggcaccaatg ggctgcacca tcaccctgcc 300
caccgcatgg gcatggggca gttcccgagc ccccatcacc accagcagca gcagccccag 360
cacgccttca acgcccataat gggcgagcac atacactacg gcgcgggcaa catgaatgcc 420
acgagcggca tcaggcatgc gatggggccg gggactgtga acggagggca cccccgagc 480
gcgctggccc ccgcgccag gtttaacaac tcccagttca tgggtcccc ggtggccagc 540
cagggaggct ccctgccggc cagcatgcag ctgcagaagc tcaacaacca gtatttcaac 600
catcaccctt acccccacaa ccactacatg ccggttttgc accctgctgc aggccaccag 660
atgaacggga caaacagca cttccgagat tgcaacccca agcacagcgg cggcagcagc 720
acccccggcg gctcgggcgg cagcagcacc cccggcggt ctggcagcag ctggggcggc 780
ggcgcgggca gcagcaacag cggcgggcgc agcggcagcg gcaacatgcc cgcctccgtg 840
gcccacgtcc ccgctgcaat gctgccgccc aatgtcatag aactgattt catcgacgag 900
gaagtcttta tgcctttggt gatagaaatg ggtttggacc gcatcaagga gctgccgaa 960
ctctggctgg ggcaaacga gtttgatttt atgacggact tcgtgtgcaa acagcagccc 1020
agcagagtga gctgttgact cgatcgaaac cccggcgaaa gaaatcaaac cccaacttc 1080
ttcggcgtga attaaaagaa acattccctt agacacagta tctcactttt cagatcttga 1140
aagggttgag aacttggaag caaagtaaac tataaacttg taaaaattgg ttttaaaaaa 1200
aattgctgcc actttttttt cctgtttttg ttctgttttt gtagccttga cattcaccca 1260
cctcccttat gtagttgaaa tatctagcta acttgggtctt ttctgttgtt tgtttttact 1320
cctttccctc actttctcca gtgctcaact gtttagatatt aatcttggca aactgcttaa 1380
tcttgtggat tttgtagatg gtttcaaatt actgaactgc attcagattt acgagtgaag 1440
ggaaaaattg cattagttgg ttgcatgaac ttcgaggggc agatattact gcacaaactg 1500
ccatctcgct tcattttttt aactatgcat ttgagtacag actaattttt aaaatatgct 1560
aaactggaag attaaacaga tgtgggcccac actgttcttg atcaggaaag tcatactgtt 1620
cactttcaag ttggtgttcc ccccgccgcg cccccccacc cccatatgta cagatgataa 1680
taggggtgtg aatgtcgtca gtggcaaaaca tttcacagat ttttattttg tttctgtctt 1740
caacattttt gacactgtgc taatagttat attcagtaaa tgaaaagata ctactgtgtt 1800
gaaagctttt taggaaattt tgacagtatt tttgtacaaa acattttttt gaaaaaatac 1860
ttgttaattt attctatttt aatttgccaa tgtcaataaa aagttaagaa ataaaaaaaa 1920
aaaa 1924

<210> 64
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 2049176CB1

<400> 64
ggcctgggtcc gcagcgccct gcgcccaccc gccccggacg tggggcccaa gccccgtga 60
agatgggtgtc ctggatgatc tccagagccg tgggtgctgg gtttggaatg cttttatcctg 120
catattattc atacaaagct gtgaaaacaa aaaacgtgaa ggaatatgtt cgatggatga 180
tgtactggat tgtttttgct ctctatactg tgattgaaac agtagccgat caaacagtgt 240
cttgggtttcc cctgtactat gagctgaaga ttgcttttgt catatggctg cttttccctt 300
ataccaaagg agcaagttta atatatagaa aattccctta tccacttctt tcttcaaagg 360
aaagggagat tgatgattat attgtacaag caaaggaacg aggctatgaa accatggtaa 420

WO 01/07471

PCT/US00/19948

```

acttttgacg gcaaggttta aaccttgacg ctactgctgc tgttactgca gcagtaaaga 480
gccaaggagc aataactgaa cgtttaagaa gcttcagtat gcatgattta acaactatcc 540
aaggtgatga gectgtggga caaagaccat accaacctct accagaagca aaaaagaaaa 600
gtaaaccagc ccccgatgaa tcagcagggt atggaattcc actgaaagac ggagatgaga 660
aaacagatga agaagcagag gggccatatt cagataatga gatgttaaca cacaaagggc 720
ttcgaagatc gcaaagcatg aaatctgtga aaaccaccaa aggccgcaaa gaggtgcggt 780
acgggtcact aaaatacaaaa gtgaagaaac gaccacaagt gtatttttag tcatctacac 840
gtcaaataatc ccaagacaga ttatgctaaa tacatcgact tcatcttcta acatgatata 900
ttcaggattt acacattaaa atgattattt aaattgtggc agtgatgg 948

```

<210> 65

<211> 2035

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2686765CB1

<400> 65

```

gaccgtggcc ctgaccgcc aacccccgct tgccccaag ccgggaacca cagtggcctc 60
aggagtgact gcacggagtg atgcaggaca agtgacaggt gggcatggag ctgccgcagc 120
aacatcagca tcagcaggac aggtcctga ggaccctca ggccctggca caggccctc 180
tgggacttgt gaggtccgg tagctgtcgt gaccgtgacc ccagctccgg agcctgctga 240
aaactctcaa gacctgggct ccacgtccag cctgggacct ggcatctctg ggccctcagg 300
gcaggccccg gacacgtga gttacttgg ctcctgtgag ctcatgtctg ggaccttgg 360
gtccttggcg gatgatgtga gctccatggg ctcagattca gagataaacg ggctggccct 420
gcgcaagacg gacaagtatg gcttccttgg gggcagccag tactcgggca gcctagagag 480
ctccattccc gtggacgtgg ctcggcagcg ggagctcaaa tggctggaca tgttcagtaa 540
ctgggataag tggctgtcac ggcgattcca gaaggtgaag ctgcgctgcc ggaaggggat 600
ccctcctct ctcagagcca aagcctggca gtacctgtct aatagcaagg aacttctgga 660
gcagaaccca ggaaagtgtg aggagctgga acgggctcct ggggacccca agtggtgga 720
tgtgattgag aaggacctgc accgccagtt cctttccac gagatgtttg ctgctcagg 780
ggggcatggg caacaggacc tgtaccgaat cctgaaggcc tacaccatct accggcctga 840
cgagggttac tgccaggccc agggccccgt ggctgcggtc ctgctcatgc acatgcctgc 900
ggagaagcct tttggtgct ggggtgcag ctgcgacaag tacctccag gttactacag 960
tgcagggtcg gaggccattc agctggacgg ggagatctt tttgactcc tgcgcggggc 1020
ctccccgtcg gcgcctcgcc acctgcagcg gcagcgcat gaccctgtgc tctacatgac 1080
ggagtggttc atgtgcattc tcgcccgcac cctgccttgg gcgtcgggtg tgcgtgtctg 1140
ggacatgttt ttctgtgaag gcgttaagat catcttccgg gtggccctgg tccgtctcg 1200
ccacacgctg ggctcagtg agaagctgcg ctccgtgcaa ggcatgtatg agaccatgga 1260
gcagctgctg aacctgccc agcagtgcat gcaggaagac ttcttgggtg atgaggtgac 1320
caatctgccc gtgacagaag cactgattga gcgggagaat gcagcccagc tcaagaagtg 1380
gcgggaaacg cggggggagc tgcagtatcg gccctcacgg cgactgcatg ggtccccggc 1440
catccacgag gacgcgggc ggcaacagcc accctgggc cctcctcca gcctcctcag 1500
cctccttggc ctcaagagcc gaggtcccg gccagctgga ggggccccgt ccccgccg 1560
ccccgtccgc agagccagt ctgggcctgc cccagggcct gtgggtcact ctgagggact 1620
gcateccatc ctccctcac ccactggcaa tagcacccc ttgggttcca gcaaggagac 1680
ccggaagcag gagaaggagc ggcagaaaca ggagaaggag cggcagaaac aggagaagga 1740
gcggggagaag gagcggcaga agcaggagaa agagcgagag aagcaggaaa aggagcgaga 1800
gaagcaggag aaggagcggc agaagcagga gaagaaggct caaggccgga agctttcgct 1860
gcgtcgaaag gcagatgggc cccagggccc ccatgatggg ggggacaggc cctcagccga 1920
ggccccggcag gacgcttact tctgacctct gccctggggc tggactgcat ggccccctc 1980
tttccctcag ccaagaacag gcctggccca aggtgccacc ccctagcacc ttgtc 2035

```

<210> 66

<211> 766

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3215187CB1

WO 01/07471

PCT/US00/19948

<400> 66

```

cttggaggga gtgcggtcct ctagggaggc atcggggctcc taggggcttc ttggcgtgtg 60
tgggtgggatt ggggtccgcc ggccatggcc ttcactttcg ctgcgtttctg ctacatgctg 120
tctctgggtgc tgtgcgctgc gctcatcttc ttcgccatct ggcacataat tgcctttgat 180
gagttaagga cagatttttaa gagccccata gaccagtgca atcctgttca tgcgagggaa 240
cggttgagga acatcgagcg catctgcttc cttctgcgaa agctgggtgct gccagaatac 300
tccatccata gcctcttctg cattatgttc ctgtgtgcgc aagagtgggt cacgctgggg 360
ctgaatgtcc ctctactttt ctatcacttc tggagggtatt tccactgtcc agcagatagc 420
tcagaactag cctacgaccc accggtgggtc atgaatgccg acactttgag ttactgtcag 480
aaggaggcct ggtgtaagct ggcttctat ctcctctcct tcttctacta cctttactgc 540
atgatctaca ctttagtgag ctcttaacgc aaagaccatg cacatcatca gagactgaga 600
tgggagaggc ctgagacgga gaggtgcatt tctgctgggt actggaggag ggaccagaat 660
gaggatacgt gagatataga cccggcaggc agtcagactg aatgggagct ggaatcacgc 720
agcagctggg agccgagtta accctgcgtg tctgtgtcac cctggt 766

```

<210> 67

<211> 2503

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3500375CB1

<400> 67

```

tgtcctcggc ggccctgggtg gctactgccc ctgctgctgt cgtaggcgag gacggctgtt 60
agtgtctgtg ctgttggttc gtcgcggcgg cgaaggagga ggaggaagag ggcgaggcga 120
caagagaaga aggaggcagg cgcggcggca gcggcggcgc cccgagccgg cggaggcgag 180
gggggggaag atggcggacg tgcttagcgt cctgcgacag tacaacatcc agaagaagga 240
gattgtggtg aagggagacg aagtgatctt cggggagttc tcttggtgcca agaattgtga 300
gaccaactat gttgtttggg ggactggaaa ggaaggccaa cccagagagt actacacatt 360
ggattccatt ttattttctac ttaataacgt gcacctttct catcctgttt atgtccgacg 420
tgcagctact gaaaatattc ctgtgggttag aagacctgat cgaaaagatc tacttgata 480
tctcaatggt gaagcgtcaa catcggcaag tatagacaga agcgtccct tagaaatagg 540
tcttcagcga tctactcaag tcaaacgagc tgcagatgaa gttttagcag aagcaaagaa 600
accacgaatt gaggatgaag agtgtgtgcg ccttgataaa gagagattgg ctgccggttt 660
ggagggtcac aaagaaggga ttgtacagac tgaacagatt aggtctttgt ctgaagctat 720
gtcagtgga aaaattgctg caatcaaagc caaaattatg gctaagaaaa gatctactat 780
caagactgat ctagatgatg acataactgc ccttaaacag aggagttttg tggatgctga 840
ggtagatgtg acccgagata ttgtcagcag agagagagta tggaggacac gaacaactat 900
cttacaagac acaggaaaga atttttccaa gaacattttt gcaattcttc aatctgtaaa 960
agccagagaa gaaggcggtg cacctgaaca gcgacctgcc ccaaatgcag cacctgtgga 1020
tcccactttg cgcaccaaac agcctatccc agctgcctat aacagatacg atcaggaaag 1080
attcaaagga aaagaagaaa cgggaaggctt caaaattgac actatgggaa cctaccatgg 1140
tatgacactg aaatctgtaa cggagggtgc atctgccggg aagactcaga ctctgcagc 1200
ccagccagta ccaagaccag tttctcaagc aagacctccc ccaaatacaga agaaaggatc 1260
tcgaacaccc attatcataa ttcttgacg taccacctct ttaataacca tgcttaatgc 1320
aaaagacctt ctacaggacc tgaaatttgt cccatcagat gaaaagaaga aacaagggtg 1380
tcaacgagaa aatgaaactc taatacaaag aagaaaagac cagatgcaac cagggggcac 1440
tgcaattagt gttacagtac cttatagagt agtagaccag ccccttaaac ttatgectca 1500
agactgggag cgcgtttag cctgttttgt gcagggtcct gcatggcagt tcaaagggtg 1560
gccatggctt ttgcctgatg gatcaccagt tgatatatt gctaaaatta aagccttcca 1620
tctgaagtat gatgaagttc gtctggatcc aaatgttcag aaatgggatg taacagtatt 1680
agaactcagc tatcacaac gtcatttgga tagaccagt ttcttacggt tttgggaaac 1740
attggacagg tacatggtaa agcataaatc gcacttgaga ttctgaatta tttggctcct 1800
ccatttcttg aaattgagac tcaagcttta tgaatttata aagaacttaa aaatgaagaa 1860
ggtcacagat tgatctttaa taagacctta ttgatgctt tgtgcttcaa ggagatgata 1920
cctgtcatcc atataagcaa actttttggc ttacaactat ttttttaata ttagccttct 1980
agtctgtaat ggaaattgta tattttgata gaagttttt ctccattggg taaattagca 2040
ttacttaaaa tttgtttctt tagaaaataa atgcagggtt taaatgtgtg tatatttaga 2100
gattataagg ctctctgagc catcttctga tttttcattg ctctataatt ctttttactg 2160
aaaatactat gttatgaatg gtattaaatt ttagtctctg gaacatccaa aaccaagcaa 2220
agggatgtga ctattttgaa tgaatcagaa tgtcaacttg tatgtacact atatctacac 2280

```

WO 01/07471

PCT/US00/19948

```

ttactcatta tttaaaaaga ataatgaaaa atctagatca attcttcaat ttgattgaac 2340
tggttcagcct tttcaagatt tctttattta caaatgatta cattttaaag aatgtacatt 2400
cttctcactg actttggtga ttttgaaacc tagaatgatg tgtttctatc tgtaatatct 2460
ttccatttga aaaaaatctc aaaacacaga ttaaaaccac aaa 2503

```

<210> 68
 <211> 541
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 5080410CB1

```

<400> 68
atggcgctcca tgcgggagag cgacacgggc ctgtggctgc acaacaagct gggggccacg 60
gacgagctgt gggcgccgcc cagcatcgcg tccctgctca cggccgcggt catcgacaac 120
atccgtctct gcttccatgg cctctcgctc gcagtgaagc tcaagttgct actcgggacg 180
ctgcacctcc cgcgcgcgac ggtggacgag cctcctattt tgccaatgaa gggcgcccta 240
atggagatca tccagctcgc cagcctcgac tcggaccctt ggggtgctcat ggtcgccgac 300
atcttgaagt cctttccgga cacaggctcg cttaacctgg agctggagga gcagaatccc 360
aacgttcagg atattttggg agaacttaga gaaaagggtg gtgagtgtga agcgtctgcc 420
atgctgccac tggagtgccg gtacttgaac aaaaacgccc ctgacgaccc tcgcgggacc 480
cctcactccc ccgggtgaag cattttcagt taaagcggaa acccaagagc gccacgctgc 540
g

```

<210> 69
 <211> 937
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 5218248CB1

```

<400> 69
gactacgacc aaaacaaagg agcggcgggc gggagcggac ttaccttacc ttctctgcct 60
tcggcgcgct tctcagccgg gccgcccacc caaaggagcc gtccgactat gtctaactatg 120
gagaaacacc tggttaacct gaagttcgcg gccaaagaac tgagtaggag tgccaaaaaa 180
tgcgataagg aggaaaaggc cgaaaaggcc aaaattaaaa aggccattca gaagggcaac 240
atggaagttg cgaggatata cgcgaaaaat gccatccgcc agaagaacca ggcgggtgaat 300
ttcttgagaa tgagtgcgag agtcgatgca gtggctgcca ggggtccagac ggcgggtgacg 360
atgggcaagg tgaccaagtc gatggctggg gtggttaagt cgatggatgc gacattgaag 420
accatgaatc tggagaagat ttctgctttg atggacaaat tcgagcacca gtttgagact 480
ctggacgtcc agacgcagca aatggaagac acgatgagca gcacgacgac gctcaccact 540
ccccagaacc aagtggatat gctgctccag gaaatggcag atgaggcggg cctcgacctc 600
aacatggagc tgccgcaggg ccagaccggc tccgtgggca cgagcgtggc ttcggcggag 660
caggatgaac tgtctcagag actggcccgc cttegggatc aagtgtgacg gcagaacccg 720
ctctgaggtt tcttgcccat agccaccctt tgaaatgctc tctgtgtgtt agagagatac 780
tataccctag aaactctgaa cacgccagaa tgctgaaatg cccttctacc tttgggttta 840
cagccccctc cacataaatt aagaaattca gtatttctgc actcttagct gtattctaaa 900
gttctgtata gctcgtaatg atgggtatatt tatagca 937

```

<210> 70
 <211> 823
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 058336CB1

<400> 70

WO 01/07471

PCT/US00/19948

```

cccatcacgg cgtagtgcaa gctaaaatta accctcacta aagggaataa gcttgcgggc 60
gccgggcgaa tggtcggcag ctgcgaggcc aagagagacc ccaggacaca cacagctgcc 120
tcccgggtgc agaagaagac cccggcctga gagtggatg gcgtttaatg attgcttcag 180
tttgaactac cctggcaacc cctgcccagg ggacttgatc gaagtgttcc gtccctggcta 240
tcagactagg gccctgtact tgggtgatgg ttacgttatc aacatagcac ctgtagatgg 300
cattcctgcg tcctttacaa gcgccaagtc tgtattcagc agtaaggccc tggtgaaaat 360
gcagctcttg aaggatgttg tgggaaatga cacatacaga ataaacaata aatacgatga 420
aacgtacccc cctctccctg tggaagaaat cataaagcgg tcagagtttg taattggaca 480
ggaggtggcc tataacttac ttgtcaacaa ctgtgaacat tttgtgacat tgcttcgcta 540
tggagaagga gtttcagagc aggccaaacc agcgataagt accgttgagt ttgtgacagc 600
tgctgttggg gtcttctcat tcctgggctt gtttccaaaa ggacaaagag caaaatacta 660
ttaacaattt accaaagaga tattgatatt gaaggaattt gggaggagga aaagaaacct 720
ggggtgaata cttattttca gtgcatcatt actgttccag attcctatga tggatggcag 780
actctttaat aaattgctta ctgatattat cttaaaaaaa aaa 823

```

<210> 71

<211> 1033

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1511488CB1

<400> 71

```

gcgccagggg ttccagctgc acgtcccagg ctctccagcg cgcggcaggc cggggcgggg 60
cgaggagagc tgcgggggaca acgcctgtgg ctgggtccgg aggtgcgggt gcggcgcggg 120
acaagcgggc agcatgctca gggcggtcgg gaggcctactg cgccttgggc gcgggctaac 180
agtccgctgc ggccccgggg cgcctctcga ggccacgcga cggcccgcac cggctcttcc 240
gccccggggg ctccccctgct actccagcgg cggggccccc agcaattctg ggccccaagg 300
tcacggggag attcacggag tccccacgca gcgcaggcct tcgcagttcg acaagaaaat 360
cctgctgtgg acagggcgtt tcaaategat ggaggagatc ccgcctcgga tcccgccaga 420
aatgatagac accgcaagaa acaaagctcg agtgaaagct tgttacataa tgattggact 480
cacaattatc gcctgctttg ctgtgatagt gtcagccaaa agggctgtag aacgacatga 540
atccttaaca agttggaact tggcaaaaga agctaagtgg cgtgaagaag ctgcattggc 600
tgcacaggct aaagctaaat gatattctaa gtgacaaagt gttcacctga ataccatccc 660
tgtcatcagc aacagtagaa gatgggaaaa atagaatatt taccaaaaata tctgccatgg 720
ttttattttg gtaacaagaa gcacaatgtc ttttttattt ttatttttta gtaaactttt 780
actgaagtat accatgcatt caaaaagtgg acaaaaactgt atacagtctg atagatatatt 840
atgtcgtgaa cacctgtgta accactgcca aagtgaagat gtagaatatt ggcaacactt 900
cacagcctca ttctgcctt ttctcagcca ttacctccca aacatagcag tttttctgag 960
tttcatcacc tttgattcat tttgcctgtt tttgaacttt atataaatgg atttatacat 1020
taaaaaaaaa aaa 1033

```

<210> 72

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1638819CB1

<400> 72

```

ggcacttccg gcggcgcgct gcaggcgcgg ggaacaccaa tggcggggta cttgaagctg 60
gtgtgtgttt ccttttcagcg tcaagggttc cacactgttg ggagtcgctg caagaatcgg 120
acaggcgctg agcacctgtg gctgaccgga catctcaggg acccatttgt gaaggctgcg 180
aagggtggaga gttaccgggtg tcgaagcgcc ttcaagctcc tggaggtgaa cgagaggcac 240
cagattctgc ggccccgcct tcgggtgtta gactgtgggg cagctcctgg ggcctggagt 300
cagggtggcg tgcagaaggt caacgcgcga ggcacagatc ccagctctcc tgttggttcc 360
gtgcttgggg tagatcttct tcacatatc cccctggaag gagcaacttt tctgtgacct 420
gctgacgtga ctgaccgag aacctcagc agaatectcg aggtgcttcc tggcaggaga 480
gcagatgtga ttctgagcga catggcgccc aatgccacag ggttcgggga cctcgatcat 540

```

WO 01/07471

PCT/US00/19948

```

gacaggctca tcagcctgtg cctgaccctt ctcagcgtga ccccagacat cctgcaacct 600
gggggggacat tcctttgtaa aacctgggct ggaagtcaaa gccgtcgggt acagaggaga 660
ctgacagagg aattccagaa tgtaaggatc atcaaacctg aagccagcag gaaagagtca 720
tcagaagtgt acttcttggc cacacagtac cacggaagga agggcactgt gaagcagtga 780
ggatttcttg tgccattttc ataatggtca ttagctcctt ttaagctaga aacgtagcct 840
gagctcctga agagttcctg ggagatttga gctgattttg gagatggagc aggacaagtg 900
gggagtctct ctctctctct ctctctctct ctttttaacc aaaaagagat gacaaaacta 960
agttcagggg ccatggaaaa tgaaaaagtc cgctatattg tgatttggga agagaaagt 1020
atcaagagaa agaggtgagg atggaaggat ggagaaaaac agactgtggg aaggatcaga 1080
aggaatccgc cgaggcaggg atgggtgtgc ccatgtgtgc cttgacggga cttcatctta 1140
tagactgtta aactgtcaca cacaacagg ctttccaccc ctgctctgag agcaccacgc 1200
acagatttcc agttcttagt gtggctgttt aaagtagaaa atctgggggc tgggtgaggc 1260
cactcatgcc tgtaaaccca gggctttaga aggtgaggc tgggggattg cttgaagtca 1320
ggagttcaag accaacctgg gcaacatagc aacacccccc atgtctacaa aaatgaaaaa 1380
ccaaaaagca aacaaaaaga aaaatctgaa atttccatct ggggattaac ttctgtcttt 1440
ctggtgaaca atatagcaat tcacgcattc ttcaagcagc aaaagttccc ggaacaatta 1500
gggaagacgt atggtctgaa tttatccagg cagtgggtct gctttggttt ttgctggaaa 1560
tttatatcag tgtctgggct cccaagaaca taaatgtaat tgccaaagca aaaaaaaaaa 1620
aa

```

<210> 73

<211> 2449

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1655123CB1

<400> 73

```

cgttgccggg ctctccggaa ggagacgtgg cggcggttgg gccggtgata cccgggcgct 60
ttatagtcct gccgcctcct cctccaccct cccctcctcc tcctctcctc ctggagcaga 120
ggaggttgtg gcggtggctg gagaaagcgg cggcgaggga tggaggaagg agggcgccggc 180
gtacggagtc tgggtcccggg cgggcgggtg ttactggtcc tctgcggcct cctggaggcg 240
tccggcgccg gccgagccct tcctcaactc agcgatgaca tccctttccg agtcaactgg 300
cccggcaccg agttctctct gcccacaaact ggagttttat ataaagaaga taattatgtc 360
atcatgacaa ctgcacataa agaaaaatat aaatgcatac ttccccttgt gacaagtggg 420
gatgaggaag aagaaaagga ttataaaggc cctaatacaa gagagctttt ggagccacta 480
tttaaacaaa gcagttgttc ctacagaatt gagtcttatt ggacttacga agtatgtcat 540
ggaaaaacaca ttccggcagta ccatgaagag aaagaaaactg gtcagaaaaat aaatattcac 600
gagtactacc ttgggaatat gttggccaag aaccttctat ttgaaaaaga acgagaagca 660
gaagaaaagg aaaaatcaaa tgagattccc actaaaaata tcgaagggtca gatgacacca 720
tactatcctg tgggaatggg aaatggtaca ccttgtagtt tgaaacagaa cgggcccgaga 780
tcaagtactg tgatgtacat atgtcatect gaatctaagc atgaaattct ttcatgtact 840
gaagttacaa cttgtgaata tgaagtgttc attttgacac cactcttggt cagtcacctc 900
aaatataggt tcagagcatc tcctgtgaat gacatatatt gtcaatcact gccaggatct 960
ccatttaagc ccctcaccct gaggcagctg gagcagcagg aagaaatact aagggtgcct 1020
tttaggagaa ataaagagga agatttgcaa tcaactaaag aagagagatt tccagcgatc 1080
cacaagtcga ttgctatttg ctctcagcca gtgctcactg ttgggacaac ccacatatcc 1140
aaattgacag atgaccaact cataaaagag ttctttagtg gttcttactg ctttcgtggg 1200
ggtgtcgggt ggtggaaata tgaattctgc tatggcaaac atgtacatca ataccatgag 1260
gacaaggata gtgggaaaac ctctgtggtt gtcgggacat ggaaccaaga agagcatatt 1320
gaatgggcta agaagaatac tgctagagct tatcatcttc aagacgatgg taccagaca 1380
gtcaggatgg tgtcacattt ttatggaaat ggagatattt gtgatataac tgacaaaacca 1440
agacaggtga ctgtaaaact aaagtgcata gaatcagatt cacctcatgc tgttactgta 1500
tatatgctag agcctcactc ctgtcaatat attcttgggg ttgaatctcc agtgatctgt 1560
aaaatccttag atacagcaga tgaaaatgga cttctttctc tccccacta aaggatatta 1620
aagttagggg aaagaaaaga tcattgaaag tcatgataat ttctgtccca ctgtgtctca 1680
ttatagagtt ctcagccatt ggacctcttc taaaggatgg tataaaatga ctctcaacca 1740
ctttgtgaat acatatgtgt atataagagg ttattgataa acttctgagg cagacatttg 1800
tctcgctttt ttctattttt gttgtgtctt ataaactgac tgtttttctt tgtttggata 1860
ctgtgattcc aaaataaate tcatccaagc aagttagagt ccagcctaata caaatgtcat 1920
aattgttgta cctattgaaa gtttttaaat aatagattta ttatgtaaat tatagtatat 1980

```

WO 01/07471

PCT/US00/19948

```

gtaagtagct aatgaagtaa agatcatgaa gaaagaaatt gataggtgta aatgagagac 2040
catgtaaaaat atgtaaattc tagtacctga aatcctttca acagattttt atatagcaac 2100
tgctctctgc aagtagttaa actagaaact gggcacatgg tagaggctca catggggagtt 2160
gtcctcacc c ttgttaattc caagaaactc ttatttataa taggttgctt ctctctcaga 2220
acttttatct attacttttt tcttcttatg agtatgttta ctctcagagt atctatctga 2280
tgtagacagt tgggtgatgct tctgagactc agaatggttt actctaacaa aacactgtgc 2340
tgtctatccc ttgtacttgc ctactgtaat atggattttca cttctgaaca gtttacagca 2400
caatatattat tttaaagtga ataaaatgtc cacaagcaaa aaaaaaaaaa 2449

```

<210> 74

<211> 1689

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2553926CB1

<400> 74

```

aagtaatctt agggattgtg ggaaggcagc tgaactcggc gcctggaaag atggaggcag 60
cggagacaga ggcggaagct gcagccctag aggtcctggc tgagggtggca ggcattcttg 120
aacctgtagg cctgcaggag gaggcagaac tgccagccaa gatcctgggt gagtttcttg 180
tggaactctca gaagaaagac aagctgctct gcagccagct tcaggtagcg gatttctctg 240
agaacatcct ggctcaggag gacactgcta agggctctga ccccttggct tctgaagaca 300
cgagccgaca gaaggcaatt gcagctaagg aacaatggaa agagctgaag gccacctaca 360
gggagcacgt agaggccatc aaaattggcc tcaccaaggc cctgactcag atggaggaag 420
cccagaggaa acggacacaa ctccgggaag cctttgagca gctccaggcc aagaaacaaa 480
tggccatgga gaaacgcaga gcagtcacaga accagtggca gctacaacag gagaagcatc 540
tgcagcatct ggccggagggt tctgcagagg tgaggggagcg taagacaggg actcagcagg 600
agcttgacgg ggtgtttcag aaacttggaa acctgaagca gcaggcagaa caggagcggg 660
acaagctgca gaggtatcag accttccctc agcttctgta taccctgcag ggtaagctgt 720
tgttccctga ggctgaggct gaggcagaga atcttccaga tgataaacc cagcagccga 780
ctcgacccca ggagcagagt acaggagaca ccatggggag agaccctggt gtgtccttca 840
agttctccaa ggctgttggt ctacaacctg ctggagatgt aaatttgcca tgacttctctg 900
gaggacagca gcatggagaa agatcctaga aaaggcctct gacttccctc acctcccaac 960
catcattaca ggaaagactg tgaactcctg agttcagctt gatttctgac tacatcccag 1020
caagctctgg catctgtgga ttaaaatccc tggatctctc tcagttgtgt atttgttcat 1080
cttcatatgc tggcaggaac aactattaat acagatactc agaagccaat aacatgacag 1140
gagctgggac tgggttgaac acagggtgtg cagatgggga gggggtagct gccttggggc 1200
tcttatgatg cagacatggt gaatttaatt caaggaggag gagaatgttt taggcagggt 1260
gttatatgtg ggaagataat tttattcatg gatccaaatg tttgttgagt cctttctttg 1320
tgctaagggt cttgcggtga accagaatta taacagttag ctcatctgac tgttttagga 1380
tgtacagcct agtggttaaca ttcttggtat ctttttgtgc cttatctaaa acatttctcg 1440
atcactgggt tcagatgttc atttattata ttcttttcaa agattcagag attggctttt 1500
gtcatccact attgtatgtt ttgtttcatt gacctctagt gataccttga tctttccac 1560
tttctgtttt cggattggag aagatgtacc tttttgtca actcttactt ttatcagatg 1620
atcaactcac gtatttggat ctttatttgt tttctcaaat aaatatattaa ggttaaaaaa 1680
aaaaaaaaa 1689

```

<210> 75

<211> 2489

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2800717CB1

<400> 75

```

tgtgcccaga acgcggttag gaagtgtgtg catacgtctg aaccctaaat gggtctcagt 60
tctgtaaaact tctctctcca ctgggtggag tagggccttt aagagcagct ggaatgcagt 120
tcccctgatc agcgtaccag ttgttgccct tctgaacctc tgccagtcct ggagactgg 180
ggcctgagct ccaaccagcg ggccctcatc tacacctca ccaccgcaac ttctcaccg 240

```

WO 01/07471

PCT/US00/19948

```

agcaagaagc agctcccaga gagaaagaac gttcccacct gcctagccat gggagaggac 300
gctgcacagg ccgaaaagtt ccagcaccct gggctctgaca tgcggcagga aaagccctcg 360
agccccagcc cgatgccttc ctccacacca agccccagcc tgaacctagg gaacacagag 420
gaggccatcc gggacaactc acagggtgaac gcagtcacgg tgctcacgct cctggacaag 480
ctggtgaaca tgctagacgc tgtgcaggag aaccagcaca agatggagca gcgacagatc 540
agtttggagg gctccgtgaa gggcatccag aatgacctca ccaagctctc caagtaccag 600
gcctccacca gcaacacggg gagcaagctg ctggagaagt cccgcaaggc cagcgccac 660
acgcgcgcgg tcaaagagcg catggatagg cagtgcgcac aggtgaagcg gctggagaac 720
aaccacgcc agctcctccg acgcaaccat ttcaaagtgc tcattctcca ggaggaaaat 780
gagatccctg ccagcgtgtt tgtgaaacag cccgtttccg gtgccgtgga aggggaaggag 840
gagcttccgg atgaaaacaa atccctggag gaaaccctgc acaccgtgga cctctcctca 900
gatgatgatt tgccccacga tgaggaggcc ctggaagaca gtgccgagga aaaggtggaa 960
gaaagtaggg cagagaaaaat aaaaagatcc agcctgaaga aagtggatag cctcaagaaa 1020
gcattttctc gccagaacat cgagaaaaag atgaacaagc tggggacaaa gatcgatatc 1080
gtagagagga gagagaagat taagaaatct ctcacgtcaa atcaccagaa aatatcctca 1140
ggaaaaagct ccccttcaa ggtttctccc ctactttcg ggcggaagaa agtccgagag 1200
ggagaaagcc atgcagaaaa tgagaccaag tcagaagacc tgcctagcag tgagcagatg 1260
ccaaatgacc aggaagagga gtcctttgca gagggtcatt ccgaagcgtc cctcgccagc 1320
gctctggtgg aaggggaaat tgcagaggag gctgctgaga aggcgacctc cagggggagt 1380
aactcgggga tggacagcaa catcgacttg actattgtgg aagatgaaga ggaggagtca 1440
gtggccctgg aacaggcaca gaaggtacgc tatgagggtg gctacgcgct aacatccgag 1500
gaggcggagc gctccgatgg ggaccccggt tgctgtgctc aagcgggcag ccagggtcta 1620
tcctgagctt agagccaccg tgccatcctg tgcctccact cctgcgttcc tgtccaggca 1680
agaacaaact cttgcacatc tccagcacga ctcaccact caggttttac catgaaagcg 1740
gtaatcattg accatatagt catagtaaga cacacgagac caggttttac aatgtctcca 1800
acctgtcacg gactccactt ttaatttgcct cttaggttct atctctgtag aatgtctcca 1860
agattgaaga agaaactgag cagttgaaaa atgctaactc ctttgactta gtcagaaaaa 1920
aacagaggat aattaagata ctagtcatga aaagtgattc attctttttt gtcattccat 1980
aagcttgctg aatagtgtac cggtaatata ttgtatttcc accgtactct gtgaatctaa 2040
ttattattct ttaagtgttg atatataata tacataaata tgtaagctaa acatataact 2100
atatgtttta agaagaaaac atctacgaaa ggtaaaaaga gatgatcagt tggttgttta 2160
cttgctagaa accattgttt tattgcaaac gaaggaaaaa tgaagagatt ataaaagtca 2220
gctaataag taagatacgt agtaaaagtca ggactattca aaaagtaaga aagaaaattt 2280
ggaaaatgag agaaacagga aacaaagaat gccgaaaaga atgaaaacag agaaaaaatg 2340
tatgtgcttg aaagtaaaat acttacaata gtagecttaac tatttcactc tttaaataaa 2400
aataactaaag aagttcgtat atcctggaat aacatgtcat cttcaaaata tttttatttt 2460
ctaataatttt taataataaa cattttatag tgtaaagct gtatttttct taataaataa 2489
aggacattac aaatatttct ttaaaaaaa

```

<210> 76

<211> 898

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5664154CB1

<400> 76

```

cctctggcga tgacaacagc cacacgtgat cggccaacac tgagtcttac ctcgttgttg 60
cgtcagaacc gccgtcgctc gctcccttct cggcagtggt acctgttccc ggtgtccctg 120
aggacgtgcg ggccaggtag ggccccgaaa gtaggaagcg gagggggagc aggtttgcgg 180
ggccaagtgt tgcggcgacg cacctcacgt cgagaatcgg gaggaggaga ctgcaaggat 240
aggcccagga gtaatggagt ccaaagagga acgagcgta aacaatctca tcgtggaaaa 300
tgtcaaccag gaaaatgatg aaaaagatga aaaggagcaa gttgctaata aaggggagcc 360
cttgcccta cctttgaatg ttagtgaata ctgtgtgcc agaggaacc gtaggcggtt 420
ccgcgttagg cagcccatcc tgcagtatag atgggacata atgcataggc ttggagagcc 480
acaggcaagg atgagagagg agaatatgga aaggattggg gaggaggtga gacagctgat 540
ggaaaagctg agggaaaagc agttgagtca tagtctgcgg gcagtcagca ctgatcccc 600
tcacatgac catcacgatg agttttgcct tatgccctga atcctgatgg tttccctgaa 660
gttaataggg agacccttgc ttccataact tacacatttg tgggtgtacct ttgtcgtaaa 720
cgttttgatg ttctgtgggtc toctattacc agcttctaaa tgaatgttgt 780
ttttgacca gtttgtaagt ttctgtcagc aggagagttt tacctattgc atggaaagat 840

```

WO 01/07471

PCT/US00/19948

gctcattata tattgtgaag ttaataaaac agtttttaaaa agcaaaaaaa aaaaaaaa 898

<210> 77
<211> 1236
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 017900CB1

<400> 77
cctcggtact gacctctgca gagccgggtg gagccattg acgtccagcg aacgacgtga 60
gcagcgatgg acggtcgggt gcagctgata aaggccctcc tggccttgcc gatccggcct 120
gcgacgcgtc gctggaggaa cccgattccc tttcccagaga cgtttgacgg cgataccgac 180
cgactccccg agttcatcgt gcagacgggc tctacatgt tcgtggacga gaacacgttc 240
tccagcgacg ccctgaaggt gacgttcctc atcaccgcc tcacagggcc cgccctgcag 300
tgggtgatcc cctacatcaa gaaggagagc cccctcctca atgattaccg gggctttctg 360
gccgagatga agcgagtctt tggatgggag gaggacgagg acttctaggc cgggagacct 420
tcgggcctgg gggcgggtgc tctggggagg gtccgctgtg ttactggccg ccgccagggt 480
cgccaccggc gccctccctc cgcgcctccc tccccctcga gccgccgcga tgtccctgc 540
gctcctgttc cctcccgct agtgcttgcc tttgttccag gaatagcgt ccaggctcct 600
gctgccgccc ctgggcctca ctctggagcg agccgccgcc ctctccttcc agccagccag 660
ccccctccat gtacatttgg acgtctgctt gcgctccagc tgcaagctgg gctcctgtta 720
cacactggac agaccacca ctgccgcgcg tgccaagccc tctcctccc accagactgc 780
cagacgacta catcattctg cccacagacc tgcgtgcca cagccatcgc catccatcgc 840
atcccaccga cagactgctg ctctagtga tctggactca cctcggaggt atctgggctg 900
gccacagtcc ctggacagt atccagacag ctggccgccc cccaagggat ctgtcacctt 960
cagcgagacc tatttctctc ccacccccag aaacctcttg tgttcttgcc taggcccagg 1020
tgttcctggc agccaaatcg agtctctcat tttctcttgt ggaccagtta gttttgcca 1080
taacgcagta ttctgagttt gcaactgtct ctctgatgtg tgccctttgt tcaacacagt 1140
aacccttgca ttctgctctg ctctaataca ctacctggag aaagtctttt ccttattttt 1200
aataaatgtc agacattatt gaaaagaaaa aaaaaa 1236

<210> 78
<211> 1634
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 035102CB1

<400> 78
gtttgactcc cgtgcgggtg ggcccagcag ccacaaagct cccgctgcca ttgctccttg 60
tactcccgcc gtcactgcc ctgtccaacc cctccccgg ggcttgccg gcggtccca 120
cacccctcgg ccggtgtacg cgctctgcac ctgcctgccc gaaaacatgt tgcagacacc 180
agagagcagg gggctcccgg tcccgcaggc cgagggggag aaggatggcg gccatgatgg 240
tgagaccggg gcccgaccg cctcgcagga gcgccccaa gaggagcttg gcgcccgggag 300
ggaggagggg gctgcggagc ccgcctcac ccggaaggc gcgagggcct tggcggccaa 360
atccttggca aggcgcagg cctaccggc gctgaatcg acggtggcg agttggtgca 420
gttctcctcg gtgaaagaca agaagaagag tccatcaca cgctcggaga tgggtgaaata 480
cgttatttga gacttgaaga ttctgttccc ggacatcat gcaagggccg cagagcatct 540
gcggtatgtc tttggttttg agctgaaaca gtttgaccgc aagcaccaca cttacatcct 600
gatcaacaaa ctaaaacctc tggaggagga ggaggaggag gaggatcttg gaggagatgg 660
ccccagattg ggtctgttaa tgatgatcct gggccttat tatatgagag gtaaatgcgc 720
cagggaggcc caggctcggg agatgctgcg tcggttggg gtgcaaccct caaagtata 780
tttctctttt gggatatcga agaggcttat tatggaagat tttgtgcagc agcgatatct 840
cagttacagg cgggtgcctc acaccaatcc accagcatat gaattctctt ggggtccccg 900
aagcaacctg gaaatcagca agatggaagt cctggggttc gtggccaaac tgcataagaa 960
ggaaccgcag cactggccag tgcagtaccg tgaggcccta gcagacgagg ccgacagggc 1020
cagagccaag gccagagctg aagccagtat gagggccagg gccagtgcta gggccggcat 1080
ccacctctgg tgagggttgg tgaaaagtgt gccagtgggt ccccgtagg acgaactact 1140

WO 01/07471

PCT/US00/19948

```
gtcctgagtc ataagtaata tgggtggggc gaggggtctta tttctgtaga aatcgtgtga 1200
ctttaaggat ttagattttg tatcttatgt tttgtaacat ttaataatta ctgttaaaat 1260
gctgttttga aatgagattg gtctactttt tctgttagga ttttattgta gagttttgct 1320
ggttttgtaa aatggatgga agaactttgt atttatactg tgattttgaa cagattatgc 1380
aacattggaa ggaaggctgt actttgatgg tttgaaggaa ctcagcagta tgatgatctg 1440
gttccagggg aaaaaaatag ctggttggtg tctagcccc caacactttt gtctgttgtg 1500
tataaaagaa gaaagactgg catgtacctt catttgctta gctattttgag tatctagaga 1560
aaaattaaaa tgcaatgagt tagcagtata ccctggcaca ctttaataaat taaacatttg 1620
tggaaaaaaa aaaa
```

<210> 79

<211> 1258

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 259983CB1

<400> 79

```
tcccgccag cggtagcaac tgcagaactg caggagacta tctttctaga caaggcagtt 60
gaggaggagg gagcgcttga gggggactgg cctggcgtgc actccgcacc tcggggacat 120
tattgcgcgt ggaacggctg cttttggaag gcacaacttc ctgaatggac catgactccc 180
accaaagatc cctgtctctg attcaccaaa cagcttcaac cctgaaacca ggacgagaag 240
ttgacaacat ctgagtggac agctaattga cctaagactt cagaccaggc ctactattgc 300
ccagaagaaa agatgtttgg ttttcacaag ccaaagatgt accgaagtat agagggctgc 360
tgtattttgca gagctaagtc ctccagttct cgattcactg acagtaaacg ctatgaaaag 420
gacttccaga gctgttttgg attgcatgag actcgttcag gagacatctg caatgcctgt 480
gtcctgcttg tgaaaagatg gaagaagttg ccagcaggat caaaaaaaaaa ctggaatcat 540
gtggttagatg caagggctgg acccagtcata aagactacat tgaaaccaa gaaagtgaag 600
actctatctg ggaacaggat aaaaagcaac cagatcagta aactgcagaa ggaatttaaa 660
cgtcataatt ctgatgctca cagtaccacc tcaagtgcct cccagctca atctccttgt 720
tacagtaacc agtcagatga cggctcagat acagagatgg cttctggttc taacagaaca 780
ccagtttttt ctttttttaga tctcacttac tggaaaagac agaagatatg ttgtgggac 840
atctataaag gccgttttgg ggaagtccct attgacacac atctcttcaa gccttgctgc 900
agcaataaga aagcagctgc tgagaagcca gaggagcagg ggccagagcc tctgcccac 960
tccactcagg agtgggtgact gaggttttta tgtagaaggg gaacaaaaaa aaaaatatct 1020
gaattttgaa aaaccacaaa gctacaaact gaccctcttt tttttttgag acggagtttt 1080
gctcttgtaa ccagggctgg agtgcatgg cgtgatcttg gctcactgca acttccgtct 1140
cccgggggtc aggtgattct cctgcctcag cctcccaagt agctgggttt ataggtgccc 1200
gctacagacc cggctaattt tttagtttta gtagagacgg gggttcacca cgttgggc 1258
```

<210> 80

<211> 2223

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 926810CB1

<400> 80

```
aaaagccgcc gcggtgcct taggaacggc gctgcctcgt ctctgctacc cctgggtggg 60
cgccctgcg aagcagctcc ttcgggcagc cccgggtcgc ttagcggcca aggaggcttc 120
agttctttgc cgcctgcaag gcggagacca gaaggcggaa tccacagctg gcgacgggg 180
agcatctgct gtccaccagc ggagcacagg ccatcaaagc cgcactctgaa cttgaattct 240
gtgcagctga ttgcagagct ggaccggat ctgcgacccc ctgtggacag aggttgaccg 300
taccgccggag aggagctttc tcacggaggg cactgggttg agaggctgga agtgaaataa 360
agacgcgctc ttgtttcaga gttcgtcccc tgctgagata ggaaggcaga gccacctcct 420
ctcctctccc acctgcagat taagcttttc taaaaagcct aggcattctt ttatattcag 480
ataccctatc gtcgtcagtc atggctagca tcattgcacg tgtcggtaac agccggcgcc 540
tgaatgcacc cttgccgcct tgggccatt ccattgctgag gtccctgggg agaagtctcg 600
gtcctataat ggccagcatg gcagacagaa acatgaagtt gttctcgggg aggggtggtg 660
```

WO 01/07471

PCT/US00/19948

```

cagcccaagg ggaagaaacc tttgaaaact ggctgaccca agtcaatggc gtcctgccag 720
attggaatat gtctgaggag gaaaagctca agcgcttgat gaaaaccctt aggggcccctg 780
cccgcgaggt catgcgtgtg cttcaggcga ccaaccctaa cctaagtgtg gcagatttct 840
tgcgagccat gaaattgggtg tttggggagt ctgaaagcag tgtgactgcc catggtaaat 900
tttttaacac cctacaagct caagggggaga aagcctccct ttatgtgatc cgtttagagg 960
tgcagctcca gaacgctatt caggcaggca ttatagctga gaaagatgca aaccggactc 1020
gcttgacgca gctcctttta ggcgggtgagc tgagtaggga cctccgactc agacttaagg 1080
attttctcag gatgtatgca aatgagcagg agcggcttcc caactttctg gaggtaatca 1140
gaatggtaag ggaggaagag gattgggatg atgcttttat taaacggaag cgtccaaaaa 1200
ggtctgagtc aatggtggag agggcagtc ggcctgtggc atttcagggc tccccaccga 1260
tagtgatcgg cagtgtgtgac tgcaatgtga tagagataga tgataccctc gacgactccg 1320
atgaggatgt gatcctgggtg gagtctcagg accctccact tccatccttg ggtgcccctc 1380
ccctcagaga cagggccaga cctcaggatg aagtgtgggt cattgattcc cccacaatt 1440
ccagggctca gtttccttcc accagtgggt gttctggcta taagaataac ggtcctgggg 1500
agatgcgtag agccaggaag cgaaaacaca caatccgctg ttcgtattgt ggtgaggaag 1560
gccactcaaa agaaacctgt gacaacgaga gtgacaaggc ccagggtttt gagaatttga 1620
tcatcactct ccaggagctg acccatactg agatggagag gtcaagagtg gcccctggcg 1680
aatacaatga cttctctgag ccactgtaag ggaccacccc caggtttcag tgaaccctta 1740
cctatatcca gcatccagta gtgggaaaaac tggggtgggg gtgggggtgg gacttctaac 1800
tgcatagaat aatccacaaa gcggctatct tttgggggtg agtagaaagg gtcttgata 1860
ccagcacatt ggagggagat agcctgacct ctgtccttgc tccttctccc tgcagcctac 1920
gggtctgttt tctgtgtgtg cccatttccct tgacagcttt attctttgtg aaagtgggtat 1980
aatttattgt taaatatttg aacaataaaa aaggtacaaa aagtgaagta caaattaccc 2040
aaatctctcc acccttatat aatcattgtc aaccctttga tgagtatat ttccctatac 2100
ctatgtaccc agatagatat atgcatagat aaaagtgatg aaatataagt gctgttctat 2160
ctgtattttt tcaccaaaca atatatgttg tgagcttcta tgacaataaa tatatatatc 2220
act 2223

```

<210> 81

<211> 1370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1398816CB1

<400> 81

```

cccacgcgtc cggccggggag gactgggtgc gcctgcaggg atcggaagcc ggttgggggtg 60
tgagaggttt tctcgctcta gggagattct tcaagcaatc actatgtcaa cagacacag 120
tgtttccctt ccttcatatg aggaagatca gggatcaaaa ctcatcga aagctaaaga 180
ggcaccattc gtaccggttg gaatagcggg ttttgacgca attgttgcat atggattata 240
taaactgaag agcaggggaa atactaaaat gtccattcat ctgatccaca tgcgtgtggc 300
agcccaaggc tttgttgtag gagcaatgac tgttggtatg ggctattcca tgtatcggga 360
attctgggca aaacctaaag cttagaagaa gagatgctgt ttggtccttg ttggaggagc 420
ttgctttagt tagatgtctt attattaaag ttacctatta ttgttgga taaactaatt 480
tgtatgggtt tagatggtaa catggcattt tgaatattgg ctctcttct tgcaggcttg 540
atttgcttgg tgaccgaatt actagtgact agtttactaa ctaggtcatt caaggaagtc 600
aagttaactt aaacatgtca cctaaatgca cttgatgggtg ttgaaatgtc caccttctta 660
aatttttaag atgaacttag ttctaaagaa gataacaggc caatcctgaa ggtactccct 720
gtttgctgca gaatgtcaga tattttggat gttgcataag agtctattt gccccagtta 780
attcaacttt tgtctgcctg ttttgaggac tggctggctc tgtagaact ctgtccaaaa 840
agtgcattga atataacttg taaagcttcc cacaattgac aatatatatg catgtgttta 900
aaccaaatcc agaaagctta aacaatagag ctgcataata gtatttatta aagaatcaca 960
actgtaaaca tgagaataac ttaaggattc tagtttagtt ttttgtaatt gcaaattata 1020
ttttgctgc tgatatatta gaataatttt taaatgtcat cttgaaatag aaatatgtat 1080
tttaagcact caccgcaaagg taaatgaaca cgttttaaat gtgtgtgttg ctaatttttt 1140
ccataagaat tgtaaacatt gaactgaaca aattacctat aatggatttg gttaatgact 1200
tatgagcaag ctggtttggc cagacagtat acccaaactt ttatataata tacagaaggc 1260
tatcacactt gtgaaattct cttgtctaat ctgaatttgc attccatggt gttaacatgg 1320
tatatgtatt gttattaaag taagtgaccc atgtcaaaaa aaaaaaaaaa 1370

```

<210> 82

WO 01/07471

PCT/US00/19948

<211> 1541
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1496820CB1

<400> 82
 gtgttaagct gacaaaatct gtacagaata ttttaattttt cctttttattt ctgtgatata 60
 aagatttgtt ttctttttcat agcaacatga accgtgaaga ccggaatgtg ctgcgtatga 120
 aagaacggga aaggcggaat caggaaattc agcagggcga agacgccttc ccacctagct 180
 ctctctcttt tgcagagcca tacaaagtta ctagcaaaga agataagtta tcaagtcgta 240
 ttcagagtat gcttggaac tacgatgaaa tgaaggattt cataggagac agatctatac 300
 caaagcttgt tgcaattccc aagcctacag taccaccatc agcagatgaa aaatctaacc 360
 caaattttctt tgaacagaga catggagggt ctcatcagag tagcaaattg actccagtag 420
 gacccgcacc cagcacttct cagtctcaga aacggctctc aggcttacag agtggacata 480
 gtageccagc gaccagcgca ggtagcagta gtggcactaa cagtagtggt cagaggcacg 540
 accgtgagtc atataacaat agtgggagca gtageccgga aaaaggccag catggatcag 600
 aacactccaa atcacgttct tccagccctg gaaaacccca ggctgtttct tcattaaact 660
 ctagtcattc caggtctcat gggaatgatc accatagcaa ggaacatcaa cgctccaaat 720
 cacctcggga cctgatgca aactgggatt ctcttcccgt tgtacctttt tcaagtgggc 780
 agcactcaac tcaatctttc ccacctcat tgatgtcaaa gtccaattca atgttacaga 840
 aacccactgc ctatgtgcgg cccatggacg gacaggagtc catggaacca aagctgtcct 900
 ctgagcacta cagcagccaa tcccatggca acagcatgac tgagctgaag cccagcagca 960
 aagcacatct caccaagctg aaaataacct cccaaccact ggatgcatca gcttctgggtg 1020
 atgtgagctg tgtggatgaa atcctaaaag agatgacgca ttcattggcct cccctctaa 1080
 cggctattca tacaccatgc aaaacagaac ctcccaaatt tccttttcca actaaggtaa 1140
 gtaaataaaa tgtatctttc ataattgaag aaaactctaa atggcttgac taaaatcata 1200
 tggattaaaa attgtcttgc cattcctatt ctagtgggag acagacagta aataagtga 1260
 taaatagata aattcagata gtgacaactg ttatgaagat aattagcagg gtaatggaac 1320
 tgagagcatc ttggatcaag aggtattaag aaagctttga aggcaatatg cgagagagat 1380
 ttaaaagaca ttaatacagc cggacacggt ggctcactcc tgtaatccca gcactttgga 1440
 aggctgagcc aagagactct cttgaggcca ggagtttgcg accagcctgg tcagcatggc 1500
 aagaccctgt ctctacccaa aattggaagg aaaaaaaaaa a 1541

<210> 83
 <211> 1372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1514559CB1

<400> 83
 cggctcgagc agctgccgaa gtcagttcct tgtggagccg gagctggggc cggattcgcc 60
 gaggcaccga ggcactcaga ggaggcgcca tgtcagaacc ggctggggat gtccgtcaga 120
 acccatgcgg cagcaaggcc tgccgcggcc tcttcggccc agtggacagc gagcagctga 180
 gccgcgactg tgatgcgcta atggcggggt gcatccagga ggcccgtgag cgatggaact 240
 tcgactttgt caccgagaca ccactggagg gtgacttcgc ctgggagcgt gtgcggggcc 300
 ttggcctgcc caagctctac ctccccactt ggctcgctgg gtggtaccct ctggaggggt 360
 gtggctcctt cccatcgctg tcacaggcgg ttatgaaatt caccctcttt cctggacact 420
 cagacctgaa ttctttttca tttgagaagt aaacagatgg cactttgaag gggcctcacc 480
 gagtgggggg atcatcaaaa actttggagt cccctcactt cctctaaggt tgggcagggt 540
 gacctgaag tgagcacagc ctagggctga gctggggacc tggtaccctc ctggctcttg 600
 atacccctct ctgtcttgtg aaggcagggg gaaggtaggg tcttgagca gaccacccg 660
 cctgccctca tggccctctt gacctgact ggggagcccg tctcagtgtt gagccttttc 720
 cctctttggc tccctgtac cttttgagga gccccagcta ccctctctct ccagctgggc 780
 tctgcaattc cctctgtctg ctgtccctgc cccttgtcct ttcccttcag taccctctca 840
 gctccagggt gctctgaggt gectgtccca cccccaccc cagctcaatg gactggaagg 900
 ggaagggaca cacaagaaga agggcaccct agttctacct caggcagctc aagcagcag 960
 cgccccctcc tctagctgtg ggggtgaggg tcccatgtgg tggcacaggc ccccttgagt 1020

WO 01/07471

PCT/US00/19948

gggggttatct	ctgtgttagg	ggtatatgat	gggggagtag	atctttctag	gagggagaca	1080
ctggccccctc	aaatcgtcca	gcgaccttc	tcatccaccc	catccctccc	cagttcattg	1140
cacttttgatt	agcagcggaa	caaggagtc	gacattttaa	gatgggtggca	gtagaggcta	1200
tggacagggc	atgccacgtg	ggctcatatg	gggctgggag	tagttgtctt	tcctggcact	1260
aacgttgagc	ccctggaggc	actgaagtgc	ttagtgtact	tggagtattg	gggtctgacc	1320
ccaaacacct	tccagctcct	gtaacatact	ggcctggact	gttttctctc	gg	1372

<210> 84

<211> 868

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1620092CB1

<400> 84

cattgagctc	accagcgcca	ccgtccccgg	cgaagttctg	cgctggtcgg	cggagtagca	60
agtggccatg	gggagcctca	gcggctctcg	cctggcagca	ggttggttca	tgtgatcctg	120
gttaatggaa	cataagttag	attttatggg	tgacagggag	agagatcagg	cttgacttga	180
gagcacgtgg	gaaaagaagg	gggctatctc	ttcgcaaaga	tttaagtatc	ttataagaac	240
tgtttgccag	tgcaattatg	agaagctgtt	ttaggttatg	tgaaagagat	gtttcctcat	300
ctctaaggct	taccagaagc	tctgatttga	agagaataaa	tggattttgc	acaaaaccac	360
aggaaagtcc	cggagctcca	tcccgcactt	acaacagagt	gcctttacac	aaacctacgg	420
attggcagaa	aaagatcctc	atatggtcag	gtcgcttcaa	aaagggaagt	gaaatcccag	480
agactgtctc	gttgagatg	cttgatgctg	caaagaacaa	gatgagagtg	aagatcagct	540
atctaattgat	tgccctgacg	gtggtaggat	gcattctcat	ggttattgag	ggcaagaagg	600
ctgccaaaag	acacgagact	ttaacaagct	tgaacttaga	aaagaaagct	cgtctgaaag	660
aggaagcagc	tatgaaggcc	aaaacagagt	agcagaggta	tccgtgttgg	ctggattttg	720
aaaatccagg	aattatgtta	taacgtgcct	gtattaaaaa	ggatgtggta	tgaggatcca	780
tttcataaag	tatgatttgc	ccaaacctgt	accatttccg	tatttctgct	gtagaagtag	840
aaataaattt	tcttaataaa	aaaaaaaa				868

<210> 85

<211> 3388

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1678765CB1

<400> 85

aactgtgtct	gcaagcagtt	tgtactcagt	ttgtcaagag	agcagcttcc	tgttttgatt	60
atataccttc	atctctgaaa	aaagacatgc	tagttaaat	tcaagatggt	ttacttagaa	120
gatgacaagg	aagatgaggt	ggtttgtaaa	ggctcattaa	gtaaaactca	agatgtttac	180
catgacaagt	ccccctctgg	tatcttgtct	caaaccatga	attatgtggg	acagctggct	240
gggcaggtga	ttgtcactgt	gaaggaactc	tacaagggca	ttaaccaggc	cacctctctc	300
gggtgcattg	atgtcatcgt	ggtacagcag	caggatggca	gctatcagtg	ttcacctttt	360
cacgttcggt	ttggaaagct	gggagtcctg	agatccaaa	agaaagtgat	tgatatagaa	420
atcaacggca	gtgcagtgg	tcttcacatg	aagttgggtg	ataacggaga	agctttcttt	480
gttgaggaga	ctgaagaaga	atatgaaaag	cttcctgctt	accttgccac	ctcaccaatt	540
cctactgaag	atcagttctt	ttaaagatatt	gacacccctt	tggtgaaatc	gggtggagat	600
gaaacaccat	ctcagagtcc	agacatctca	cacgtcttgg	aaacagagac	aatttttact	660
ccaagttctg	tgaaaaagaa	aaaacgaagg	agaaagaaat	acaaacagga	cagtaagaag	720
gaagagcagg	ccgcactctg	tgtctgcaga	gacacatgtg	atgtaggcgt	gagctccgat	780
gatgacaagg	gggccaggc	agcacgagga	tcttcaaatg	cttccttgaa	agaagaagaa	840
tgtaaagagc	ctttgtctct	ccattctggg	gatcattacc	ccttatctga	tggagattgg	900
tcccctttag	agaccaccta	tccccagaca	gcgtgtccta	agagtgatcc	agagctggag	960
gtgaaacctg	cggagagcct	gctcagatca	gagtatcaca	tggagtggac	gtggggcgga	1020
ttcccagagt	ccaccaaggt	cagcaaaaag	gaacgatctg	accatcatcc	taggaacagt	1080
acaattacac	catcagaaaa	tactcatttt	cggttaattc	ccagtgagga	caacctcatc	1140
agtgaagttg	agaaggatgc	ttccatggaa	gacactgtct	gtaccatagt	gaagcccaaa	1200

WO 01/07471

PCT/US00/19948

```

gccggcgggg tccacagtgg gggcagtggg gatggggccg gcagcggggg cccgggagca 960
cagaaccacg tgaaggagag atgagcccc cgggcccggac aggggcacac gtgtgcaaag 1020
agacggtggt gtgtgttctc tcctgcattc gcgtgtgcac acatgtgctg ggcacgcgtg 1080
tggtagaggtc tgagaggggc cgggctgca ctggtgtggg ctgcacaggc acagacgcag 1140
acggccccgg ccgtgtcctg tggccccctg tcggatggat gcgtgccgtt tgtagagaag 1200
agcctttggg cccattcact cgttcagcag acacgcattg gactgatgct ttgagttttc 1260
ttctgtgggg ttttcctttc tctggtctcc gtgcagcccc tgccctccct cgggtgctgc 1320
tggccgcaaa ggaggaactc gtggggggag ggtgtgattt gcagacctgg gtctctgctc 1380
tgctctgggg gtggggcctg ctatcacaga gacctcctt cctctcacc cctcctctcc 1440
caggcctcgc caggagtctt ggctgttggc agctcagagg tgggggaggg ctgtggtgtg 1500
agtgccttgc acctgtcctc gctcctgtca ccccttctct ctgcctctc catgcccagg 1560
gaacacccat ggtgcagtcc tcaggcaagg ccaggacggg gctgaggccc tgcgtggaga 1620
tgctgcacca gcggaaggct gagaccgcgt taccttagtt catctgttca ctcgtaataa 1680
aaagaattct ctcagaaaaa aaaaaaa 1707

```

<210> 87

<211> 1752

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1806454CB1

<400> 87

```

cccgggtgcg ccgcggcgct gggggcggca ggttgcggcg gcgcccggagc ggggtctccag 60
gctggcgagc gccaggaca ggcattgtgt tgggactggc ggccatggag ctgaagggtg 120
gggtggatgg catccagcgt gtggtctgtg ggggtctcaga gcagaccacc tgccaggaag 180
tggtcacatgc actagcccaa gcaataggcc agactggccg ctttgtgctt gtgcagcggc 240
ttcgggagaa ggagcggcag ttgctgccac aagagtgtcc agtgggcgcc caggccacct 300
tcggacagtt tgccagcgt gtccagtgtt tcctgaggcg cacaggggccc agcctagctg 360
ggagggcctc ctacagacagc tgtccacccc cggaacgctg cctaattcgt gccagcctcc 420
ctgtaaagcc acgggctgcg ctgggctgtg agccccgcaa aacactgacc cccgagccag 480
ccccagcct ctacgcctc gggcctgctg cccctgtgac acccacacca ggctgctgca 540
cagacctgcg gggcctggag ctccagggtg agaggaatgc tgaggagctg ggccatgagg 600
ccttctggga gcaagagctg cgccgggagc aggcccgga gcgagagga caggcacgcc 660
tgcaggcact aagtgcggcc actgctgagc atgccgccc gctgcaggcc ctggacgctc 720
aggcccgtgc cctggaggct gagctgcagc tggcagcggg ggcccctggg cccccctcac 780
ctatggcatc tgccactgag cgcctgcacc aggacctggc tgttcaggag cggcagagtg 840
cggaggtgca gggcagcctg gctctggtga gccgggccct ggaggcagca gagcgacct 900
tgcaggctca ggctcaggag ctggaggagc tgaaccgaga gctccgtcag tgcaacctgc 960
agcagttcat ccagcagacc ggggctgcgc tgccaccgcc cccacggcct gacagggggc 1020
ctcctggcac tcaggtcgga gtggttcttg ggggaggctg ggaggtgagg acctggcca 1080
gccccactcc aagctgactt cccaacccac agggccctct gcctccagcc agagaggagt 1140
cctccttggg cgtccctctc ggtccctctg ggggcaccgg gccctcctgt ggctgcagcc acctcagct 1200
tctgtgcccc acctccccct ggggcaccgg ggcctcctgt aggttagcagc agctcctgcc 1320
ccagagtggg gtctcttggc agcccagccc caggctctgt gacagcctag tgagggctgc 1380
aagaccatcc tgcccggacc acagaaggag agttggcggg cacagagggc tcctctgcca 1440
ggcagtggga agccctgggt ttggcctcag gagctggggg tgcagtgggg gactgcccta 1500
gtccttgcca ggtcgccagc accctggaga agcatggggc gtaccagct cggaacttgc 1560
caggcccaa aggccacgac tgcctgttgg ggacaggaga tgcattgaca gtgtgtacac 1620
gctgtgggca tgtgcttgcc tgcgggagag gtccttcaat gtgtgtacac agcaagagca 1680
tgtgtgtgcc acttccccct ccccaacgtg aaaacctcaa taaactgccc gaagcagctt 1740
gaaaaaaaaa aa 1752

```

<210> 88

<211> 2461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

WO 01/07471

PCT/US00/19948

<223> Incyte ID No: 1806850CB1

<400> 88

```

ctgaaagaga gattggaggc ttttacaaga gattttcttc ctcacatgaa agaggaagag 60
gagggtttttc agcccatgtt aatggaatat tttacctatg aagagcttaa gtatattaaa 120
aagaaagtga ttgcacaaca ctgctctcag aaggatactg cagaactcct tagaggtctt 180
agcctatgga atcatgctga agagcgacag aagtttttta aatattccgt ggatgaaaag 240
tcagataaag aagcagaagt gtcagaacac tccacaggta taacctatct tcctcctgag 300
gtaatgctgt caattttcag ctatcttaat cctcaagagt tatgtcgtat cagtcaagta 360
agcatgaaat ggtctcagct gacaaaaacg ggatcgcttt ggaaacatct ttaccctgtt 420
cattgggcca gaggtgactg gtatagtggg cccgcaactg aacttgatac tgaacctgat 480
gatgaatggg tgaaaaatag gaaagatgaa agtcgtgctt ttcatgagtg ggatgaagat 540
gctgacattg atgaatctga agagtctgcg gaggaatcaa ttgctatcag cattgcacaa 600
atggaaaaac gtttactcca tggcttaatt cataacgttc taccatattg tggtaactct 660
gtaaaaacct tagtattagc atacagctct gcagtttcca gcaaaatggg taggcagatt 720
ttagagcttt gtcctaacct ggagcatctg gatcttacct agactgacat ttcagattct 780
gcatttgaca gttgggtcttg gcttgggttg tgccagagtc ttcggcatct tgatctgtct 840
ggttgtgaga aaatcacaga tgtggcccta gagaagattt ccagagctct tggaaattctg 900
acatctcatc aaagtggcct tttgaaaaca tctacaagca aaattacttc aactgcgtgg 960
aaaaataaag acattaccat gcagtcacc aagcagtatg cctgtttgca cgatttaact 1020
aacaagggca ttggagaaga aatagataat gaacaccctt ggactaagcc tgtttcttct 1080
gagaatttca cttctcctta tgtgtggatg ttagatgctg aagatttggc tgatattgaa 1140
gatactgtgg aatggagaca tagaaatgtt gaaagtcttt gtgtaatgga aacagcatcc 1200
aacttttagt gtccacctc tggttgtttt agtaaggaca ttgttggact aaggactatg 1260
tctgtttggc agcgatttg tcttctcca gcctttgcgt attgttgtca ctcattttgt 1320
tgtacaggaa cagctttaag aactatgtca tcactcccag aatcttctgc aatgtgtaga 1380
aaagcagcaa ggactagatt gcctagggga aaagacttaa tttactttgg gagtgaaaaa 1440
tctgatcaag agactggacg tgtacttctg tttctcagtt tatctggatg ttatcagatc 1500
acagaccatg gtctcagggg tttgactctg ggaggagggc tgccttattt ggagcacctt 1560
aatctctctg gttgtcttac tataactggg gcaggcctgc aggatttggg ttcagcatgt 1620
ccttctctga atgatgaata cttttactac tgtgacaaca ttaacggtec tcatgctgat 1680
accgccagtg gatgccagaa tttgcagtgt ggttttcgag cctgctgceg ctctggcgaa 1740
tgacccttga cttctgatct ttgtctactt catttagctg agcaggcttt ctttcatgca 1800
ctttactcat agcacatttc ttgtgttaac catccctttt tgagcgtgac ttgttttggc 1860
cccatttctt acaacttcag aaatcttaat ttaccagtga attgtaatgt tgtttctctt 1920
gcaaattata cttttgggtt agaaagggat taggtctttt caaaaggggtg agaacagtct 1980
tacatttttc ttttaaatga aatgctttaa agaatgttgg taatgccatg tcatttaaag 2040
tatttcatag ataattttga gtttttaaagt ccatggagggt gatttggtct ctttacacat 2100
taacactgta ccaagctttg cagatctttt ccgacacaca tgtctgaaga cttattttca 2160
aagacagcac atttttgaa actaatctct tttccgtaat atttccctta ttccaatgat 2220
tctcagaagg ccaattcaaa caaaccaca ttttaaggtt tttaggatta tagaataaat 2280
tggcttctga gtgttagctc agtgagctag gaaagcacca atcgatattt gtttccctta 2340
gggatacttt gttctcacca ctgtccctat gtcacaaat ttgggagaga ttttttaaaa 2400
taccacaatc atttgaagaa atgtataaat aaaatctact ttgaggactt taaaaaaaaa 2460
a
2461

```

<210> 89

<211> 965

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1851534CB1

<400> 89

```

ctttcagaaa aacccttggt gctgctgtaa caaattacaa caaacttaat ggcttaaaac 60
gacacagatt tattctttta catttcttga tgtctgacat gggactaaaa tcaaggtgtc 120
agcggcagag gcccgatgag agaaagggaa agttaaggat gctggagcag aacaatggat 180
ttctcttttc ctttcatgca agggatcatg ggaaacacaa ttcagcaacc acctcaactc 240
attgactccg ccaacatccg tcaggaggat gcctttgata acaacagtga cattgtgaa 300
gatgggtggc agacaccata tgaagctact ttgcagcaag gctttcagta ccagctaca 360
acagaagatc ttcctccact cacaaatggg tatccatcat caatcagtgt gtatgaaact 420

```

WO 01/07471

PCT/US00/19948

```

caaaccaaaccagtcata taatcagtat cctaattgggt cagccaatgg ctttggtgca 480
gttagaaaact ttagccccac tgactattat cattcagaaa ttccaaacac aagaccacat 540
gaaattcttg aaaaaccttc cctccacag ccaccacct ctccttcggt accacaaact 600
gtgattccaa agaagactgg ctccactgaa attaaactaa aaataacca aactatccag 660
aatggcaggg aattgtttga gtcttccctt tgtggagacc ttttaaata agtacaggca 720
agtgagcaca cgaaatcaaa gcatgaaagc agaaaagaaa agaggaaaaa aagcaacaag 780
catgactcat caagatctga agagcgcaag tcacacaaaa tccccaaatt agaaccagag 840
gaacaaaata tgaccaaag agaggggtga cactgtatca gaaaaacca gggaagaacc 900
agtactaaaa gaggggaagc ccagttcagc caatactatc ttctgttcca acaacggtag 960
tgtcc

```

<210> 90

<211> 2555

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1868749CB1

<400> 90

```

agcacgtccc actctatgac cagtgggagg atgtgatgaa agggatgaag gtggaggtgc 60
tcaacagtga tgctgtgctc ccagccggg tgactggat cgcctctgtc atccagacag 120
cagggtatcg ggtgctgctt cggtatgaag gctttgaaaa tgacgccagc catgacttct 180
ggtgcaacct gggaacagtg gatgtccacc ccattggctg gtgtgccatc aacagcaaga 240
tcctagtgcc ccacaggacc atccatgcca agttcaccca ctggaagggc tacctcatga 300
aacggctggt gggctccagg acgcttcccg tggatttcca catcaagatg gtggagagca 360
tgaagtaccc ctttaggcag ggcattgccc tggaaagtgg ggacaagtcc caggtgtcac 420
gcactcgcat ggctgtggtg gacacagtaa tcgggggtcg cctacggctc ctctacgagg 480
atggtgacag tgacgacgac ttctggtgcc acatgtggag ccccttgatc caccagtggt 540
gttggtcacg acgtgtgggc cacggcatca agatgtcaga gaggcgaagt gacatggccc 600
atcacccac cttccggaag atctactgtg atgccgttcc ttacctctc aagaaggtag 660
gagcagtcta cacagaaggc ggttggtttg aggaagggat gaagctggag gccattgacc 720
ccctgaatct gggcaacatc tgcgtggcaa ctgtctgtaa gggtctcctg gatggatacc 780
tgatgatctg tgtggacggg gggccctcca cagatggctt ggactggttc tgctaccatg 840
cctcttccca cgccatcttc ccggccacct tctgtcagaa gaatgacatt gagctcacac 900
cgccaaaagg ttatgaggca cagactttca actgggagaa ctacttgagg aagaccaagt 960
cgaaagccgc tccatcgaga ctctttaaca tggattgccc aaaccatggc ttcaagggtg 1020
gcatgaagct ggaggccgtg gacctgatgg agccccggct catctgtgtg gccacggtga 1080
aacgagtggg gcatcggtc ctcagcatcg actttgacgg ctgggacagc gattacgacc 1140
agtgggtgga ctgcgagtc ccagacatct acccgtcgg ctggtgtgag ctcaccggct 1200
accagctcca gcctcctgtg gccgcagaac cggccacacc gctgaaggcc aaagaggcca 1260
caaagaagaa aaagaaacag tttgggaaga aaaggaaaag aatcccgcgc actaagacgc 1320
gacccctcag acaggggtcc aagaagcccc tgcaggagga cgaccctcag ggtgccagga 1380
agatctcgtc ggagcctgtt cctggcgaga tcattgctgt gcgtgtgaag gaagagcatc 1440
tagacgtggc ctgcgccgac aaggcttcaa gtccagagct gcctgtctcc gtcgagaaca 1500
tcaagcagga aacagacgac tgagccttcc tgcctccagc ctggcttcta gctggaagcc 1560
agcccagcgt ttctctacca ccaccaccat gcctccacct gactttggct tggagactga 1620
tcctctctgt gtaattctg cccggtgctg tgaaggctgg acggtggagg acctgctggg 1680
gtctcctggg accgcctgt tgettetgcc ctcccctgtg gaaaggctta tatgacgggc 1740
cgcctgaggg ccagaaactc gtctgtgaac cacttttcc agccagagtt cccaaagctg 1800
gaacgctagc tgctgtctt tccttaagat ggctccccc cgacccgcca cggccctcag 1860
ttgccaggga tggggccacc actgtcacac tgtggaatac aagacagtga actctgtctg 1920
cctgaacgag tcatgtaaat taagtcttag agcagctctc tgagcaggat aaggtccctc 1980
gacagtgagt tgtgtggtgg gggcagcctc tgcctcaaaa attcaccaag cagaatgcct 2040
ctcagcctca tgtgttggtc ctctgctcct cctagctccc cagggatgtt ggggacccag 2100
cttgctcggc cagctaagaa cagtgacca ggatgtggat tttggcgacc tgtgtggtgg 2160
ccttgagctg ctttctgtgt ttgtgaggac tgactcccat ttctaaagg aaatgcccc 2220
ggggaggaca ttgggaggaa gatggcctga gtgtgcactt tggctctgct acctgctcct 2280
gaagccccgc taaaaataat tcatccaaga ttcttttgta gttaaagggt ccagttctga 2340
ctggagcctc tagagagctg ggcttgtatg ttcttttggc cttttgttcc tacctaaatg 2400
aagaaacctat gccgtgaggg ccctggaaca cagaacctc aagacaagga tgacagagct 2460
ggaggacaca tctagctgcc attgcaacct cactgggctc cccagactct gtgtgtgaga 2520

```


WO 01/07471

PCT/US00/19948

```

gtggcagtgc tgaccttggt gggccaaggg acccactgaa ggtcctggaa ggtgttgttg 3120
cagcagtcca cgccagtgtg gacaaggggt aggagctggt ttcacctgag gacctgctgg 3180
agtggctgcg gcctttctgt gctgatgacg cctggccggt gcggccccgc attcacgtgc 3240
tgcagatttt ggggcaatca tttcacctga ctgaggagga cagcaagctc ctctgtttct 3300
ttagaactga agccattctc aaagcctcct ggccccagag acaggtagac atagctgaca 3360
ttgagaatga agagaaccgc tactgtctat tcatggaact cctggaatct agtcaccacg 3420
aggctgaatt tcagcacttg gttttacttt tgcaagcttg gccacctatg aaaagtgaat 3480
atgtcataac caataatcca tgggtgagac tagctacagt gatgctaacc agatgtacga 3540
ttggaacaa ggaaggattg gggaatgaag ttttgaaaat gtgtcgctct ttgtataaca 3600
ccaagcagat gctgcctgca gaggggtgtga aggagctgtg tctgctgctg ctttaaccagt 3660
ccctcctgct tccatctctg aaactttctc tcgagagccg agatgagcat ctgcacgaga 3720
tggcactgga gcaaatcacg gcagtcacta cgggtgaatga ttccaattgt gaccaagaac 3780
ttctttccct gctcctggat gccaaagctgc tgggtgaagtg tgtctccact cccttctatc 3840
cacgtattgt tgaccacctc ttggctagcc tccagcaagg gcgctgggat gcagaggagc 3900
tggcagaca cctgcgggag gccggccatg aagccgaagc cgggtctctc cttctggccg 3960
tgagggggac tcaccaggcc ttcagaacct tcagtacagc cctccgcgca gcacagcact 4020
gggtgtgagg gccacctgtg gccctgctcc ttagcagaaa aagcatctgg agttgaatgc 4080
tgttcccaga agcaacatgt gtatctgccc attgttctcc atggttccaa caaattgcaa 4140
ataaaactgt atggaacga tgaaaaaaaa aa 4172

```

<210> 92

<211> 4037

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2259032CB1

<400> 92

```

tcggagtgcc gcccgcgccc ccgagtcggt ctccagccgc cggccggccg tgccgggtgtc 60
cgtaggcgct gcgccctcgg ccggggcccat gtgtgtgcgg cccgcccagag gccgcccggg 120
ctttgcctcc accagcgccc tggcctccgc tcgggcctcc acacgggcct ccgaagagct 180
gccgcgacgc ccggcccgcga gggcaggtaa agagattata aatcttccac tgaatgaaaa 240
aaattttctt aaagctgcac atactccaag aaaaaaacca caaatgtttt tctgttttgc 300
ctgaatacat gatttaaaca agagatttcc acagaagctc tgccggccgtc acgatgttct 360
ggaagtttga cttgaacacc acgtcccatg ttgacaagct gctggacaag gagcatgtga 420
cgctgcagga gttaatggat gaagatgaca tcttgccagga gtgtaaggct cagaaccaga 480
agctgctgga ctccctgtgc aggcagcagt gcatggagga gctggtgagc ctcatcacac 540
aggatccgcc cctggacatg gaggagaagg tccgcttcaa atatccaaac acagcctgtg 600
agcttctgac ttgtgatgtg ccgcagatca gcgaccgcct cggtgggggac gagagcctgc 660
tgagcctcct gtacgacttc ttggaccatg agccgcctct caatcctctg ctgccagtt 720
ttttcagcaa gaccattggc aatctcattg caagaaaaac cgaacagggtg attacgtttt 780
tgaagaagaa ggacaagttc atcagcctgg tgttgaagca catcggcacc tcagcgctta 840
tggacctgct gctgcgcctg gtcagctgtg ttgagccagc cgggctccgg caggacgtcc 900
tgcactggct gaatgaagag aaggtcaccc agaggcttgt ggagttgatc cccccagcc 960
aggatgaaga taggcagtca aatgcttctc agactctctg tgacatagtt aggctgggca 1020
gagaccaggg cagtcagctg caagaggctc tggagccaga cccgctcctc acagcgtggt 1080
agtccaggca ggactgtgtg gagcagcttc tgaagaacat gtttgatgga gaccggacgg 1140
agagctgcct cgtcagtggtg actcaggtgt tactcacctt gctggaaacc aggggggttg 1200
ggacagaggg cttgggtggac tccttttctc agggactgga aaggtcatac gctgtcagca 1260
gcagcgtact acacggcacc gagcctcggc tgaaggactt ccaccagctc ctgctcaacc 1320
cgcccaagaa gaaagcgatc ctgaccacca ttggtgtgct ggaggagccc ctggggaatg 1380
cccgtctgca tggcgcccgc ctcatggcag cactgctgca cacaaacaca cccagcatca 1440
accaggagct ctgccggctc aacacgatgg acttactgct ggacttgctt ttaagtaca 1500
cctggaataa ctttttgcac ttccaagtgc aactatgcat agccgctatt ctctcccacg 1560
ctgcccgtga ggagaggaca gaagccaggg gatccgagag cagggtggag cctccgcatg 1620
agaacgggaa ccggagcctg gagactcccc agccggccgc cagcctccct gacaacacaa 1680
tggtgaccca cctgttccag aagtgtgtgc tgggtgcagag gatcctggag gcctgggaag 1740
ccaacgacca cacgcaggca gcgggtggca tgagacgtgg gaacatgggc cacctcacac 1800
ggatcgccaa ccgcggtggtg cagaacctgg agcggggccc tgtgcagacg cacatcagcg 1860
aggtctccg agggctccct gcggactcgg gtggcgcgtg ggagagcttc gtgaggaga 1920
cgctgacgga gacgaaccgc aggaacactg tggacctggc cttctctgac taccagatcc 1980

```

WO 01/07471

PCT/US00/19948

```

agcagatgac agccaacttc gtggatcagt ttggcttcaa tgatgaggag tttgccgacc 2040
aggacgacaa catcaatgcc ccggtttgaca ggatcgacaga gatcaacttc aacatcgacg 2100
ctgacgagga cagtcaccagc gcagctctgt ttgaggcctg ctgcagtgcac cgcaccagc 2160
cctttgatga tgatgaggac gaggacatct gggaggacag tgacactcgc tgtgctgccc 2220
gggtgatggc cagacccagg tttggagccc cccatgcttc agagagttgc tcaaagaatg 2280
gcccagagcg tggaggccag gatgggaagg cgagccttga agcacacaga gatgcacctg 2340
gggcaggtgc cccaccggcc cccgggaaga aggaagcccc cctgtggag ggtgactcag 2400
aagcaggcgc catgtggacg gcagtgttg atgagccagc gaactcaacg cccacagccc 2460
caggagtggg gagggacgtg ggttccagt tgtgggcagc tggcacctca gctccagagg 2520
agaaaggctg ggccaagttc actgacttcc aacctttctg ctgtccgag tcagggccca 2580
ggtgcagctc tccggtggac acagaatgca gccatgctga gggcagccgg agccaaggcc 2640
ctgagaaagc cttcagcccc gcttctccat gtgctggaa cgtgtgtgtc accaggaagg 2700
ccccctgct ggctcttgac agtagctcct ctgggggctc ccacagcgag gatggcgacc 2760
agaaggcagc gatggccatg gatgcggtga gcaggggtcc cggccgggag gccccccgc 2820
tgcccacagt ggccaggaca gaggaggctg tcggcagggg cgggtgtgtc gacagccggc 2880
tgttaagccc tgcccgcccc gcgccaaagg aagtgactgc tgccccagcc gtggctgtgc 2940
cccccgaggg tactgtggcc atcaccacag cactgagcaa ggctggcccc gccataccca 3000
ccccagcagt ctcttctgca ctggccgtgg cgtccccct agggcccatc atggcagtca 3060
cagcagcccc agccatggtg gccacctgg ggacagtgc aaaggacggg aagacagatg 3120
ccccgccaga aggagctgcc ttaaattggc cagtgtgat ctgtgccgc cgggccacgg 3180
cccacctgg tcaggctgcc tcttaatcg agaaaactac ctggtgatgc aatctttttt 3240
tttttaattt aatttaattt taaaataaat gctgcattgg taaagctggc agttgaaacc 3300
agttggacgg ccagcttgc gtctcttctg cctgagtggg cctctcaggt cactcgtgcc 3360
ctgctggagg acagaggggc acctcagcc cccccaagcc cagagcacag caataaggtc 3420
ggcctgcagg agccggggg ggggtggggc tggggggggc aggacctga gatgccacca 3480
ggacctgatg ggccaggaag ggcgtggaca tggaggctgt ttttacagtt tttttttgtt 3540
gttgttttgt ttttaagaa tacagaagga gccaaagctt tttgcacttt gtatccagct 3600
gcaagctcag ggcagagtca agggcctggg ttggaaaaac ctgactcaca ggaatgcata 3660
attgaccttc gcagctaccc aatagccctt ggagctggca ctgaaccagg ctgaacagatt 3720
tgactgcctt aaaaacacaa ggccctctag gcctggcagg gatgtccctg tgcccagcac 3780
agggtgcctg gcagggggag accacaggta tgcaggtggg gggacatggt gtggcactgg 3840
gggctcgaag actggtttct agcactaccg gtcacggcca tgtcgtccta gaagggtcca 3900
gaagattatt ttacgttgag tccattttta atgttctgat cacctgacag ggcaccccaa 3960
acccccaact cccaataaaa gccgtgacgt tcggacaaaa aaaaaaaaaa aaaaaaaaaa 4020
aaaaaaaaaa aaaaaaa 4037

```

<210> 93

<211> 2031

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2359526CB1

<400> 93

```

ggcggggctc ggctcgggct ccgcggggcg gcggggcgac atggcgggca acatgtaccg 60
ggtcggagat tatgtctact ttgagaattc ctccagcaac ccatacctaa taagaaggat 120
agaagaactc aacaagactg caagtggcaa cgtggaagca aaagtagtat gctttttatg 180
acgacgtgat atttccaaca cacttataat gctcgagat aagcatgcta aagaaattga 240
ggaagaatct gaaacaacag ttgaggctga cttgaccgat aagcagaaac atcagttgaa 300
acatagggaa ctctttttgt cacgccagta tgaatctctg cccgcaacac atatcagggg 360
aaagtgcagt gttgcccttc tgaatgagac agaatcagta ttgtcatatc ttgataagga 420
ggataccttc ttctactcat tggctctatga cccctcattg aaaacactat tagctgacaa 480
aggtgaaatc agagtgggac ctagatatca agcagacatt ccagaaatgc tgttagaagg 540
agaatcagat gagagggaac aatcaaaaat ggaagttaaa gtttgggatc caaatagccc 600
acttacggat cgacagattg accagttttt agttgtagca cgtgctgttg ggacattcgc 660
cagagccctg gattgcagca gttctgtgag gcagcctagt ttgcatatga gtgctgctgc 720
agcttcccga gacatcacct tgtttcacgc tatggataca ttgtatagac acagctatga 780
tttgagcagt gccattagt tcttagtacc actcggagga cctgttttat gcagagatga 840
aatggaggaa tggtcagcct ctgaagctag cttatttgaa gaggcactgg aaaaatattg 900
caaagacttc aatgacatac ggcaagattt tcttcttgg aaatcattga ctagcatcat 960
tgaatattat tacatgtgga aaactactga cagatatgtg caacagaaac gtctaaaagc 1020

```


WO 01/07471

PCT/US00/19948

```

aagaaggtag atcctgtcca ttcattaatt gctttgatta ctaggagggt ttctgttcag 1380
ttttgttttt aaatgtcttg ctgatctagt tctttcagat ggaataacct tccagtcctt 1440
tagagagtgg aactagtcca tataaccag cttcagtagc aaaagtagaa gccgccacat 1500
cttttcattt ctccaagagg agagtgggga aggttcccat gaccagctgg gcagtcagga 1560
tttctctagg cattctaagt tgaaataagt gtagactgct gtcaaggagg cttcatcaga 1620
agatgtatag catttgaatg tctaatagata atgcatatca ttagaatcca agctttgaaa 1680
atctctgatt aatgctcatg tattttcttta tctttgtttt tccttgtgaa gaaagacttt 1740
caccactgtc tgagtgatga tgctgttgat aaggatgatg tcgatgacta ctatattgca 1800
tctctcagga acagctgatg ggaaggagg ggctgctgag ttcccttggt ctagctagca 1860
gcacgctcct cagagagggg gccgagttac agacagcagc cgcattctca tgcaaaatta 1920
gttttaaaact gctagtgtgg gcacggttac cttttgcctg ggtgataccg aagaattggt 1980
gaggatttag tatgctccgt agagacagtt cagccagtc tttctgcatt ggagagactt 2040
ctcata
2046

```

<210> 97

<211> 2660

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2797839CB1

<400> 97

```

gtggcgagtg ccggccgaaa gctaggtccg gattgcacgt ggagggccgc ccgaaggcca 60
ctctcggaca ttaaccgcga ttctgtacca tggggcgcaa gttggaccct acgaaggaga 120
agcggggggc aggccgaaag gcccggaagc agaagggtgc cgagacagaa ctctgtcagat 180
tcttgccctg agtaagtgc gaaaattcca agaggctgtc tagtcgtgct cgaaagaggg 240
cagccaagag gagattgggc tctgttgaag cccctaagac aaataagtct cctgaggcca 300
aaccattgct tggaaagcta ccaaaaggga tctctgcagg agctgtccag acagctggta 360
agaagggacc ccagtcctta tttaatgctc ctcgaggcaa gaagcgccca gcacctggca 420
gtgatgagga agaggaggag gaagactctg aagaagatgg tatggtgaac cacggggacc 480
tctggggctc cgaggacgat gctgatacgg tagatgacta tggagctgac tccaactctg 540
aggatgagga ggaaggtgaa gcgttgctgc ccattgaaa agctgtctcg aagcagaagg 600
cccgggaagc tgctgctggg atccagtgga gtgaagagga gaccgaggac gaggaggaga 660
agaaagaagt gacccctgag tcaggccccc caaaggtgga agaggcagat gggggcctgc 720
agatcaatgt ggatgaggaa ccatttctgc tgccccctgc tggggagatg gagcaggatg 780
cccaggctcc agacctgcaa cgagttcaca agcggatcca ggatattgtg ggaattctgc 840
gtgatttttg ggctcagcgg gaggaagggc ggtctcgttc tgaataacct aaccggctca 900
agaaggatct ggccatttac tactcctatg gagacttctt gcttggcaag ctcatggacc 960
tcttccctct ctctgagctg gtggagttct tagaagctaa tgaggtgcct cggcccgtca 1020
ccctccggac caataccttg aaaaccgcac gccgagacct tgcacaggct ctaatcaatc 1080
gtgggggttaa cctggatccc ctgggcaagt ggtcaaagac tggactagtg gtgtatgatt 1140
cttctgtgcc cattggtgct acccccagat acctggctgg gcactacatg ctgcaggag 1200
cctccagcat gttgcccgtc atggccttgg caccacagga acatgagcgg atcctggaca 1260
tgtgttgtgc ccctggagga aagaccagct acatggccca gctgatgaag aacacgggtg 1320
tgatccttgc caatgacgcc aatgctgagc ggctcaagag tgttgtgggc aacttgcac 1380
ggctgggagt caccaacacc attatcagcc actatgatgg gcgccagttc ccaaggtgg 1440
tggggggctt tgaccgagta ctgctggatg ctccctgcag tggcactggg gtcactcca 1500
aggatccagc cgtgaagact aacaaggatg agaaggacat cctgcgctgt gctcacctcc 1560
agaaggattt gctcctgagt gctattgact ctgtcaatgc gacctccaag acaggaggct 1620
acctggttta ctgcacctgt tctatcacag tagaagagaa tgagtgggtg gtgactatg 1680
ctctgaaaaa gaggaatgtg cgactgggtc ccacgggcct agactttggc caggaagggt 1740
ttaccgctt tcgagaaagg cgcttccacc ccagctctgcg ttctaccga cgcttctacc 1800
ctcataccca caatatggat gggttcttca ttgccaaagt caagaaattt tccaattcta 1860
tccctcagtc ccagacagga aattctgaaa cagccacacc tacaaatgta gacttgccct 1920
aggctatccc caagtctgag aacagcagcc agccagccaa gaaagccaag gggcgtgcaa 1980
agacaaagca gcagctgcag aaacagcaac atcccaagaa ggctccttc cagaagctga 2040
atggcatctc caaaggggca gactcagaat tgtccactgt accttctgtc acaaagacc 2100
aagcttctc cagcttccag gatagcagtc agccagctgg aaaagccgaa gggatcaggg 2160
agccaaaggt gactgggaag ctaaaagcac gatcacctaa attacagtcc tccaagaaag 2220
tgtcttctc caggcagaat gccctccca agggcagaga cacaacaaca ccgctgtgtg 2280
tatccccatc caagactcag gccaccctga aacctaaagga ccatcatcag ccccttgga 2340

```

WO 01/07471

PCT/US00/19948

gggccaagg	ggttgagaag	cagcagttgc	cagagcagcc	ttttgagaaa	gctgccttcc	2400
agaaacagaa	tgataccccc	aagggggcctc	agcctccccc	tgtgtctccc	atccgttcca	2460
gccgcccccc	accagcaaa	aggaagaaat	ctcagtcacg	gggcaacagc	cagctgctgc	2520
tatcttagat	ggttgaaaac	tagacgggtg	gctcactgcc	attgtcacca	ggttggaact	2580
cttgctctctg	tgaggatgcc	ttctctactg	tgcataccca	tgaaatttaa	tacacatttt	2640
aaaacctctg	aaaaaaaaaa					2660

<210> 98

<211> 4610

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2959521CB1

<400> 98

ggggccccga	cgcatgaggg	gggtcgggcg	gcgtgtctac	gcggacgcac	cggctaagct	60
gcttctgccg	ccgccggccg	cctgggacct	tgcggtgagg	ctgcgcgggg	ccgaggccgc	120
ctccgagcgc	caggtttatt	cagtcaccat	gaagctgctg	ctgctgcacc	cggccttcca	180
gagctgcctc	ctgctgaccc	tgcttggtct	atggagaacc	acccctgagg	ctcacgcttc	240
atccctgggt	gcaccagcta	tcagcgtctg	ctccttctctg	caggatctaa	tacatcggtg	300
tgccgagggg	gacagcctca	ctctgcagca	gctgaaggcc	ctgctcaacc	acctggatgt	360
gggagtgggc	cggggtaatg	tcacccagca	cgtgcaagga	cacaggaacc	tctccacgtg	420
ctttagttct	ggagacctct	tcactgcccc	caatttcagc	gagcagtcgc	ggattgggag	480
cagcgagctc	caggagtctt	gccccaccat	cctccagcag	ctggattccc	gggcctgcac	540
ctcggagaa	caggaaaacg	aggagaatga	gcagacggag	gagggggcgg	caagcgtctg	600
tgaagtgtgg	ggatacggtc	tcctctgtgt	gaccgtcatc	tcctctctgt	ccctcctggg	660
ggccagcgtg	gtgcccttca	tgaagaagac	cttttacaag	aggctgctgc	tctacttcat	720
agctctggcg	attggaaccc	tctactccaa	cgcctctctc	cagctcatcc	cggaggcatt	780
tggtttcaac	cctctggaag	attattatgt	ctccaagtct	gcagtgggtg	ttgggggctt	840
ttatcttttc	tttttcacag	agaagatctt	gaagattctt	cttaagcaga	aaaatgagca	900
tcacatgga	cacagccatt	atgcctctga	gtcgtctccc	tccaagaagg	accaggagga	960
gggggtgatg	gagaagctgc	agaacgggga	cctggaccac	atgattcctc	agcactgcag	1020
cagtgcagctg	gacggcaagg	cgcccatggg	ggacgagaag	gtcattgtgg	gctcgtcttc	1080
tgtgcaggac	ctgcaggctt	cccagagtgc	ttgctactgg	ctgaaagggtg	tccgctactc	1140
tgatatcggc	actctggcct	ggatgatcac	tctgagcgac	ggcctccata	atttcatcga	1200
tgccctggcc	atcgggtgctt	ccttcaactgt	gtcagttttc	caaggcatca	gcacctcggt	1260
ggccatcctc	tgtgaggagt	tcccacatga	gctaggagac	tttgtcatcc	tgctcaacgc	1320
tgggatgagc	atccaacaag	ctctcttctt	caacttctct	tctgcctgct	gctgctacct	1380
gggtctggcc	tttggcatcc	tgcccgccag	ccacttctct	gccaactgga	tttttgcgct	1440
agctggagga	atgttcttgt	atatttctct	ggctgatatg	ttccctgaga	tgaatgaggt	1500
ctgtcaagag	gatgaaagga	agggcagcat	cttgattcca	tttatcatcc	agaacctggg	1560
cctcctgact	ggattcacca	tcattggtgt	cctcaccatg	tattcaggac	agatccagat	1620
tgggtagggc	tctgccaaga	gectgtggga	ctggaagtgc	ggccctgggc	tgcccgatcg	1680
ccagccccgag	gacttaccat	ccacaatgca	ccacggaaga	ggccgttcta	tgaaaaactg	1740
acacagactg	tattcctgca	ttcaaagtgc	agccgtttgt	aaaatgctgt	atcctaggaa	1800
taagctgccc	tggttaaccag	tctctagcta	gtgcctcttg	ccctctcttc	acctcctttt	1860
ctctcagtga	ctctggaacc	tgaatgcagc	ttacaagaca	agcctgactt	ttttctctga	1920
ttaccttggc	ctcctcttgg	aaccagtgtc	gaaaggtttt	gaatccttta	cccaacaatg	1980
caaaaataga	gccaatgggt	ataacttggc	tagaaatata	aagagttaga	tccatagtgt	2040
ggggcccatg	actctagctg	ggcaccttgg	acctccagct	ggccaataga	agagacagga	2100
gacaggaagc	cttccccattt	tttcaaagtc	tgtttaattg	cctattactt	ctctcaaaga	2160
gaacctgaag	tcagaacaca	tgagcagggt	gagagggtgag	gcaagggtca	tcctgaatgg	2220
gagaggaagt	cgaaccactg	ctgtgtgtct	tgtcaggatg	ctcacttggt	cctactgaga	2280
tgctggatat	tgatttttga	acagcaccgc	gtgtttcacg	gctgtccgag	tgagctaacg	2340
tgccggtgtg	gctgcctgga	cctcctcttt	caggttaacg	ctgacagaat	ggaggctcag	2400
gctgtctgca	agaaaacagt	tggtttggct	gtgattttga	cctcctcttc	ccactgcca	2460
tcttctaaga	gactttgtag	ctgcctccta	gaagcacatt	ctgagcacat	ttgagacctc	2520
tgtgttagag	gggagactgc	acaaaactatc	ctccccagag	ttgagacgtc	tgagaggtgg	2580
caagctgact	tgtagaaatg	gggtgcccatt	tatgctctac	ttagacaagg	gtaatcagaa	2640
atggaatcag	tgcaggcaaa	atttaggatt	tgcgccttcc	ataaatcaaa	gcattgactaa	2700
tagggggtct	ctgaaatgta	agggcacaaa	cttcacttag	ggcatcgag	atgtttgcag	2760

WO 01/07471

PCT/US00/19948

```

aatggttggc ctaatgatta tgctacagat gggttttaaa tgaccctgtc aggttactgc 2820
ttccttgcaa aaaaagtcga atcctgcatt gaattgaata tgaatttctc taactctctc 2880
cagaaaaatgg atggagataa cttgtcttta aaactgtagg ccagccttag ccactgtgga 2940
gcccttgccct ccgagctctg gcttcaaggg gagctcttct ccagggtcac taggtgaatt 3000
gatttattat tatcatattg ataatgtgag attctttagc cactttgggg agcctgtctc 3060
tccagaagcc tttcttagtg gtgcccacag ttggagccca ggggccatgt ttgcaaactg 3120
attcatgtgc atggctgaca ggagtactgg ttcactacca atgcctgagc ttttctctta 3180
catagaaaaa ctgtccgctc tcagtaatca caagcagcat ccgttttgtt ttctcttctt 3240
gggagacatc tgtcaaacca ggaatattct tgaaaagaac gtgagcagga aaaactgctg 3300
gtgatacttt ttttaagttt tgtttttatc ttgctgttg gcttcaatac atttgagaat 3360
acgctgaaga gggaaaattt cagtgatgga gattctagat taaatatcag gactgatttc 3420
ctggtggggag gattatgggc cagttttacc aaagaaccaa ttccttgaat gttggaatct 3480
aactttttat attgtcatta ttattgttgt ttttaaaggg ttctttgtct tttctgtttt 3540
atttttctca agctgcttcc aggagctagc agaaaataac tcaaagttga agactctgga 3600
agattttgct ttaacctaac tcgcattgat gtattaaatt tataatttta gcattcccaa 3660
tagatcctat cattccttaa acataatacc ctttgtcttg gagtagaata ctaagttaga 3720
gttagtggat ttctagttta ggagaggagc tcaaaactat aatctttaac aaattgaaaa 3780
atgaaatagg gtgttttccc tttttgtgca cacctatatt accttaagaa atttccctcc 3840
atagacagct gcctcaaagg gaaatcctct ttaaaccgta gttggcgag aggtcagtc 3900
tagtcggagc ttaggagggg cggagagcct caccatcgct gacttgagtc gccactgatt 3960
gtggcaacag ctttgccctca tgagtcaaaa attggcaatt tcttttgatt tttagtgtt 4020
gaatttgctg tttcaagcat ttgtacatat tagaagtcta aggagtagca agtcagtggg 4080
aggacttttt cacccttggc attagcagct tcgacctcat tttccagatg caccagctcc 4140
tattaataag ttagcaagga aagtgtatgt cacgtgcagg aacagtgagg cagggacagg 4200
ggttctgctc cttctcactt caccaccggc acacagcttg cccctgtctt tgcccccaaa 4260
ggtattttgt gtctagtgtc aaattggagc tattcttcac tggctcctaa ccttgggttt 4320
taaaaagaag gcttctctgt ttgggtagcg taagagctga gtatagtaag tctcttcca 4380
aagagatggc aatatgctgg gcatctactt taaaacaaag ttgtctgatt tttgcaagag 4440
aggttaggat tttattgttc ttatttccct ttacagttct gcagttccat cacagtattt 4500
ttttaataaa ctcaggtgta tgagaagaaa ttagaaaaga aaattaactt atgtggactg 4560
taaattgttt atttgtaaga ttctataaat aaagctatat tctgtaaaac 4610

```

<210> 99

<211> 1889

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3082014CB1

<220>

<221> unsure

<222> 1809, 1848, 1853, 1880

<223> a, t, c, g, or other

<400> 99

```

acgtagaaga tggagagaag gaggtggtat tgagagatgc tgtggggagg gagagtgggg 60
ctcaccgggg ttttccaatc tctctcctat agggggaaat gcagtgtgac cctcttgaat 120
gagacagata tcttgagcca gtacctggaa aaggaggact gcttttttta ctactggtg 180
tttgaccccg tgcagaagac acttctcgct gatcaggcg agattagagt tggttgcaaa 240
taccaagctg agatcccaga tcgcctagta gagggagaat ctgataatcg gaaccagcag 300
aagatggaga tgaaggctctg ggaccagac aacctctca cagaccggca gatcgaccag 360
tttcttgttg tggcccgagc tgtgggaacc tttgcaagag ccctagattg tagcagctcc 420
attcggcagc caagcttgca catgagtgc gctgctgcct ccgagatat cactctgttt 480
cacgccatgg atacctgca aaggaacggc tacgacctgg ctaaggccat gtcgaccctg 540
gtaccccagg gagggccggg gctgtgtcgg gatgagatgg aggaatggtc agcctcagag 600
gccatgctat ttgaggaggc cctagagaag tatgggaagg acttcaatga tattcgccag 660
gattttctac cctggaagtc acttgccagc atagtccagt tttattacat gtggaaaacc 720
acagaccggg atattcagca gaaaagggtg aaagctgctg aagcagacag caaactgaaa 780
caggtctaca ttcccaccta cactaagcca aaccctaacc agatcatttc tgtgggttca 840
aaacctggca tgaattgggc tggatttcag aagggcctga cttgtgagag ttgccacacc 900
acacagtctg ctcagtggta tgcctggggc ccacctaaca tgcagtgcg cctctgtgct 960

```

WO 01/07471

PCT/US00/19948

```

tctctgttga tctactggaa gaagtatggg ggactgaaga cccaactca gcttgagggg 1020
gccactcggg gcaccacgga gccacactca aggggtcatt tatccagacc tgaagctcaa 1080
agtctctctc cttacacaac cagcgccaac agggccaagc tactggctaa gaacagacaa 1140
actttcctgc ttcagaccac aaagctgacc cgtcttgcca gacgcatgtg caggaccta 1200
ttacagccaa ggagggccgc ccgacggcct tatgctccta tcaatgccaa tgccatcaaa 1260
gcagagtgtc ccattcgact tcctaaggcc gccaaagactc cattgaagat tcaccctctg 1320
gtgcggctgc ccctggcaac tatcgtcaaa gatctggtgg ccagggcacc cctgaaacca 1380
aaaacacctc ggggtaccaac gacaccgatc aacagaaacc agctgtccca gaaccgggga 1440
ctgggggggca ttatggtgaa acgggcctat gagactatgg caggggagagg gggtcctttc 1500
tctgccaatg gaaggcctct ggcttcaggg attcgttcaa gctcacagcc agcagccaag 1560
cgtcagaaac taaaccacgc tgatgccccc aatcctgtgg tgtttgtggc cacaaggat 1620
accagggccc tacggaaggc tctgacccat ctggaaatgc ggcgagctgc tcgccgaccc 1680
aacttgcccc tgaagggtgaa gccaacgctg attgcagtgc ggccccctgt cctctctact 1740
gcaccctcac atcctgccag caccaatgag cctattgtcc tggaggactg agcactgttg 1800
ggaaaggang tgggctgaga aggtagaggt ggatgccagc ggcaccanac ctnccttcc 1860
ttctgtgtcg aaggagtgan gagtgatta                                     1889

```

<210> 100

<211> 2032

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3520701CB1

<400> 100

```

gccggggccg agccgctgtt cggctgacag ttgaggatgg ccggagccga gggcgccgct 60
gggcggcagt cggagctgga gcccggtgga tcgttggtcg acgtccttga ggaggacgag 120
gagctggaga atgaggcgtg cgctgtcctg ggcggcagcg actccgagaa gtgctcctac 180
tctcagggct cagtaaagag acaagcacta tatgcctgta gtacctgcac ccagagggga 240
gaagaaccag caggaatttg tttagcttgc agttatgaat gtcatggaag tcacaaacta 300
tttgagctat acacaaaaag aaattttcgt tgtgattgtg gaaacagcaa gtttaaaaaat 360
ttggaatgca aattacttcc tgacaaagca aaggtaaatt ctggcaataa gtacaatgac 420
aacttttttg gattgtactg catttgcaag agaccttacc ctgacccctga agacgagatt 480
ccagatgaga tgatccagtg cgtagtctgt gaagactggg tccatggaag gcatcttggg 540
gccattcccc ctgagagtgg ggattttcag gagatgggat gccaggcctg catgaaacgt 600
tgttcttttt tgtgggctta tgctgcacaa ttggcagtaa ccaaaatatc cactgaggat 660
gatggattgg tgcggaacat tgatggaata ggtgatcagg aagtatatca acctgaaaaat 720
ggagagcacc aagatagtag cctcaaagag gatgttccag aacagggaaa ggaatgatgc 780
cgggagggtta aagtagagca gaacagtga ccatgtgccg gctctagtcc tgaatctgat 840
ctccagacag tgtttaagaa tgaaagcctc aacgcagaat caaaatctgg ctgcaaactt 900
caggagctta aagctaagca gcttataaag aaagacactg ccacctattg gcccctgaac 960
tggcgtagca agttgtgtac ctgccaagac tgtatgaaaa tgtatggaga tctagatgtc 1020
ttattcctga cagatgaata cgacacagtt ctggcttatg aaaacaaagg gaagattgcc 1080
caggccactg acaggagcga tcccctaatt gataccctta gcagcatgaa tagagtccag 1140
caagtggaa ccatctgtga atacaatgat ttgaagactg aacttaaaga ctatctcaag 1200
agatttgctg atgaaggcac ggttggttaag agagaggaca ttcagcagtt ctttgaagag 1260
tttcagtcaa aaaagagaag aagagtggat gggatgcagt attactgcag ctagagtggg 1320
gtatgaagct ttctcattca agccaatgaa aatgcgcttc ccattcttgg aataaaaagag 1380
gtgtgggttca catttggtcc ctttccgtc ctectctgtt tggagaggcc tcgcgctccc 1440
ttcattctct ttagctgcag tagccaccgt gtggatgctg acttcacagc cagcgtctct 1500
tgtgactcag ctgatgcagc tcattccaca gacttcgcca gtgtactcct actccagtgc 1560
acccaggggt atttgcatag tttttaagtt tgattttgtt ttgagaaagc aaattgggtg 1620
cttgtttaat gatctgttat ttcactccca gatgtgtgtg ttttgccaca gagctgttgc 1680
cttcagaac ctctccgca ggcacacagg aaggtctctc tcccgtcacc tagaactctc 1740
acagggtcccc tcgccccctt gattgtggtg ccttgggtca aagcttctc aagcctgttc 1800
tgctccttct ttcacgtccc tgttttctga ggtttgggtc tagcttagaa aggatcttgg 1860
ggcttggttt ctctagcccc aacctccaga gtagccagga ctgatgggtt tctgggtctg 1920
atgtctgtca caggcgagga gattaacaga tgacagggtt gaggaagcaa gcctttgtta 1980
tgaattttac taatacagtt caagtgaat tttcgttcat gattctattg gc 2032

```

<210> 101

WO 01/07471

PCT/US00/19948

<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 4184320CB1

<400> 101
aatgaaagca acaggagctg ctccggggac tgctttttgcc agtaccacaga atcagtgtgc 60
aggctcagaa atcctggata gaaagagcat tttataaaaag agaattgtgtc cacatcatac 120
ccagcaccaa agacccccat aggtgttgct gtgggcgtct gataggccag catgttggcc 180
tcacccccag tatctccgtg cttcagaatg agaaaaatga aagtcgcctc tcccgaatg 240
acatccagtc tgaaaagtgg tccatcagca aacacactca actcagccct acggatgctt 300
ttgggacat tgagttccaa ggaggtggcc attccaacaa agccatgtat gtgcgagtat 360
cttttgatac aaaacctgat ctctctttac acctgatgac caaggaatgg cagttggagc 420
ttcccaagct tctcatctct gtccatgggg gcctgcagaa ctttgaactc cagccaaaac 480
tcaagcaagt ctttgggaaa gggctcatca aagcagctat gacaactgga gcgtggatat 540
tcaactggag ggtaaacaca ggtgttattc gtcagtgttg cgatgccttg aaggatcatg 600
cctctaagtc tcgaggaaaag atatgcacca taggtattgc cccctgggga attgtggaaa 660
accaggagga cctcattgga agagatgttg tccggccata ccagaccatg tccaatccca 720
tgagcaagct cactgttctc aacagcatgc attcccactt cattctggct gacaacggga 780
ccactggaaa atatggagca gaggtgaaac ttcgaagaca actggaaaag catatttcac 840
tccagaagat aaacacaaga tgccctgccg ttttctctct tgaactccgc ttgttttatt 900
cattttgggg tagttgccag ttagactcag ttggaatcgg tcaagggtgtt cctgtggtgg 960
cactcatagt ggaaggagga cccaatgtga tctcgattgt tttggagtac cttcgagaca 1020
cccctcccgt gccagtgggt gtctgtgatg ggagtggacg ggcacggac atcctggcct 1080
ttgggcataa atactcagaa gaaggcgggt aggttaacttt ccaggcccca tggagaacc 1140
ctaaagcctg tttggaaacg agggatagag tggattatgt tttcagtagc tcaaccaaga 1200
cctcaaatac aaacaagcta tgaacaaatt gtctaaaaaa tgtctgtcat gggagggctg 1260
tggtgaagaa cagagaaaca tattctaat gtccctgtgaa gtgggaaatt ctatgaaagc 1320
tacacggata ataaaaaggg tgaggaaaaag agagga 1356

<210> 102
<211> 580
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 4764233CB1

<400> 102
cacaacgcag gcaccgactt cagtgtgcat gttccttgga cacctgcctc agtgtgcatg 60
ttcactgggc atcttccctt cgaccccttt gccacgtgg tgaccgctgg ggagctgtga 120
gagtgtgagg ggcacgttcc agcgtcttgg actctttctc tcctactgag acgcagccta 180
taggtccgca ggccagtcct cccaggaact gaaatagtga aatatgagtt ggcgaggaag 240
atcaacatat aggcctaggc caagaagaag tttacagcct cctgagctga ttggggctat 300
gcttgaaccc actgatgaag agcctaaaga agagaaaacca cccactaaaa gtcggaatcc 360
tacacctgat cagaagagag aagatgatca ggggtgcagct gagattcaag tgcctgacct 420
ggaagccgat ctccaggagc tatgtcagac aaagactggg gatggatgtg aaggtggtac 480
tgatgtcaag gggaagattc taccaaaagc agagcacttt aaaatgccag aagcaggtga 540
agggaaatca caggttttaa ggaagataag ctgaaacaac 580

<210> 103
<211> 1487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 4817352CB1

WO 01/07471

PCT/US00/19948

<400> 103

```

ccgggagggc ggggtctcgg gtggccgcgc gccagggcgc tggacggcag caggatgggg 60
aaggcgaagg tccccgcctc caagcgcgcc ccgagcagcc ccgtggctaa gccgggtcct 120
gtcaagacgc tcactcggaa gaaaaacaag aagaaaaaaa ggttttggaa aagcaaggcg 180
cggaagtaa gcaagaagcc agcaagcggc cccggtgctg tggcgacc tccaaaggca 240
ccagaagact tttctcaaaa ctggaaggcg ctgcaagagt ggctgctgaa aaaaaaatct 300
caggccccag aaaagcctct tgatcatctc cagatgggtt caaaaagaa gcccaaaatt 360
atccagcaaa acaaaaaaga gacctgcct caagtgaagg gagaggagat gccggcagga 420
aaagaccagg aggcagcag gggctctgtt ccttcagggt ccaagatgga caggaggcg 480
ccagtacctc gcaccaaggc cagtgaaca gagcacaata agaaaggaac caaggaaagg 540
acaaatggtg atattgttcc agaacgaggg gacatcgagc ataagaagcg gaaagctaag 600
gaggcagccc cagccccacc caccgaggaa gacatctggt ttgacgacgt ggaccagcg 660
gatatcgaag ctgccatagg tccagaggcg gccaatagat cgaggaaaca gttgggtcag 720
agcgagggca gcgtcagcct cagcctcgtg aaagagcagg ccttcggcgg cctgacaaga 780
gccttagcct tggactgtga gatggtgggc gtgggcccta agggggagga gacatggcc 840
gccgtgtgt ccactgtgaa ccagtatggg aagtgcgttt atgacaagta cgtcaaacca 900
accgagcccc tgacggacta taggacagcg gtcagtggga ttcggcctga gaacctcaag 960
cagggagaag agcttgaagt tgttcagaag gaagtggcag agatgctgaa gggcagaatt 1020
ctagtggggc acgctctgca taatgacctt aaggtactat ttcttgatca tccaaaaaag 1080
aagattcggg acacacagaa atataaacct ttcaagagtc aagtaaagag tggaggcccg 1140
tctctgagac tactttcaga gaagatcctt gggctccagg tccagcaggc ggagcactgt 1200
tcaattcagg atgccaggc agcaatgagg ctgtacgtca tggatgaaga ggagtgggag 1260
agcatggccc gagacaggcg cccctgctg actgctccag accactgcag tgacgacgcc 1320
tagcagtcct gccctgctgc tgcctgcgcc ccgtacaga ggcaatgtga ccagtcacag 1380
ggacagatca catctcccca gattggcaac tctggtgaaa ctttttcaga atcatggcag 1440
aggggcgtgg cgtggtgcta ctgagaagac ctcttcctg ttgacga 1487

```

<210> 104

<211> 2257

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5040573CB1

<400> 104

```

gcgccggctc cggctgcagt tcccgggtcc ctccggccacc gaagccaccc tgccctggtg 60
aaagggtccc cgcaccgccc ggtgctcccc atctgcctgg cgttgtgcgc agagctggaa 120
agcatggctg ttataaatga attctgattt tggggagcag atgccaactt agagcctcgt 180
accaatctct ctgtctttaa aagatgaggt gacttgggtga ttttcttggaa aaattatagg 240
tgcccagcta agacctgaat gccatcacc tcccaggggc tctgcagttt tctcgtggtg 300
aacccttgat ggatttgttg ttgcttgaga aatggcgatg atcgaattgg ggtttggaag 360
acagaatttt catccattaa agagggaagag ttcatgtctg ttgaaactca tagctgttgt 420
ctttgctgtg cttctatttt gtgaattttt aatctattac ttagcgatct ttcagtgtaa 480
ttggcctgaa gtgaaaacca cagcctctga tgggtgaacag accacacgtg agcctgtgct 540
caaagccatg tttttggctg acaccattt gcttggggaa ttcctaggcc actggctgga 600
caaattacga agggaatggc agatggagag agcgttccag acagctctgt ggttctgca 660
gccggaagtc gtcttcatcc tgggggatat ctttgatgaa ggggaagtga gcaccctga 720
ggcctggggc gatgatgtgg agcgttttca gaaaatgttc agacacccaa gtcattgata 780
gctgaaggta gttgctggaa accatgacat tggcttccat tatgagatga acacatacaa 840
agtagaacgc tttgagaaaag tgttcagctc tgaagactg ttttcttggaa aaggcattaa 900
ctttgtgatg gtcaacagcg tggcgctgaa cggggatggc tgtggcatct gctctgaaac 960
agaagcagag ctcatgaaag tttctcacag actgaactgc tcccagagc aggcacgtgg 1020
ctccagccgg tgtggacctg ggcctctgct gccacgtct gcccctgtcc tctcgagca 1080
ttatcctctg tatccgagaa gtgatgctaa ctgttctggg gaagacgtg ctctccaga 1140
ggaaagggag atcccattta aggagaacta tgacgtgctt tcacgggagg catcacaaaa 1200
gctgctgtgg tggctccagc cgcgcctggt tctcagtggc cacacgcaca gcgcctgcga 1260
ggtgcaccac gggggccgag tccccgagct cagcgtccca tctttcagtt ggaggaaacag 1320
aaacaacccc agtttcatca tgggtagcat cagcccaca gactacaccc tctccaagt 1380
ctacctccca cgtgaggatg tggttttgat catctactgt ggagtgggtg gcttccttgt 1440
gttctccaca ctcactcact ttggccttct agcctcact tttcttctg gtttgaactt 1500
gctcggaaaag cgtaagacaa gatgaagagc aggcgccatt ataaatatca aagcccaaga 1560

```


WO 01/07471

PCT/US00/19948

aatggaactt	tgggcagaga	tcatgttaga	atcaagtgga	tgatgagacc	aattacaggc	1620
cgtctctctg	cacagcacag	aaattctcaa	tcaactgaaat	gagtaactgc	aaaataaata	1680
gttgattgtg	ctgttctcat	gctataaaag	tggacaggta	ctctacaaca	aatctgtttt	1740
ctcattttta	tcaaatatat	gtatcatcaa	aggttgcata	tgtacagtat	gtaaatgcta	1800
ttaatgtcgt	cactcacatg	cacgacagtc	cttgttcccc	caggaagggc	ctggtggccc	1860
cagcacacac	ttgggattat	gtgtatacat	aaataaatat	tgggctgttt	ccctcttcc	1920
gtgaagtggg	tctcaaattc	ctatgtactg	taaagctgta	cccttaaaag	tacagatgtg	1980
gccgggcaca	gtggctcaca	cctgtaatcc	cagcactttg	ggaggctgag	gcggtgggat	2040
cacttgagg	caggagttca	agaccagcct	ggccaacatg	gtgaaacctc	gtctccgcta	2100
gaaatacaaa	aattagccaa	gcatggtagc	aagtgcctat	aataccagct	gaggctgagg	2160
caggagaatc	ccttgagccc	gggaggcgga	ggttgcatg	agccaagatc	atgccactgc	2220
actctagcct	gggcaacaga	gtgagtcctg	ctcaaac			2257

<210> 105

<211> 2550

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5627029CB1

<400> 105

cggaagtatt	cccattttgc	gttgtctggg	ctcggcgcca	gccgggctcg	gagtggacgt	60
gccactatgg	ggtcgtccaa	gaagcatcgc	ggagagaagg	aggcgcccg	gacgacggcg	120
gcggccggca	ccgggggtgc	caccgagcag	ccgcccgcc	accgggaaca	caaaaaacac	180
aagcaccgga	gtggcggcag	tggcggtagc	ggtggcgaa	gacggaagcg	gagccgggaa	240
cgtggggg	agcgcgggag	cggcgggcgc	ggggccgaag	ctgaggcccc	gagcagcacg	300
cacgggcggg	agcgcagcca	ggcagagccc	tccgagcgcc	gcgtgaagcg	ggagaagcgc	360
gatgacggct	acgaggccgc	tgccagctcc	aaaactagct	caggcgatgc	ctcctcactc	420
agcatcgagg	agactaacia	actccgggca	aagttggggc	tgaaaccctt	ggaggttaat	480
gccatcaaga	aggaggcggg	caccaaggag	gagcccgtag	cagctgatgt	catcaaccct	540
atggccttgc	gacagcgaga	ggagctgcgg	gagaagctgg	cggctgccaa	ggagaagcgc	600
ctgctgaacc	aaaagctggg	gaagataaag	accctaggag	aggatgaccc	ctggctggac	660
gacactgcag	cctggatcga	gaggagccgg	cagctgcaga	aggagaagga	cctggcagag	720
aagagggcca	agttactgga	ggagatggac	caagagtttg	gtgtcagcac	tctggtggag	780
gaggagttcg	ggcagaggcg	gcaggacctg	tacagtgcgc	gggacctgca	gggcctcact	840
gtggagcatg	ccattgatcc	cttccgagaa	ggggagacaa	tgattcttac	cctcaaggac	900
aaaggcgtgc	tgcaggagga	ggaggacgtg	ctggtgaacg	tgaacctggt	ggataaggag	960
cgggcagaga	aaaatgtgga	gctgcggaag	aagaagcctg	actacctgcc	ctatgccgag	1020
gacgagagcg	tggacgacct	ggcgacgcaa	aaacctcgct	ctatcctgtc	caagtctgac	1080
gaagagcttg	aaggggagcg	gccacattcc	ttccgcttgg	agcaggggcg	cacggctgat	1140
ggcctgcggg	agcgggagct	ggaggagatc	cgggccaagc	tgcggctgca	ggctcagtc	1200
ctgagcacag	tggggccccc	gctggcctcc	gaataacctca	cgcctgagga	gatggtgacc	1260
tttaaaaaga	ccaagcgag	ggtgaagaaa	atccgcaaga	aggagaagga	ggtagtagtg	1320
cgggcagatg	acttgctgcc	tctcggggac	cagactcagg	atggggactt	tgggtccaga	1380
ctgcggggac	ggggtcgccc	ccgagtgtcc	gaagtggagg	aggagaagga	gcctgtgcct	1440
cagccctgc	cgtcggacga	cacccgagtg	gagaacatgg	acatcagtga	tgaggaggaa	1500
ggtggagctc	caccgccggc	gtccccgcag	gtgctggagg	aggacgaggc	ggagctggag	1560
ctgcagaagc	agctggagaa	gggacgccgg	ctgcgacagt	tacagcagct	acagcagctg	1620
cgagacagtg	acgagaaggt	ggtggagatt	gtgaagaagc	tggagtctcg	ccagcggggc	1680
tgggaggagg	atgaggatcc	cgagcggaa	ggggccatcg	tggtcaacgc	cacgtccgag	1740
ttctgccgca	ccttggggga	gatccccacc	tacgggctgg	ctggcaatcg	cgaggagcag	1800
gaggagctca	tggactttga	acgggatgag	gagcgctcag	ccaacgggtg	ctccgaatct	1860
gacggggagg	agaacatcgg	ctggagcacg	gtgaacctgg	acgaggagaa	gcagcagcag	1920
gatttctctg	cttctccac	caccatcctg	gacgaggaac	cgatcgtgaa	tagggggctg	1980
gcagctgccc	tgctcctgtg	tcagaacaaa	gggtgctgtg	agaccacagt	gcagaagggtg	2040
gcccgggtga	aggcccccaa	caagtcgctg	ccctcagccg	tgtactgcat	cgaggataag	2100
atggccatcg	atgacaagta	cagccggagg	gaggaatacc	gaggcttcac	acaggacttc	2160
aaggagaagg	acggctacaa	acccgacgtt	aagatcgaat	acgtggatga	gacggggccg	2220
aaactcacac	ccaaggaggc	tttccggcag	ctgtcgcacc	gcttccatgg	caaggggtca	2280
ggcaagatga	agacagagcg	gcgcatgaag	aggtggagcg	aggaggcgct	cctgaagaag	2340
atgagctcca	gcgacacgcc	cctgggcacc	gtggccctgc	tccaggagaa	gcagaaggct	2400

WO 01/07471

PCT/US00/19948

```

cagaagaccc cctacatcgt gctcagcggc agcggcaaga gcatgaacgc gaacaccatc 2460
accaagtgc agcgcctcc cgccccggcc ctgcctcaac cttcatatta aataaagctc 2520
ctccttatt ttttcaaaaa aaaaaaaaaa 2550

```

```

<210> 106
<211> 2566
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Incyte ID No: 5678487CB1

```

```

<400> 106
cggctcgagg tgaggactac aactcccgac gtgcaaagcg agggccagtg ggtgggaaga 60
gcccccaaga gctctgtgcg ggattctagg ctccccctgtg acagccgcgg caggaagcag 120
gcgggcgctc cccggccaca ggctgttgt tctcggaagg gagaaagctg gacatttccc 180
cacgtaactc ccagctctgg gcctagagtg cgtgcatggc gaagtccccg gagaactcta 240
ccctggagga gattctgggg cagtatcaac ggagtcctcc ggaacatgcc agcagaagca 300
ttcaccaact gacatgtgcc ctgaaagaag gcgatgtcac tattggagaa gatgcacca 360
atctttcttt tagcaccagt gtgggaaatg aggacgccag gacagcctgg cccgaattac 420
aacagagcca tgctgttaat cagctcaaag atttggtgcg ccaacaagca gataaggaaa 480
gtgaagtatc tccgtcaaga agaagaaaaa tgtccccctt gaggtcatta gaacatgagg 540
aaaccaatat gcctactatg cagcaccttg ttcatactat taatgaccag tctcaatata 600
ttcatcattt agaggcagaa gttaagttct gcaaggagga actctctgga atgaaaaata 660
aaatacaagt agttgtgctt gaaaacgaag ggctccagca acagctaaaa tctcaaagac 720
aagaggagac actgagggaa caaacacttc tggatgcac cggaacatg cacaattctt 780
ggattacaac aggtgaagat tctgggggtg gcgaaacctc caaaagacca ttttcccatg 840
acaatgcaga ttttggcaaa gctgcatctg ctggtgagca gctagaactg gagaagctaa 900
aacttactta tgaggaaaag tgtgaaattg aggaatccca attgaagttt ttgaggaacg 960
acttagctga atatcagaga acttggtgaag atcttaaaga gcaactaaag cataaagaat 1020
ttcttctggc tgctaatact tgtaaccgtg ttggtggtct ttgtttgaaa tgtgctcagc 1080
atgaagctgt tctttcccaa acccatacta atgttcatat gcagaccatc gaaagactgg 1140
ttaaagaaag agatgacttg atgtctgcac tagtttccgt aaggagcagc ttggcagata 1200
cgcagcaaag agaagcaagt gcttatgaac aggtgaaaca agttttgcaa atatctgagg 1260
aagccaattt tgaaaaaacc aaggctttaa tccagtgtga ccagttgagg aaggagctgg 1320
agaggcaggc ggagcgactt gaaaaagatc ttgcatctca gcaagagaaa agggccattg 1380
agaaagacat gatgaaaaag gaaataacaa aagaaaggga gtacatggga tcaaagatgt 1440
tgatcttgtc tcagaatatt gcccactgg agggccaggt ggaaaaggtt acaaaggaaa 1500
agatttcagc tattaatcaa ctggaggaaa ttcaaagcca gctggcttct cgggaaatgg 1560
atgtcacaaa ggtgtgtgga gaaatgcgt atcagctgaa taaaaccaac atggagaagg 1620
atgaggcaga aaaggagcac agagagttca gagcaaaaac taacagggat cttgaaatta 1680
aagatcagga aatagagaaa ttgagaatag aactggatga aagcaaaca cacttggaac 1740
aggagcagca gaaggcagcc ctggccagag agggatgcct gagactaaca gaactgctgg 1800
gcgaatctga gcaccaactg cacctcacca gacaggaaaa agatagcatt cagcagagct 1860
ttagcaagga agcaaaggcc caagcccttc agggccagca aagagagcag gagctgacac 1920
agaagataca gcaaattgga gccagcatg acaaaaactga aaatgaacag tatttgttgc 1980
tgacctccca gaatacattt ttgacaaagt taaaggaaga atgctgtaca ttagccaaga 2040
aactggaaca aatctctcaa aaaaccagat ctgaaatagc tcaactcagt caagaaaaaa 2100
ggtatacata tgataaattg ggaaagttac agagaagaaa tgaagaattg gaggaacagt 2160
gtgtccagca tgggagagta catgagacga tgaagcaaag gctaaggcag ctggataagc 2220
acagccaggc cacagcccag cagctggtgc agctcctcag caagcagaac cagcttctcc 2280
tggagaggca gagcctgtcg gaagaggtgg accggctgcg gacccagtta cccagcatgc 2340
cacaatctga ttgctgacct ggatggaaca gagtgaata aatgatttac aaagagatat 2400
ttacattcat ctggtttaga cttaatatgc cacaacgcac cacgacctc ccagggtgac 2460
accgcctcag cctgcagtgg ggctggtcct catcaacgcg ggcgctgtcc ccgcacgcag 2520
tcgggctgga gctggagct gactctagct gagcagagct cctggt 2566

```

```

<210> 107
<211> 3022
<212> DNA
<213> Homo sapiens

```


WO 01/07471

PCT/US00/19948

<221> misc_feature

<223> Incyte ID No: 5992432CB1

<400> 108

gtcgtcgaaa	agaagtcaat	aacgtgggcc	tgctcgtcaa	aaatgattta	accaatagaa	60
aacgggtctg	gctcggaggg	gcggggccgtc	agtggtagac	gtcataagcg	cgcgactctc	120
tcctgtacct	gggcatccag	aaaaatggtg	gtgatggcgc	gactttcgcg	gccccgagcgg	180
ccggaccttg	tcttcgagga	agaggacctc	ccctatgagg	aggaaatcat	gcggaaccaa	240
ttctctgtca	aatgctggct	tcgctacatc	gagttcaaac	agggcgcccc	gaagcccagg	300
ctcaatcagc	tatacgagcg	ggcactcaag	ctgctgccct	gcagctacaa	actctggtac	360
cgatacctga	aggcgcgctcg	ggcacagggtg	aagcatcgct	gtgtgaccga	ccctgcctat	420
gaagatgtca	acaactgtca	tgagagggcc	tttgtgttca	tgcacaagat	gcctcgtctg	480
tggctagatt	actgccagtt	cctcatggac	caggggcgcg	tcacacacac	ccgccgcacc	540
ttcgaccgtg	ccctccgggc	actgcccact	acgcagcact	ctcgaatttg	gccccctgtat	600
ctgcgcttcc	tgcgctcaca	cccactgcct	gagacagctg	tgcgaggcta	tcggcgcttc	660
ctcaagctga	gtcctgagag	tgcagaggag	tacattgagt	acctcaagtc	aagtgaccgg	720
ctggatgagg	ccgcccagcg	cctggccacc	gtggtgaacg	acgagcgttt	cgtgtctaa	780
gccggcaagt	ccaactacca	gctgtggcac	gagctgtgcg	acctcatctc	ccagaatccg	840
gacaaggtag	agtccttcaa	tgtggacgcc	atcatccgcg	ggggcctcac	ccgcttcacc	900
gaccagctgg	gcaagctctg	gtgttctctc	gccgactact	acatccgcag	cggccatttc	960
gagaaggctc	gggacgtgta	cgaggaggcc	atccggacag	tgatgaccgt	gcgggacttc	1020
acacaggtgt	ttgacagcta	cgcccagttc	gaggagagca	tgatcgctgc	aaagatggag	1080
accgcctcgg	agctggggcg	cgaggaggag	gatgatgtgg	acctggagct	gcgcctggcc	1140
cgcttcgagc	agctcatcag	ccggcgcccc	ctgctcctca	acagcgtctt	gctgcgccaa	1200
aaccacacc	acgtgcacga	gtggcacaag	cgtgtcgcgc	tgcaccaggg	ccgcccccg	1260
gagatcatca	acacctacac	agaggctgtg	cagacggtgg	accccttcaa	ggccacaggc	1320
aagccccaca	ctctgtgggt	ggcgtttgcc	aagttttatg	aggacaacgg	acagctggac	1380
gatgcccgtg	tcctcctgga	gaaggccacc	aaggtgaact	tcaagcaggt	ggatgacctg	1440
gcaagcgtgt	ggtgtcagtg	cggagagctg	gagctccgac	acgagaacta	cgatgaggcc	1500
ttgcggctgc	tgcgaaaggc	cacggcgctg	cctgccccgc	gggcccagta	ctttgatggg	1560
tcagagcccc	tgcagaaccg	cgtgtacaag	tcactgaagg	tctggtccat	gctgcgcgac	1620
ctggaggaga	gcctcggcac	cttccagtc	accaaggccg	tgtacgaccg	catcctggac	1680
ctgcgtatcg	caacacccca	gatcgtcatc	aactatgcca	tgttcctgga	ggagcacaag	1740
tacttcgagg	agagcttcaa	ggcgtagcag	cgcggcacat	cgctgttcaa	gtggcccaac	1800
gtgtccgaca	tctggagcac	ctacctgacc	aaattcattg	cccgcctatg	gggcccgaag	1860
ctggagcggg	cacgggacct	gtttgaacag	gctctggacg	gctgcccccc	aaaatatgcc	1920
aagaccttgt	acctgctgta	cgcacagctg	gaggaggagt	ggggcctggc	ccggcatgcc	1980
atggccgtgt	acgagcgtgc	caccagggcc	gtggagcccc	cccagcagta	tgacatgttc	2040
aacatctaca	tcaagcgggc	ggccgagatc	tatgggggtca	cccacaccgc	cgcatctac	2100
cagaaggcca	ttgaggtgct	gtcggacgag	cacgcgcgtg	agatgtgcct	gcggtttgca	2160
gacatggagt	gcaagctcgg	ggagattgac	cgcgccccgg	ccatctacag	cttctgctcc	2220
cagatctgtg	acccccggac	gaccggcgcg	ttctggcaga	cgtggaagga	ctttgaggtc	2280
cggcattggca	atgaggacac	catcaaggaa	atgctgcgta	tccggcgagc	cgtgcaggcc	2340
acgtacaaca	cgcaggtcaa	cttcatggcc	tcgcagatgc	tcaaggctctc	gggcagtgcc	2400
acgggcaccg	tgtctgacct	ggccccctgg	cagagtggca	tggacgacat	gaagctgctg	2460
gaacagcggg	cagagcagct	ggcggttgag	gcggagcgtg	accagccctt	gcgcgcccag	2520
agcaagatcc	tgttcgtgag	gagtgacgcc	tcccgggagg	agctggcaga	gctggcacag	2580
caggtcaacc	ccgaggagat	ccagctgggc	gaggacgagg	acgaggacga	gatggacctg	2640
gagcccaacg	aggttcggct	ggagcagcag	agcgtgccag	ccgcagtgtt	tgggagcctg	2700
aaggaagact	gacccgtccc	tccccctccc	ccccctccca	ccccctcccc	aatacagcta	2760
cgtttgtaca	tcaaaaaaaaa	aaaaaaaa				2787

Docket No.: PF-0722 USN

**DECLARATION AND POWER OF ATTORNEY FOR
UNITED STATES PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if more than one name is listed below) of the subject matter which is claimed and for which a United States patent is sought on the invention entitled

CELL CYCLE AND CELL PROLIFERATION PROTEINS

the specification of which:

 / / is attached hereto.

 / / was filed on _____ as application Serial No. _____ and if this box contains an X / /, was amended on _____.

 /X / was filed as Patent Cooperation Treaty international application No. PCT/US00/19948 on July 21, 2000, if this box contains an X / /, was amended on under Patent Cooperation Treaty Article 19 on _____ 2001, and if this box contains an X / /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge my duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any foreign application(s) for patent or inventor's certificate indicated below and of any Patent Cooperation Treaty international applications(s) designating at least one country other than the United States indicated below and have also identified below any foreign application(s) for patent or inventor's certificate and Patent Cooperation Treaty international application(s) designating at least one country other than the United States for the same subject matter and having a filing date before that of the application for said subject matter the priority of which is claimed:

20010915 09:44:30

Docket No.: PF-0722 USN

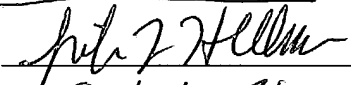
LEGAL DEPARTMENT
INCYTE GENOMICS, INC.
3160 PORTER DRIVE, PALO ALTO, CA 94304

TEL: 650-855-0555 FAX: 650-849-8886 or 650-845-4166

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.


First Joint Inventor:

100

Full name: Jennifer L. Hillman
Signature: 
Date: September 21, 2001
Citizenship: United States
Residence: Mountain View, California ^{CA}
P.O. Address: 230 Monroe Drive, #17
Mountain View, California 94040

Second Joint Inventor:

200

Full name: Preeti Lal
Signature: 
Date: September 10, 2001
Citizenship: India
Residence: Santa Clara, California ^{CA}
P.O. Address: P.O. Box 5142
Santa Clara, California 95056

Docket No.: PF-0722 USN

**LEGAL DEPARTMENT
 INCYTE GENOMICS, INC.
 3160 PORTER DRIVE, PALO ALTO, CA 94304**

TEL: 650-855-0555 FAX: 650-849-8886 or 650-845-4166

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

First Joint Inventor: Full name: Jennifer L. Hillman
 Signature: _____
 Date: _____, 2001
 Citizenship: United States
 Residence: Mountain View, California
 P.O. Address: 230 Monroe Drive, #17
Mountain View, California 94040

Second Joint Inventor: Full name: Preeti Lal
 Signature: _____
 Date: _____, 2001
 Citizenship: India
 Residence: Santa Clara, California
 P.O. Address: P.O. Box 5142
Santa Clara, California 95056

Docket No.: PF-0722 USN

Third Joint Inventor:

Full name: Y. Tom Tang

Signature: _____

Date: _____, 2001

Citizenship: United States

Residence: San Jose, California

P.O. Address: 4230 Ranwick Court
San Jose, California 95118

Fourth Joint Inventor:

Full name: Henry Yue

Signature: _____

Date: _____, 2001

Citizenship: United States

Residence: Sunnyvale, California

P.O. Address: 826 Lois Avenue
Sunnyvale, California 94087

Fifth Joint Inventor:

Full name: Janice Au-Young

Signature: _____

Date: _____, 2001

Citizenship: United States

Residence: Brisbane, California

P.O. Address: 233 Golden Eagle Lane
Brisbane, California 94005

Docket No.: PF-0722 USN

Sixth Joint Inventor:

Full name: Olga Bandman
Signature: _____
Date: _____, 2001
Citizenship: United States
Residence: Mountain View, California
P.O. Address: 366 Anna Avenue
Mountain View, California 94043

Seventh Joint Inventor:

Full name: Yalda Azimzai
Signature: _____
Date: _____, 2001
Citizenship: United States
Residence: Castro Valley, California
P.O. Address: 5518 Boulder Canyon Drive
Castro Valley, California 94552

Eighth Joint Inventor:

Full name: Junming Yang
Signature: _____
Date: _____, 2001
Citizenship: China
Residence: San Jose, California
P.O. Address: 7125 Bark Lane
San Jose, California 95129

Docket No.: PF-0722 USN

Ninth Joint Inventor:

Full name: Dyung Aina M. Lu

Signature: _____

Date: _____, 2001

Citizenship: United States

Residence: San Jose, California

P.O. Address: 233 Coy Drive
San Jose, California 95123

Tenth Joint Inventor:

Full name: Mariah R. Baughn

Signature: _____

Date: _____, 2001

Citizenship: United States

Residence: San Leandro, California

P.O. Address: 14244 Santiago Road
San Leandro, California 94577

Eleventh Joint Inventor:

Full name: Chandra Patterson

Signature: _____

Date: _____, 2001

Citizenship: United States

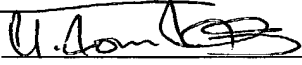
Residence: Menlo Park, California

P.O. Address: 490 Sherwood Way, #1
Menlo Park, California 94025

Docket No.: PF-0722 USN

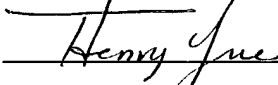
Third Joint Inventor:

300

Full name: Y. Tom Tang
Signature: 
Date: September 10, 2001
Citizenship: United States
Residence: San Jose, California ^{CA}
P.O. Address: 4230 Ranwick Court
San Jose, California 95118

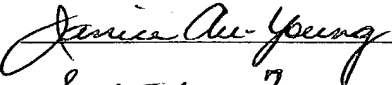
Fourth Joint Inventor:

400

Full name: Henry Yue
Signature: 
Date: September 24, 2001
Citizenship: United States
Residence: Sunnyvale, California ^{CA}
P.O. Address: 826 Lois Avenue
Sunnyvale, California 94087

Fifth Joint Inventor:

500

Full name: Janice Au-Young
Signature: 
Date: September 7, 2001
Citizenship: United States
Residence: Brisbane, California ^{CA}
P.O. Address: 233 Golden Eagle Lane
Brisbane, California 94005

Docket No.: PF-0722 USN

600

Olga Bandman

Oleg Boedunov

12 September, 2001

United States

Mountain View, California

366 Anna Avenue
Mountain View, California 94043

200

Yalda Azimzaj

Yaldır Özgenç

September 13, 2001

United States

Castro Valley, California

5518 Boulder Canyon Drive
Castro Valley, California 94552

800

Junming Yang

23

September 17, 2001

China

San Jose, California

7125 Bark Lane
San Jose, California 95129

Docket No.: PF-0722 USN

Ninth Joint Inventor:

900

Full name: Dyung Aina M. Lu
Signature: [Signature]
Date: Sept 7, 2001
Citizenship: United States
Residence: San Jose, California
P.O. Address: 233 Coy Drive
San Jose, California 95123

Tenth Joint Inventor:

1000

Full name: Mariah R. Baughn
Signature: [Signature]
Date: September 5, 2001
Citizenship: United States
Residence: San Leandro, California
P.O. Address: 14244 Santiago Road
San Leandro, California 94577

RECEIVED
10 JUL 2002
Legal Staff
International Division

Eleventh Joint Inventor:

1100

Full name: Chandra Patterson Arvizu CA 9/10/01
Signature: [Signature]
Date: September 10, 2001
Citizenship: United States
Residence: Menlo Park, California
P.O. Address: 490 Sherwood Way, #1
Menlo Park, California 94025

Docket No.: PF-0722 USN

Twelfth Joint Inventor:

1200

Full name:

Purvi Shah

Signature:

Purvi Shah

Date:

Sept. 20, 2001

Citizenship:

India

Residence:

CA
San Jose, California

P.O. Address:

859 Salt Lake Drive
San Jose, California 95133

Docket No.: PF-0722 USN

Twelfth Joint Inventor:

Full name: Purvi Shah

Signature: _____

Date: _____, 2001

Citizenship: India

Residence: San Jose, California

P.O. Address: 859 Salt Lake Drive
San Jose, California 95133

Docket No.: PF-0722 USN

Country	Number	Filing Date	Priority Claimed
_____	_____	_____	// Yes // No
_____	_____	_____	// Yes // No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
60/145,075	July 21, 1999	Expired
60/153,129	September 8, 1999	Expired
60/164,647	November 10, 1999	Expired

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of Title 35, United States Code §112, I acknowledge my duty to disclose material information as defined in Title 37 Code of Federal Regulations, §1.56(a) which occurred between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
_____	_____	_____

I hereby appoint the following:

Lucy J. Billings	Reg. No. 36,749
Michael C. Cerrone	Reg. No. 39,132
Diana Hamlet-Cox	Reg. No. 33,302
Richard C. Ekstrom	Reg. No. 37,027
Barrie D. Greene	Reg. No. 46,740
Lynn E. Murry	Reg. No. 42,918
Shirley A. Recipon	Reg. No. 47,016
Susan K. Sather	Reg. No. 44,316
Michelle M. Stempfen	Reg. No. 41,327
David G. Streeter	Reg. No. 43,168
Stephen Todd	Reg. No. 47,139
P. Ben Wang	Reg. No. 41,420

respectively and individually, as my patent attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Please address all communications to:

Docket No.: PF-0722 USN

**DECLARATION AND POWER OF ATTORNEY FOR
UNITED STATES PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if more than one name is listed below) of the subject matter which is claimed and for which a United States patent is sought on the invention entitled

CELL CYCLE AND CELL PROLIFERATION PROTEINS

the specification of which:

 / is attached hereto.

 / was filed on _____ as application Serial No. _____ and if this box contains an X /, was amended on _____.

 X / was filed as Patent Cooperation Treaty international application No. PCT/US00/19948 on July 21, 2000, if this box contains an X /, was amended on under Patent Cooperation Treaty Article 19 on _____ 2001, and if this box contains an X /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge my duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any foreign application(s) for patent or inventor's certificate indicated below and of any Patent Cooperation Treaty international applications(s) designating at least one country other than the United States indicated below and have also identified below any foreign application(s) for patent or inventor's certificate and Patent Cooperation Treaty international application(s) designating at least one country other than the United States for the same subject matter and having a filing date before that of the application for said subject matter the priority of which is claimed:

PCT/US00/19948

1/93

WO 01/07471

PCT/US00/19948

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1210462CD1

<400> 2

Met	Leu	Thr	Gln	Leu	Lys	Ala	Lys	Ser	Glu	Gly	Lys	Leu	Ala	Lys	
1				5					10					15	
Gln	Ile	Cys	Lys	Val	Val	Leu	Asp	His	Phe	Glu	Lys	Gln	Tyr	Ser	
				20					25					30	
Lys	Glu	Leu	Gly	Asp	Ala	Trp	Asn	Thr	Val	Arg	Glu	Ile	Leu	Thr	
				35					40					45	
Ser	Pro	Ser	Cys	Trp	Gln	Tyr	Ala	Val	Leu	Leu	Asn	Arg	Phe	Asn	
				50					55					60	
Tyr	Pro	Phe	Glu	Leu	Glu	Lys	Asp	Leu	His	Leu	Lys	Gly	Tyr	His	
				65					70					75	
Thr	Leu	Ser	Gln	Gly	Ser	Leu	Pro	Asn	Tyr	Pro	Lys	Ser	Val	Lys	
				80					85					90	
Cys	Tyr	Leu	Ser	Arg	Thr	Pro	Gly	Arg	Ile	Pro	Ser	Glu	Arg	His	
				95					100					105	
Gln	Ile	Gly	Asn	Leu	Lys	Lys	Tyr	Tyr	Leu	Leu	Asn	Ala	Ala	Ser	
				110					115					120	
Leu	Leu	Pro	Val	Leu	Ala	Leu	Glu	Leu	Arg	Asp	Gly	Glu	Lys	Val	
				125					130					135	
Leu	Asp	Leu	Cys	Ala	Ala	Pro	Gly	Gly	Lys	Ser	Ile	Ala	Leu	Leu	
				140					145					150	
Gln	Cys	Ala	Cys	Pro	Gly	Tyr	Leu	His	Cys	Asn	Glu	Tyr	Asp	Ser	
				155					160					165	
Leu	Arg	Leu	Arg	Trp	Leu	Arg	Gln	Thr	Leu	Glu	Ser	Phe	Ile	Pro	
				170					175					180	
Gln	Pro	Leu	Ile	Asn	Val	Ile	Lys	Val	Ser	Glu	Leu	Asp	Gly	Arg	
				185					190					195	
Lys	Met	Gly	Asp	Ala	Gln	Pro	Glu	Met	Phe	Asp	Lys	Val	Leu	Val	
				200					205					210	
Asp	Ala	Pro	Cys	Ser	Asn	Asp	Arg	Ser	Trp	Leu	Phe	Ser	Ser	Asp	
				215					220					225	
Ser	Gln	Lys	Ala	Ser	Cys	Arg	Ile	Ser	Gln	Arg	Arg	Asn	Leu	Pro	
				230					235					240	
Leu	Leu	Gln	Ile	Glu	Leu	Leu	Arg	Ser	Ala	Ile	Lys	Ala	Leu	Arg	
				245					250					255	
Pro	Gly	Gly	Ile	Leu	Val	Tyr	Ser	Thr	Cys	Thr	Leu	Ser	Lys	Ala	
				260					265					270	
Glu	Asn	Gln	Asp	Val	Ile	Ser	Glu	Ile	Leu	Asn	Ser	His	Gly	Asn	
				275					280					285	
Ile	Met	Pro	Met	Asp	Ile	Lys	Gly	Ile	Ala	Arg	Thr	Cys	Ser	His	
				290					295					300	
Asp	Phe	Thr	Phe	Ala	Pro	Thr	Gly	Gln	Glu	Cys	Gly	Leu	Leu	Val	
				305					310					315	
Ile	Pro	Asp	Lys	Gly	Lys	Ala	Trp	Gly	Pro	Met	Tyr	Val	Ala	Lys	
				320					325					330	
Leu	Lys	Lys	Ser	Trp	Ser	Thr	Gly	Lys	Trp						
				335					340						

<210> 3

<211> 418

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1305252CD1

<400> 3

WO 01/07471

PCT/US00/19948

```

Met Leu Tyr Leu Glu Asp Tyr Leu Glu Met Ile Glu Gln Leu Pro
1      5      10      15
Met Asp Leu Arg Asp Arg Phe Thr Glu Met Arg Glu Met Asp Leu
20     25     30
Gln Val Gln Asn Ala Met Asp Gln Leu Glu Gln Arg Val Ser Glu
35     40     45
Phe Phe Met Asn Ala Lys Lys Asn Lys Pro Glu Trp Arg Glu Glu
50     55     60
Gln Met Ala Ser Ile Lys Lys Asp Tyr Tyr Lys Ala Leu Glu Asp
65     70     75
Ala Asp Glu Lys Val Gln Leu Ala Asn Gln Ile Tyr Asp Leu Val
80     85     90
Asp Arg His Leu Arg Lys Leu Asp Gln Glu Leu Ala Lys Phe Lys
95     100    105
Met Glu Leu Glu Ala Asp Asn Ala Gly Ile Thr Glu Ile Leu Glu
110    115    120
Arg Arg Ser Leu Glu Leu Asp Thr Pro Ser Gln Pro Val Asn Asn
125    130    135
His His Ala His Ser His Thr Pro Val Glu Lys Arg Lys Tyr Asn
140    145    150
Pro Thr Ser His His Thr Thr Thr Asp His Ile Pro Glu Lys Lys
155    160    165
Phe Lys Ser Glu Ala Leu Leu Ser Thr Leu Thr Ser Asp Ala Ser
170    175    180
Lys Glu Asn Thr Leu Gly Cys Arg Asn Asn Asn Ser Thr Ala Ser
185    190    195
Ser Asn Asn Ala Tyr Asn Val Asn Ser Ser Gln Pro Leu Gly Ser
200    205    210
Tyr Asn Ile Gly Ser Leu Ser Ser Gly Thr Gly Ala Gly Ala Ile
215    220    225
Thr Met Ala Ala Ala Gln Ala Val Gln Ala Thr Ala Gln Met Lys
230    235    240
Glu Gly Arg Arg Thr Ser Ser Leu Lys Ala Ser Tyr Glu Ala Phe
245    250    255
Lys Asn Asn Asp Phe Gln Leu Gly Lys Glu Phe Ser Met Ala Arg
260    265    270
Glu Thr Val Gly Tyr Ser Ser Ser Ser Ala Leu Met Thr Thr Leu
275    280    285
Thr Gln Asn Ala Ser Ser Ser Ala Ala Asp Ser Arg Ser Gly Arg
290    295    300
Lys Ser Lys Asn Asn Asn Lys Ser Ser Ser Gln Gln Ser Ser Ser
305    310    315
Ser Ser Ser Ser Ser Ser Leu Ser Ser Cys Ser Ser Ser Ser Thr
320    325    330
Val Val Gln Glu Ile Ser Gln Gln Thr Thr Val Val Pro Glu Ser
335    340    345
Asp Ser Asn Ser Gln Val Asp Trp Thr Tyr Asp Pro Asn Glu Pro
350    355    360
Arg Tyr Cys Ile Cys Asn Gln Val Ser Tyr Gly Glu Met Val Gly
365    370    375
Cys Asp Asn Gln Asp Cys Pro Ile Glu Trp Phe His Tyr Gly Cys
380    385    390
Val Gly Leu Thr Glu Ala Pro Lys Gly Lys Trp Tyr Cys Pro Gln
395    400    405
Cys Thr Ala Ala Met Lys Arg Arg Gly Ser Arg His Lys
410    415

```

<210> 4

<211> 297

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

WO 01/07471

PCT/US00/19948

<223> Incyte ID No: 1416289CD1

<400> 4

Met	Ala	Tyr	Asn	Val	Ile	Ile	Ile	Tyr	Phe	Asn	Phe	Arg	Cys	Leu
1				5					10					15
Glu	Trp	Leu	Leu	Asn	Asn	Leu	Met	Thr	His	Gln	Asn	Val	Glu	Leu
				20					25					30
Phe	Lys	Glu	Leu	Ser	Ile	Asn	Val	Met	Lys	Gln	Leu	Ile	Gly	Ser
				35					40					45
Ser	Asn	Leu	Phe	Val	Met	Gln	Val	Glu	Met	Asp	Ile	Tyr	Thr	Ala
				50					55					60
Leu	Lys	Lys	Trp	Met	Phe	Leu	Gln	Leu	Val	Pro	Ser	Trp	Asn	Gly
				65					70					75
Ser	Leu	Lys	Gln	Leu	Leu	Thr	Glu	Thr	Asp	Val	Trp	Phe	Ser	Lys
				80					85					90
Gln	Arg	Lys	Asp	Phe	Glu	Gly	Met	Ala	Phe	Leu	Glu	Thr	Glu	Gln
				95					100					105
Gly	Lys	Pro	Phe	Val	Ser	Val	Phe	Arg	His	Leu	Arg	Leu	Gln	Tyr
				110					115					120
Ile	Ile	Ser	Asp	Leu	Ala	Ser	Ala	Arg	Ile	Ile	Glu	Gln	Asp	Ala
				125					130					135
Val	Val	Pro	Ser	Glu	Trp	Leu	Ser	Ser	Val	Tyr	Lys	Gln	Gln	Trp
				140					145					150
Phe	Ala	Met	Leu	Arg	Ala	Glu	Gln	Asp	Ser	Glu	Val	Gly	Pro	Gln
				155					160					165
Glu	Ile	Asn	Lys	Glu	Glu	Leu	Glu	Gly	Asn	Ser	Met	Arg	Cys	Gly
				170					175					180
Arg	Lys	Leu	Ala	Lys	Asp	Gly	Glu	Tyr	Cys	Trp	Arg	Trp	Thr	Gly
				185					190					195
Phe	Asn	Phe	Gly	Phe	Asp	Leu	Leu	Val	Thr	Tyr	Thr	Asn	Arg	Tyr
				200					205					210
Ile	Ile	Phe	Lys	Arg	Asn	Thr	Leu	Asn	Gln	Pro	Cys	Ser	Gly	Ser
				215					220					225
Val	Ser	Leu	Gln	Pro	Arg	Arg	Ser	Ile	Ala	Phe	Arg	Leu	Arg	Leu
				230					235					240
Ala	Ser	Phe	Asp	Ser	Ser	Gly	Lys	Leu	Ile	Cys	Ser	Arg	Thr	Thr
				245					250					255
Gly	Tyr	Gln	Ile	Leu	Thr	Leu	Glu	Lys	Asp	Gln	Glu	Gln	Val	Val
				260					265					270
Met	Asn	Leu	Asp	Ser	Arg	Leu	Leu	Ile	Phe	Pro	Leu	Tyr	Ile	Cys
				275					280					285
Cys	Asn	Phe	Leu	Tyr	Ile	Ser	Pro	Glu	Lys	Lys	Asn			
				290					295					

<210> 5

<211> 184

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1558289CD1

<400> 5

Met	Glu	Ser	Phe	Ser	Ser	Lys	Ser	Leu	Ala	Leu	Gln	Ala	Glu	Lys
1				5					10					15
Lys	Leu	Leu	Ser	Lys	Met	Ala	Gly	Arg	Ser	Val	Ala	His	Leu	Phe
				20					25					30
Ile	Asp	Glu	Thr	Ser	Ser	Glu	Val	Leu	Asp	Glu	Leu	Tyr	Arg	Val
				35					40					45
Ser	Lys	Glu	Tyr	Thr	His	Ser	Arg	Pro	Gln	Ala	Gln	Arg	Val	Ile
				50					55					60
Lys	Asp	Leu	Ile	Lys	Val	Ala	Ile	Lys	Val	Ala	Val	Leu	His	Arg
				65					70					75

WO 01/07471

PCT/US00/19948

Asn	Gly	Ser	Phe	Gly	Pro	Ser	Glu	Leu	Ala	Leu	Ala	Thr	Arg	Phe			
				80					85					90			
Arg	Gln	Lys	Leu	Arg	Gln	Gly	Ala	Met	Thr	Ala	Leu	Ser	Phe	Gly			
				95					100					105			
Glu	Val	Asp	Phe	Thr	Phe	Glu	Ala	Ala	Val	Leu	Ala	Gly	Leu	Leu			
				110					115					120			
Thr	Glu	Cys	Arg	Asp	Val	Leu	Leu	Glu	Leu	Val	Glu	His	His	Leu			
				125					130					135			
Thr	Pro	Lys	Ser	His	Gly	Arg	Ile	Arg	His	Val	Phe	Asp	His	Phe			
				140					145					150			
Ser	Asp	Pro	Gly	Leu	Leu	Thr	Ala	Leu	Tyr	Gly	Pro	Asp	Phe	Thr			
				155					160					165			
Gln	His	Leu	Gly	Lys	Ile	Cys	Asp	Gly	Leu	Arg	Lys	Leu	Leu	Asp			
				170					175					180			
Glu	Gly	Lys	Leu														

<210> 6
 <211> 173
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1577739CD1

Met	Asp	Val	Arg	Arg	Val	Leu	Val	Lys	Ala	Glu	Met	Glu	Lys	Phe			
1				5					10					15			
Leu	Gln	Asn	Lys	Glu	Leu	Phe	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Ile			
				20					25					30			
Cys	Cys	Cys	Cys	Arg	Ala	Lys	Phe	Pro	Leu	Phe	Ser	Trp	Pro	Pro			
				35					40					45			
Ser	Cys	Leu	Phe	Cys	Lys	Arg	Ala	Val	Cys	Thr	Ser	Cys	Ser	Ile			
				50					55					60			
Lys	Met	Lys	Met	Pro	Ser	Lys	Lys	Phe	Gly	His	Ile	Pro	Val	Tyr			
				65					70					75			
Thr	Leu	Gly	Phe	Glu	Ser	Pro	Gln	Arg	Val	Ser	Ala	Ala	Lys	Thr			
				80					85					90			
Ala	Pro	Ile	Gln	Arg	Arg	Asp	Ile	Phe	Gln	Ser	Leu	Gln	Gly	Pro			
				95					100					105			
Gln	Trp	Gln	Ser	Val	Glu	Glu	Ala	Phe	Pro	His	Ile	Tyr	Ser	His			
				110					115					120			
Gly	Cys	Val	Leu	Lys	Asp	Val	Cys	Ser	Glu	Cys	Thr	Ser	Phe	Val			
				125					130					135			
Ala	Asp	Val	Val	Arg	Ser	Ser	Arg	Lys	Ser	Val	Asp	Val	Leu	Asn			
				140					145					150			
Thr	Thr	Pro	Arg	Arg	Ser	Arg	Gln	Thr	Gln	Ser	Leu	Tyr	Ile	Pro			
				155					160					165			
Asn	Thr	Arg	Thr	Leu	Asp	Phe	Lys										
				170													

<210> 7
 <211> 591
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1752768CD1

Met	Val	Pro	Val	Ala	Val	Thr	Ala	Ala	Val	Ala	Pro	Val	Leu	Ser			
1				5					10					15			
Ile	Asn	Ser	Asp	Phe	Ser	Asp	Leu	Arg	Glu	Ile	Lys	Lys	Gln	Leu			

WO 01/07471

PCT/US00/19948

	20		25		30
Leu Leu Ile Ala Gly	Leu Thr Arg Glu Arg Gly Leu Leu His Ser				
35		40			45
Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser	Leu Pro Ala Leu Pro				
50		55			60
Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp Ala					
65		70			75
Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val					
80		85			90
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ser					
95		100			105
Lys Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser Gly					
110		115			120
Glu Lys Lys Lys Asp Asp Glu Thr Val Asp Ser Leu Gly Pro Leu					
125		130			135
Glu Lys Gly Gln Val Lys Asn Glu Ala Leu Arg Glu Leu Arg Val					
140		145			150
Glu Leu Ser Lys Lys His Gln Ala Arg Glu Leu Asp Gly Phe Gly					
155		160			165
Leu Tyr Leu Tyr Gly Val Val Leu Arg Lys Leu Asp Leu Val Lys					
170		175			180
Glu Ala Ile Asp Val Phe Val Glu Ala Thr His Val Leu Pro Leu					
185		190			195
His Trp Gly Ala Trp Leu Glu Leu Cys Asn Leu Ile Thr Asp Lys					
200		205			210
Glu Met Leu Lys Phe Leu Ser Leu Pro Asp Thr Trp Met Lys Glu					
215		220			225
Phe Phe Leu Ala His Ile Tyr Thr Glu Leu Gln Leu Ile Glu Glu					
230		235			240
Ala Leu Gln Lys Tyr Gln Asn Leu Ile Asp Val Gly Phe Ser Lys					
245		250			255
Ser Ser Tyr Ile Val Ser Gln Ile Ala Val Ala Tyr His Asn Ile					
260		265			270
Arg Asp Ile Asp Lys Ala Leu Ser Ile Phe Asn Glu Leu Arg Lys					
275		280			285
Gln Asp Pro Tyr Arg Ile Glu Asn Met Asp Thr Phe Ser Asn Leu					
290		295			300
Leu Tyr Val Arg Ser Met Lys Ser Glu Leu Ser Tyr Leu Ala His					
305		310			315
Asn Leu Cys Glu Ile Asp Lys Tyr Arg Val Glu Thr Cys Cys Val					
320		325			330
Ile Gly Asn Tyr Tyr Ser Leu Arg Ser Gln His Glu Lys Ala Ala					
335		340			345
Leu Tyr Phe Gln Arg Ala Leu Lys Leu Asn Pro Arg Tyr Leu Gly					
350		355			360
Ala Trp Thr Leu Met Gly His Glu Tyr Met Glu Met Lys Asn Thr					
365		370			375
Ser Ala Ala Ile Gln Ala Tyr Arg His Ala Ile Glu Val Asn Lys					
380		385			390
Arg Asp Tyr Arg Ala Trp Tyr Gly Leu Gly Gln Thr Tyr Glu Ile					
395		400			405
Leu Lys Met Pro Phe Tyr Cys Leu Tyr Tyr Cys Arg Arg Ala His					
410		415			420
Gln Leu Arg Pro Asn Asp Ser Arg Met Leu Val Ala Leu Gly Glu					
425		430			435
Cys Tyr Glu Lys Leu Asn Gln Leu Val Glu Ala Lys Lys Cys Tyr					
440		445			450
Trp Arg Ala Tyr Ala Val Gly Asp Val Glu Lys Met Ala Leu Val					
455		460			465
Lys Leu Ala Lys Leu His Glu Gln Leu Thr Glu Ser Glu Gln Ala					
470		475			480
Ala Gln Cys Tyr Ile Lys Tyr Ile Gln Asp Ile Tyr Ser Cys Gly					
485		490			495

WO 01/07471

PCT/US00/19948

Glu	Ile	Val	Glu	His	Leu	Glu	Glu	Ser	Thr	Ala	Phe	Arg	Tyr	Leu
				500					505					510
Ala	Gln	Tyr	Tyr	Phe	Lys	Cys	Lys	Leu	Trp	Asp	Glu	Ala	Ser	Thr
				515					520					525
Cys	Ala	Gln	Lys	Cys	Ala	Phe	Asn	Asp	Thr	Arg	Glu	Glu	Gly	
				530					535					540
Lys	Ala	Leu	Leu	Arg	Gln	Ile	Leu	Gln	Leu	Arg	Asn	Gln	Gly	Glu
				545					550					555
Thr	Pro	Thr	Thr	Glu	Val	Pro	Ala	Pro	Phe	Phe	Leu	Pro	Ala	Ser
				560					565					570
Leu	Ser	Ala	Asn	Asn	Thr	Pro	Thr	Arg	Arg	Val	Ser	Pro	Leu	Asn
				575					580					585
Leu	Ser	Ser	Val	Thr	Pro									
				590										

<210> 8

<211> 463

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1887228CD1

<400> 8

Met	Pro	Leu	Leu	Asn	Trp	Val	Ala	Leu	Lys	Pro	Ser	Gln	Ile	Thr
1				5					10					15
Gly	Thr	Val	Phe	Thr	Glu	Leu	Asn	Asp	Glu	Lys	Val	Leu	Gln	Glu
				20					25					30
Leu	Asp	Met	Ser	Asp	Phe	Glu	Glu	Gln	Phe	Lys	Thr	Lys	Ser	Gln
				35					40					45
Gly	Pro	Ser	Leu	Asp	Leu	Ser	Ala	Leu	Lys	Ser	Lys	Ala	Ala	Gln
				50					55					60
Lys	Ala	Pro	Ser	Lys	Ala	Thr	Leu	Ile	Glu	Ala	Asn	Arg	Ala	Lys
				65					70					75
Asn	Leu	Ala	Ile	Thr	Leu	Arg	Lys	Gly	Asn	Leu	Gly	Ala	Glu	Arg
				80					85					90
Ile	Cys	Gln	Ala	Ile	Glu	Ala	Tyr	Asp	Leu	Gln	Ala	Leu	Gly	Leu
				95					100					105
Asp	Phe	Leu	Glu	Leu	Leu	Met	Arg	Phe	Leu	Pro	Thr	Glu	Tyr	Glu
				110					115					120
Arg	Ser	Leu	Ile	Thr	Arg	Phe	Glu	Arg	Glu	Gln	Arg	Pro	Met	Glu
				125					130					135
Glu	Leu	Ser	Glu	Glu	Asp	Arg	Phe	Met	Leu	Cys	Phe	Ser	Arg	Ile
				140					145					150
Pro	Arg	Leu	Pro	Glu	Arg	Met	Thr	Thr	Leu	Thr	Phe	Leu	Gly	Asn
				155					160					165
Phe	Pro	Asp	Thr	Ala	Gln	Leu	Leu	Met	Pro	Gln	Leu	Asn	Ala	Ile
				170					175					180
Ile	Ala	Ala	Ser	Met	Ser	Ile	Lys	Ser	Ser	Asp	Lys	Leu	Arg	Gln
				185					190					195
Ile	Leu	Glu	Ile	Val	Leu	Ala	Phe	Gly	Asn	Tyr	Met	Asn	Ser	Ser
				200					205					210
Lys	Arg	Gly	Ala	Ala	Tyr	Gly	Phe	Arg	Leu	Gln	Ser	Leu	Asp	Ala
				215					220					225
Leu	Leu	Glu	Met	Lys	Ser	Thr	Asp	Arg	Lys	Gln	Thr	Leu	Leu	His
				230					235					240
Tyr	Leu	Val	Lys	Val	Ile	Ala	Glu	Lys	Tyr	Pro	Gln	Leu	Thr	Gly
				245					250					255
Phe	His	Ser	Asp	Leu	His	Phe	Leu	Asp	Lys	Ala	Gly	Ser	Val	Ser
				260					265					270
Leu	Asp	Ser	Val	Leu	Ala	Asp	Val	Arg	Ser	Leu	Gln	Arg	Gly	Leu
				275					280					285
Glu	Leu	Thr	Gln	Arg	Glu	Phe	Val	Arg	Gln	Asp	Asp	Cys	Met	Val

WO 01/07471

PCT/US00/19948

```

290          295          300
Leu Lys Glu Phe Leu Arg Ala Asn Ser Pro Thr Met Asp Lys Leu
305          310          315
Leu Ala Asp Ser Lys Thr Ala Gln Glu Ala Phe Glu Ser Val Val
320          325          330
Glu Tyr Phe Gly Glu Asn Pro Lys Thr Thr Ser Pro Gly Leu Phe
335          340          345
Phe Ser Leu Phe Ser Arg Phe Ile Lys Ala Tyr Lys Lys Ala Glu
350          355          360
Gln Glu Val Glu Gln Trp Lys Lys Glu Ala Ala Ala Gln Glu Ala
365          370          375
Gly Ala Asp Thr Pro Gly Lys Gly Glu Pro Pro Ala Pro Lys Ser
380          385          390
Pro Pro Lys Ala Arg Arg Pro Gln Met Asp Leu Ile Ser Glu Leu
395          400          405
Lys Arg Arg Gln Gln Lys Glu Pro Leu Ile Tyr Glu Ser Asp Arg
410          415          420
Asp Gly Ala Ile Glu Asp Ile Ile Thr Asp Leu Arg Asn Gln Pro
425          430          435
Tyr Ile Arg Ala Asp Thr Gly Arg Arg Ser Ala Arg Arg Arg Pro
440          445          450
Pro Gly Pro Pro Leu Gln Val Thr Ser Asp Leu Ser Leu
455          460
<210> 9
<211> 270
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1988468CD1

<400> 9
Met Ala Asp His Met Met Ala Met Asn His Gly Arg Phe Pro Asp
1          5          10          15
Gly Thr Asn Gly Leu His His His Pro Ala His Arg Met Gly Met
20          25          30
Gly Gln Phe Pro Ser Pro His His His Gln Gln Gln Gln Pro Gln
35          40          45
His Ala Phe Asn Ala Leu Met Gly Glu His Ile His Tyr Gly Ala
50          55          60
Gly Asn Met Asn Ala Thr Ser Gly Ile Arg His Ala Met Gly Pro
65          70          75
Gly Thr Val Asn Gly Gly His Pro Pro Ser Ala Leu Ala Pro Ala
80          85          90
Ala Arg Phe Asn Asn Ser Gln Phe Met Gly Pro Pro Val Ala Ser
95          100          105
Gln Gly Gly Ser Leu Pro Ala Ser Met Gln Leu Gln Lys Leu Asn
110          115          120
Asn Gln Tyr Phe Asn His His Pro Tyr Pro His Asn His Tyr Met
125          130          135
Pro Asp Leu His Pro Ala Ala Gly His Gln Met Asn Gly Thr Asn
140          145          150
Gln His Phe Arg Asp Cys Asn Pro Lys His Ser Gly Gly Ser Ser
155          160          165
Thr Pro Gly Gly Ser Gly Gly Ser Ser Thr Pro Gly Gly Ser Gly
170          175          180
Ser Ser Ser Gly Gly Gly Ala Gly Ser Ser Asn Ser Gly Gly Gly
185          190          195
Ser Gly Ser Gly Asn Met Pro Ala Ser Val Ala His Val Pro Ala
200          205          210
Ala Met Leu Pro Pro Asn Val Ile Asp Thr Asp Phe Ile Asp Glu
215          220          225

```

WO 01/07471

PCT/US00/19948

Glu	Val	Leu	Met	Ser	Leu	Val	Ile	Glu	Met	Gly	Leu	Asp	Arg	Ile
			230						235					240
Lys	Glu	Leu	Pro	Glu	Leu	Trp	Leu	Gly	Gln	Asn	Glu	Phe	Asp	Phe
			245						250					255
Met	Thr	Asp	Phe	Val	Cys	Lys	Gln	Gln	Pro	Ser	Arg	Val	Ser	Cys
			260						265					270

<210> 10

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2049176CD1

<400> 10

Met	Val	Ser	Trp	Met	Ile	Ser	Arg	Ala	Val	Val	Leu	Val	Phe	Gly
1				5					10					15
Met	Leu	Tyr	Pro	Ala	Tyr	Tyr	Ser	Tyr	Lys	Ala	Val	Lys	Thr	Lys
				20					25					30
Asn	Val	Lys	Glu	Tyr	Val	Arg	Trp	Met	Met	Tyr	Trp	Ile	Val	Phe
				35					40					45
Ala	Leu	Tyr	Thr	Val	Ile	Glu	Thr	Val	Ala	Asp	Gln	Thr	Val	Ala
				50					55					60
Trp	Phe	Pro	Leu	Tyr	Tyr	Glu	Leu	Lys	Ile	Ala	Phe	Val	Ile	Trp
				65					70					75
Leu	Leu	Ser	Pro	Tyr	Thr	Lys	Gly	Ala	Ser	Leu	Ile	Tyr	Arg	Lys
				80					85					90
Phe	Leu	His	Pro	Leu	Leu	Ser	Ser	Lys	Glu	Arg	Glu	Ile	Asp	Asp
				95					100					105
Tyr	Ile	Val	Gln	Ala	Lys	Glu	Arg	Gly	Tyr	Glu	Thr	Met	Val	Asn
				110					115					120
Phe	Gly	Arg	Gln	Gly	Leu	Asn	Leu	Ala	Ala	Thr	Ala	Ala	Val	Thr
				125					130					135
Ala	Ala	Val	Lys	Ser	Gln	Gly	Ala	Ile	Thr	Glu	Arg	Leu	Arg	Ser
				140					145					150
Phe	Ser	Met	His	Asp	Leu	Thr	Thr	Ile	Gln	Gly	Asp	Glu	Pro	Val
				155					160					165
Gly	Gln	Arg	Pro	Tyr	Gln	Pro	Leu	Pro	Glu	Ala	Lys	Lys	Lys	Ser
				170					175					180
Lys	Pro	Ala	Pro	Ser	Glu	Ser	Ala	Gly	Tyr	Gly	Ile	Pro	Leu	Lys
				185					190					195
Asp	Gly	Asp	Glu	Lys	Thr	Asp	Glu	Glu	Ala	Glu	Gly	Pro	Tyr	Ser
				200					205					210
Asp	Asn	Glu	Met	Leu	Thr	His	Lys	Gly	Leu	Arg	Arg	Ser	Gln	Ser
				215					220					225
Met	Lys	Ser	Val	Lys	Thr	Thr	Lys	Gly	Arg	Lys	Glu	Val	Arg	Tyr
				230					235					240
Gly	Ser	Leu	Lys	Tyr	Lys	Val	Lys	Lys	Arg	Pro	Gln	Val	Tyr	Phe
				245					250					255

<210> 11

<211> 533

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2686765CD1

<400> 11

Met Ser Gly Thr Leu Glu Ser Leu Ala Asp Asp Val Ser Ser Met

WO 01/07471

PCT/US00/19948

1	5	10	15
Gly Ser Asp Ser Glu	Ile Asn Gly Leu	Ala Leu Arg Lys Thr	Asp
20	25	30	
Lys Tyr Gly Phe Leu	Gly Gly Ser Gln Tyr	Ser Gly Ser Leu	Glu
35	40	45	
Ser Ser Ile Pro Val	Asp Val Ala Arg	Gln Arg Glu Leu	Lys Trp
50	55	60	
Leu Asp Met Phe Ser	Asn Trp Asp Lys Trp	Leu Ser Arg Arg	Phe
65	70	75	
Gln Lys Val Lys Leu	Arg Cys Arg Lys Gly	Ile Pro Ser Ser	Leu
80	85	90	
Arg Ala Lys Ala Trp	Gln Tyr Leu Ser Asn	Ser Lys Glu Leu	Leu
95	100	105	
Glu Gln Asn Pro Gly	Lys Phe Glu Glu Leu	Glu Arg Ala Pro	Gly
110	115	120	
Asp Pro Lys Trp Leu	Asp Val Ile Glu Lys	Asp Leu His Arg	Gln
125	130	135	
Phe Pro Phe His Glu	Met Phe Ala Ala Arg	Gly Gly His Gly	Gln
140	145	150	
Gln Asp Leu Tyr Arg	Ile Leu Lys Ala Tyr	Thr Ile Tyr Arg	Pro
155	160	165	
Asp Glu Gly Tyr Cys	Gln Ala Gln Ala Pro	Val Ala Ala Val	Leu
170	175	180	
Leu Met His Met Pro	Ala Glu Lys Pro Phe	Gly Ala Trp Val	Gln
185	190	195	
Ile Cys Asp Lys Tyr	Leu Pro Gly Tyr Tyr	Ser Ala Gly Leu	Glu
200	205	210	
Ala Ile Gln Leu Asp	Gly Glu Ile Phe Phe	Ala Leu Leu Arg	Arg
215	220	225	
Ala Ser Pro Leu Ala	His Arg His Leu Gln	Arg Gln Arg Ile	Asp
230	235	240	
Pro Val Leu Tyr Met	Thr Glu Trp Phe Met	Cys Ile Phe Ala	Arg
245	250	255	
Thr Leu Pro Trp Ala	Ser Val Leu Arg Val	Trp Asp Met Phe	Phe
260	265	270	
Cys Glu Gly Val Lys	Ile Ile Phe Arg Val	Ala Leu Val Leu	Leu
275	280	285	
Arg His Thr Leu Gly	Ser Val Glu Lys Leu	Arg Ser Cys Gln	Gly
290	295	300	
Met Tyr Glu Thr Met	Glu Gln Leu Arg Asn	Leu Pro Gln Gln	Cys
305	310	315	
Met Gln Glu Asp Phe	Leu Val His Glu Val	Thr Asn Leu Pro	Val
320	325	330	
Thr Glu Ala Leu Ile	Glu Arg Glu Asn Ala	Ala Gln Leu Lys	Lys
335	340	345	
Trp Arg Glu Thr Arg	Gly Glu Leu Gln Tyr	Arg Pro Ser Arg	Arg
350	355	360	
Leu His Gly Ser Arg	Ala Ile His Glu Glu	Arg Arg Arg Gln	Gln
365	370	375	
Pro Pro Leu Gly Pro	Ser Ser Ser Leu Leu	Ser Leu Pro Gly	Leu
380	385	390	
Lys Ser Arg Gly Ser	Arg Ala Ala Gly Gly	Ala Pro Ser Pro	Pro
395	400	405	
Pro Pro Val Arg Arg	Ala Ser Ala Gly Pro	Ala Pro Gly Pro	Val
410	415	420	
Val Thr Ala Glu Gly	Leu His Pro Ser Leu	Pro Ser Pro Thr	Gly
425	430	435	
Asn Ser Thr Pro Leu	Gly Ser Ser Lys Glu	Thr Arg Lys Gln	Glu
440	445	450	
Lys Glu Arg Gln Lys	Gln Glu Lys Glu Arg	Gln Lys Gln Glu	Lys
455	460	465	
Glu Arg Glu Lys Glu	Arg Gln Lys Gln Glu	Lys Glu Arg Glu	Lys
470	475	480	

WO 01/07471

PCT/US00/19948

Gln	Glu	Lys	Glu	Arg	Glu	Lys	Gln	Glu	Lys	Glu	Arg	Gln	Lys	Gln
				485					490					495
Glu	Lys	Lys	Ala	Gln	Gly	Arg	Lys	Leu	Ser	Leu	Arg	Arg	Lys	Ala
				500					505					510
Asp	Gly	Pro	Pro	Gly	Pro	His	Asp	Gly	Gly	Asp	Arg	Pro	Ser	Ala
				515					520					525
Glu	Ala	Arg	Gln	Asp	Ala	Tyr	Phe							
				530										

<210> 12

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3215187CD1

<400> 12

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ser	Leu	Val
1				5					10					15
Leu	Cys	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25					30
Phe	Asp	Glu	Leu	Arg	Thr	Asp	Phe	Lys	Ser	Pro	Ile	Asp	Gln	Cys
				35					40					45
Asn	Pro	Val	His	Ala	Arg	Glu	Arg	Leu	Arg	Asn	Ile	Glu	Arg	Ile
				50					55					60
Cys	Phe	Leu	Leu	Arg	Lys	Leu	Val	Leu	Pro	Glu	Tyr	Ser	Ile	His
				65					70					75
Ser	Leu	Phe	Cys	Ile	Met	Phe	Leu	Cys	Ala	Gln	Glu	Trp	Leu	Thr
				80					85					90
Leu	Gly	Leu	Asn	Val	Pro	Leu	Leu	Phe	Tyr	His	Phe	Trp	Arg	Tyr
				95					100					105
Phe	His	Cys	Pro	Ala	Asp	Ser	Ser	Glu	Leu	Ala	Tyr	Asp	Pro	Pro
				110					115					120
Val	Val	Met	Asn	Ala	Asp	Thr	Leu	Ser	Tyr	Cys	Gln	Lys	Glu	Ala
				125					130					135
Trp	Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ser	Phe	Phe	Tyr	Tyr	Leu
				140					145					150
Tyr	Cys	Met	Ile	Tyr	Thr	Leu	Val	Ser	Ser					
				155					160					

<210> 13

<211> 531

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3500375CD1

<400> 13

Met	Ala	Asp	Val	Leu	Ser	Val	Leu	Arg	Gln	Tyr	Asn	Ile	Gln	Lys
1				5					10					15
Lys	Glu	Ile	Val	Val	Lys	Gly	Asp	Glu	Val	Ile	Phe	Gly	Glu	Phe
				20					25					30
Ser	Trp	Pro	Lys	Asn	Val	Lys	Thr	Asn	Tyr	Val	Val	Trp	Gly	Thr
				35					40					45
Gly	Lys	Glu	Gly	Gln	Pro	Arg	Glu	Tyr	Tyr	Thr	Leu	Asp	Ser	Ile
				50					55					60
Leu	Phe	Leu	Leu	Asn	Asn	Val	His	Leu	Ser	His	Pro	Val	Tyr	Val
				65					70					75
Arg	Arg	Ala	Ala	Thr	Glu	Asn	Ile	Pro	Val	Val	Arg	Arg	Pro	Asp
				80					85					90
Arg	Lys	Asp	Leu	Leu	Gly	Tyr	Leu	Asn	Gly	Glu	Ala	Ser	Thr	Ser

WO 01/07471

PCT/US00/19948

	95		100		105
Ala Ser Ile Asp	Arg Ser Ala Pro Leu	Glu Ile Gly Leu Gln	Arg		
	110		115		120
Ser Thr Gln Val	Lys Arg Ala Ala Asp	Glu Val Leu Ala Glu	Ala		
	125		130		135
Lys Lys Pro Arg	Ile Glu Asp Glu Glu	Cys Val Arg Leu Asp	Lys		
	140		145		150
Glu Arg Leu Ala	Ala Arg Leu Glu Gly	His Lys Glu Gly Ile	Val		
	155		160		165
Gln Thr Glu Gln	Ile Arg Ser Leu Ser	Glu Ala Met Ser Val	Glu		
	170		175		180
Lys Ile Ala Ala	Ile Lys Ala Lys Ile	Met Ala Lys Lys Arg	Ser		
	185		190		195
Thr Ile Lys Thr	Asp Leu Asp Asp Asp	Ile Thr Ala Leu Lys	Gln		
	200		205		210
Arg Ser Phe Val	Asp Ala Glu Val Asp	Val Thr Arg Asp Ile	Val		
	215		220		225
Ser Arg Glu Arg	Val Trp Arg Thr Arg	Thr Thr Ile Leu Gln	Ser		
	230		235		240
Thr Gly Lys Asn	Phe Ser Lys Asn Ile	Phe Ala Ile Leu Gln	Ser		
	245		250		255
Val Lys Ala Arg	Glu Glu Gly Arg Ala	Pro Glu Gln Arg Pro	Ala		
	260		265		270
Pro Asn Ala Ala	Pro Val Asp Pro Thr	Leu Arg Thr Lys Gln	Pro		
	275		280		285
Ile Pro Ala Ala	Tyr Asn Arg Tyr Asp	Gln Glu Arg Phe Lys	Gly		
	290		295		300
Lys Glu Glu Thr	Glu Gly Phe Lys Ile	Asp Thr Met Gly Thr	Tyr		
	305		310		315
His Gly Met Thr	Leu Lys Ser Val Thr	Glu Gly Ala Ser Ala	Arg		
	320		325		330
Lys Thr Gln Thr	Pro Ala Ala Gln Pro	Val Pro Arg Pro Val	Ser		
	335		340		345
Gln Ala Arg Pro	Pro Pro Asn Gln Lys	Lys Gly Ser Arg Thr	Pro		
	350		355		360
Ile Ile Ile Ile	Pro Ala Ala Thr Thr	Ser Leu Ile Thr Met	Leu		
	365		370		375
Asn Ala Lys Asp	Leu Leu Gln Asp Leu	Lys Phe Val Pro Ser	Asp		
	380		385		390
Glu Lys Lys Lys	Gln Gly Cys Gln Arg	Glu Asn Glu Thr Leu	Ile		
	395		400		405
Gln Arg Arg Lys	Asp Gln Met Gln Pro	Gly Gly Thr Ala Ile	Ser		
	410		415		420
Val Thr Val Pro	Tyr Arg Val Val Asp	Gln Pro Leu Lys Leu	Met		
	425		430		435
Pro Gln Asp Trp	Asp Arg Val Val Ala	Val Phe Val Gln Gly	Pro		
	440		445		450
Ala Trp Gln Phe	Lys Gly Trp Pro Trp	Leu Leu Pro Asp Gly	Ser		
	455		460		465
Pro Val Asp Ile	Phe Ala Lys Ile Lys	Ala Phe His Leu Lys	Tyr		
	470		475		480
Asp Glu Val Arg	Leu Asp Pro Asn Val	Gln Lys Trp Asp Val	Thr		
	485		490		495
Val Leu Glu Leu	Ser Tyr His Lys Arg	His Leu Asp Arg Pro	Val		
	500		505		510
Phe Leu Arg Phe	Trp Glu Thr Leu Asp	Arg Tyr Met Val Lys	His		
	515		520		525
Lys Ser His Leu	Arg Phe				
	530				

<210> 14

<211> 165

<212> PRT

<213> Homo sapiens

WO 01/07471

PCT/US00/19948

<220>

<221> misc_feature

<223> Incyte ID No: 5080410CD1

<400> 14

Met	Ala	Ser	Met	Arg	Glu	Ser	Asp	Thr	Gly	Leu	Trp	Leu	His	Asn
1				5					10					15
Lys	Leu	Gly	Ala	Thr	Asp	Glu	Leu	Trp	Ala	Pro	Pro	Ser	Ile	Ala
				20					25					30
Ser	Leu	Leu	Thr	Ala	Ala	Val	Ile	Asp	Asn	Ile	Arg	Leu	Cys	Phe
				35					40					45
His	Gly	Leu	Ser	Ser	Ala	Val	Lys	Leu	Lys	Leu	Leu	Leu	Gly	Thr
				50					55					60
Leu	His	Leu	Pro	Arg	Arg	Thr	Val	Asp	Glu	His	Pro	Ile	Leu	Pro
				65					70					75
Met	Lys	Gly	Ala	Leu	Met	Glu	Ile	Ile	Gln	Leu	Ala	Ser	Leu	Asp
				80					85					90
Ser	Asp	Pro	Trp	Val	Leu	Met	Val	Ala	Asp	Ile	Leu	Lys	Ser	Phe
				95					100					105
Pro	Asp	Thr	Gly	Ser	Leu	Asn	Leu	Glu	Leu	Glu	Glu	Gln	Asn	Pro
				110					115					120
Asn	Val	Gln	Asp	Ile	Leu	Gly	Glu	Leu	Arg	Glu	Lys	Val	Gly	Glu
				125					130					135
Cys	Glu	Ala	Ser	Ala	Met	Leu	Pro	Leu	Glu	Cys	Gln	Tyr	Leu	Asn
				140					145					150
Lys	Asn	Ala	Ala	Asp	Asp	Pro	Arg	Gly	Thr	Pro	His	Ser	Pro	Gly
				155					160					165

<210> 15

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5218248CD1

<400> 15

Met	Ser	Asn	Met	Glu	Lys	His	Leu	Phe	Asn	Leu	Lys	Phe	Ala	Ala
1				5					10					15
Lys	Glu	Leu	Ser	Arg	Ser	Ala	Lys	Lys	Cys	Asp	Lys	Glu	Glu	Lys
				20					25					30
Ala	Glu	Lys	Ala	Lys	Ile	Lys	Lys	Ala	Ile	Gln	Lys	Gly	Asn	Met
				35					40					45
Glu	Val	Ala	Arg	Ile	His	Ala	Glu	Asn	Ala	Ile	Arg	Gln	Lys	Asn
				50					55					60
Gln	Ala	Val	Asn	Phe	Leu	Arg	Met	Ser	Ala	Arg	Val	Asp	Ala	Val
				65					70					75
Ala	Ala	Arg	Val	Gln	Thr	Ala	Val	Thr	Met	Gly	Lys	Val	Thr	Lys
				80					85					90
Ser	Met	Ala	Gly	Val	Val	Lys	Ser	Met	Asp	Ala	Thr	Leu	Lys	Thr
				95					100					105
Met	Asn	Leu	Glu	Lys	Ile	Ser	Ala	Leu	Met	Asp	Lys	Phe	Glu	His
				110					115					120
Gln	Phe	Glu	Thr	Leu	Asp	Val	Gln	Thr	Gln	Gln	Met	Glu	Asp	Thr
				125					130					135
Met	Ser	Ser	Thr	Thr	Thr	Leu	Thr	Thr	Pro	Gln	Asn	Gln	Val	Asp
				140					145					150
Met	Leu	Leu	Gln	Glu	Met	Ala	Asp	Glu	Ala	Gly	Leu	Asp	Leu	Asn
				155					160					165
Met	Glu	Leu	Pro	Gln	Gly	Gln	Thr	Gly	Ser	Val	Gly	Thr	Ser	Val
				170					175					180
Ala	Ser	Ala	Glu	Gln	Asp	Glu	Leu	Ser	Gln	Arg	Leu	Ala	Arg	Leu

WO 01/07471

PCT/US00/19948

Arg Asp Gln Val 185 190 195

<210> 16
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 058336CD1

<400> 16
Met Ala Phe Asn Asp Cys Phe Ser Leu Asn Tyr Pro Gly Asn Pro
1 5 10 15
Cys Pro Gly Asp Leu Ile Glu Val Phe Arg Pro Gly Tyr Gln His
20 25 30
Trp Ala Leu Tyr Leu Gly Asp Gly Tyr Val Ile Asn Ile Ala Pro
35 40 45
Val Asp Gly Ile Pro Ala Ser Phe Thr Ser Ala Lys Ser Val Phe
50 55 60
Ser Ser Lys Ala Leu Val Lys Met Gln Leu Leu Lys Asp Val Val
65 70 75
Gly Asn Asp Thr Tyr Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr
80 85 90
Pro Pro Leu Pro Val Glu Glu Ile Ile Lys Arg Ser Glu Phe Val
95 100 105
Ile Gly Gln Glu Val Ala Tyr Asn Leu Leu Val Asn Asn Cys Glu
110 115 120
His Phe Val Thr Leu Leu Arg Tyr Gly Glu Gly Val Ser Glu Gln
125 130 135
Ala Asn Arg Ala Ile Ser Thr Val Glu Phe Val Thr Ala Ala Val
140 145 150
Gly Val Phe Ser Phe Leu Gly Leu Phe Pro Lys Gly Gln Arg Ala
155 160 165
Lys Tyr Tyr

<210> 17
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1511488CD1

<400> 17
Met Leu Arg Ala Val Gly Ser Leu Leu Arg Leu Gly Arg Gly Leu
1 5 10 15
Thr Val Arg Cys Gly Pro Gly Ala Pro Leu Glu Ala Thr Arg Arg
20 25 30
Pro Ala Pro Ala Leu Pro Pro Arg Gly Leu Pro Cys Tyr Ser Ser
35 40 45
Gly Gly Ala Pro Ser Asn Ser Gly Pro Gln Gly His Gly Glu Ile
50 55 60
His Arg Val Pro Thr Gln Arg Arg Pro Ser Gln Phe Asp Lys Lys
65 70 75
Ile Leu Leu Trp Thr Gly Arg Phe Lys Ser Met Glu Glu Ile Pro
80 85 90
Pro Arg Ile Pro Pro Glu Met Ile Asp Thr Ala Arg Asn Lys Ala
95 100 105
Arg Val Lys Ala Cys Tyr Ile Met Ile Gly Leu Thr Ile Ile Ala
110 115 120

WO 01/07471

PCT/US00/19948

Cys	Phe	Ala	Val	Ile	Val	Ser	Ala	Lys	Arg	Ala	Val	Glu	Arg	His
				125					130					135
Glu	Ser	Leu	Thr	Ser	Trp	Asn	Leu	Ala	Lys	Lys	Ala	Lys	Trp	Arg
				140					145					150
Glu	Glu	Ala	Ala	Leu	Ala	Ala	Gln	Ala	Lys	Ala	Lys			
				155					160					

<210> 18

<211> 246

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1638819CD1

<400> 18

Met	Ala	Gly	Tyr	Leu	Lys	Leu	Val	Cys	Val	Ser	Phe	Gln	Arg	Gln
1				5					10					15
Gly	Phe	His	Thr	Val	Gly	Ser	Arg	Cys	Lys	Asn	Arg	Thr	Gly	Ala
				20					25					30
Glu	His	Leu	Trp	Leu	Thr	Arg	His	Leu	Arg	Asp	Pro	Phe	Val	Lys
				35					40					45
Ala	Ala	Lys	Val	Glu	Ser	Tyr	Arg	Cys	Arg	Ser	Ala	Phe	Lys	Leu
				50					55					60
Leu	Glu	Val	Asn	Glu	Arg	His	Gln	Ile	Leu	Arg	Pro	Gly	Leu	Arg
				65					70					75
Val	Leu	Asp	Cys	Gly	Ala	Ala	Pro	Gly	Ala	Trp	Ser	Gln	Val	Ala
				80					85					90
Val	Gln	Lys	Val	Asn	Ala	Ala	Gly	Thr	Asp	Pro	Ser	Ser	Pro	Val
				95					100					105
Gly	Phe	Val	Leu	Gly	Val	Asp	Leu	Leu	His	Ile	Phe	Pro	Leu	Glu
				110					115					120
Gly	Ala	Thr	Phe	Leu	Cys	Pro	Ala	Asp	Val	Thr	Asp	Pro	Arg	Thr
				125					130					135
Ser	Gln	Arg	Ile	Leu	Glu	Val	Leu	Pro	Gly	Arg	Arg	Ala	Asp	Val
				140					145					150
Ile	Leu	Ser	Asp	Met	Ala	Pro	Asn	Ala	Thr	Gly	Phe	Arg	Asp	Leu
				155					160					165
Asp	His	Asp	Arg	Leu	Ile	Ser	Leu	Cys	Leu	Thr	Leu	Leu	Ser	Val
				170					175					180
Thr	Pro	Asp	Ile	Leu	Gln	Pro	Gly	Gly	Thr	Phe	Leu	Cys	Lys	Thr
				185					190					195
Trp	Ala	Gly	Ser	Gln	Ser	Arg	Arg	Leu	Gln	Arg	Arg	Leu	Thr	Glu
				200					205					210
Glu	Phe	Gln	Asn	Val	Arg	Ile	Ile	Lys	Pro	Glu	Ala	Ser	Arg	Lys
				215					220					225
Glu	Ser	Ser	Glu	Val	Tyr	Phe	Leu	Ala	Thr	Gln	Tyr	His	Gly	Arg
				230					235					240
Lys	Gly	Thr	Val	Lys	Gln									
				245										

<210> 19

<211> 483

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1655123CD1

<400> 19

Met	Glu	Glu	Gly	Gly	Gly	Gly	Val	Arg	Ser	Leu	Val	Pro	Gly	Gly
1				5					10					15
Pro	Val	Leu	Leu	Val	Leu	Cys	Gly	Leu	Leu	Glu	Ala	Ser	Gly	Gly

WO 01/07471

PCT/US00/19948

				20					25				30	
Gly	Arg	Ala	Leu	Pro	Gln	Leu	Ser	Asp	Asp	Ile	Pro	Phe	Arg	Val
				35					40					45
Asn	Trp	Pro	Gly	Thr	Glu	Phe	Ser	Leu	Pro	Thr	Thr	Gly	Val	Leu
				50					55					60
Tyr	Lys	Glu	Asp	Asn	Tyr	Val	Ile	Met	Thr	Thr	Ala	His	Lys	Glu
				65					70					75
Lys	Tyr	Lys	Cys	Ile	Leu	Pro	Leu	Val	Thr	Ser	Gly	Asp	Glu	Glu
				80					85					90
Glu	Glu	Lys	Asp	Tyr	Lys	Gly	Pro	Asn	Pro	Arg	Glu	Leu	Leu	Glu
				95					100					105
Pro	Leu	Phe	Lys	Gln	Ser	Ser	Cys	Ser	Tyr	Arg	Ile	Glu	Ser	Tyr
				110					115					120
Trp	Thr	Tyr	Glu	Val	Cys	His	Gly	Lys	His	Ile	Arg	Gln	Tyr	His
				125					130					135
Glu	Glu	Lys	Glu	Thr	Gly	Gln	Lys	Ile	Asn	Ile	His	Glu	Tyr	Tyr
				140					145					150
Leu	Gly	Asn	Met	Leu	Ala	Lys	Asn	Leu	Leu	Phe	Glu	Lys	Glu	Arg
				155					160					165
Glu	Ala	Glu	Glu	Lys	Glu	Lys	Ser	Asn	Glu	Ile	Pro	Thr	Lys	Asn
				170					175					180
Ile	Glu	Gly	Gln	Met	Thr	Pro	Tyr	Tyr	Pro	Val	Gly	Met	Gly	Asn
				185					190					195
Gly	Thr	Pro	Cys	Ser	Leu	Lys	Gln	Asn	Arg	Pro	Arg	Ser	Ser	Thr
				200					205					210
Val	Met	Tyr	Ile	Cys	His	Pro	Glu	Ser	Lys	His	Glu	Ile	Leu	Ser
				215					220					225
Val	Ala	Glu	Val	Thr	Thr	Cys	Glu	Tyr	Glu	Val	Val	Ile	Leu	Thr
				230					235					240
Pro	Leu	Leu	Cys	Ser	His	Pro	Lys	Tyr	Arg	Phe	Arg	Ala	Ser	Pro
				245					250					255
Val	Asn	Asp	Ile	Phe	Cys	Gln	Ser	Leu	Pro	Gly	Ser	Pro	Phe	Lys
				260					265					270
Pro	Leu	Thr	Leu	Arg	Gln	Leu	Glu	Gln	Gln	Glu	Glu	Ile	Leu	Arg
				275					280					285
Val	Pro	Phe	Arg	Arg	Asn	Lys	Glu	Glu	Asp	Leu	Gln	Ser	Thr	Lys
				290					295					300
Glu	Glu	Arg	Phe	Pro	Ala	Ile	His	Lys	Ser	Ile	Ala	Ile	Gly	Ser
				305					310					315
Gln	Pro	Val	Leu	Thr	Val	Gly	Thr	Thr	His	Ile	Ser	Lys	Leu	Thr
				320					325					330
Asp	Asp	Gln	Leu	Ile	Lys	Glu	Phe	Leu	Ser	Gly	Ser	Tyr	Cys	Phe
				335					340					345
Arg	Gly	Gly	Val	Gly	Trp	Trp	Lys	Tyr	Glu	Phe	Cys	Tyr	Gly	Lys
				350					355					360
His	Val	His	Gln	Tyr	His	Glu	Asp	Lys	Asp	Ser	Gly	Lys	Thr	Ser
				365					370					375
Val	Val	Val	Gly	Thr	Trp	Asn	Gln	Glu	Glu	His	Ile	Glu	Trp	Ala
				380					385					390
Lys	Lys	Asn	Thr	Ala	Arg	Ala	Tyr	His	Leu	Gln	Asp	Asp	Gly	Thr
				395					400					405
Gln	Thr	Val	Arg	Met	Val	Ser	His	Phe	Tyr	Gly	Asn	Gly	Asp	Ile
				410					415					420
Cys	Asp	Ile	Thr	Asp	Lys	Pro	Arg	Gln	Val	Thr	Val	Lys	Leu	Lys
				425					430					435
Cys	Lys	Glu	Ser	Asp	Ser	Pro	His	Ala	Val	Thr	Val	Tyr	Met	Leu
				440					445					450
Glu	Pro	His	Ser	Cys	Gln	Tyr	Ile	Leu	Gly	Val	Glu	Ser	Pro	Val
				455					460					465
Ile	Cys	Lys	Ile	Leu	Asp	Thr	Ala	Asp	Glu	Asn	Gly	Leu	Leu	Ser
				470					475					480
Leu	Pro	Asn												

WO 01/07471

PCT/US00/19948

<210> 20
 <211> 280
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2553926CD1

<400> 20
 Met Glu Ala Ala Glu Thr Glu Ala Glu Ala Ala Ala Leu Glu Val
 1 5 10 15
 Leu Ala Glu Val Ala Gly Ile Leu Glu Pro Val Gly Leu Gln Glu
 20 25 30
 Glu Ala Glu Leu Pro Ala Lys Ile Leu Val Glu Phe Val Val Asp
 35 40 45
 Ser Gln Lys Lys Asp Lys Leu Leu Cys Ser Gln Leu Gln Val Ala
 50 55 60
 Asp Phe Leu Gln Asn Ile Leu Ala Gln Glu Asp Thr Ala Lys Gly
 65 70 75
 Leu Asp Pro Leu Ala Ser Glu Asp Thr Ser Arg Gln Lys Ala Ile
 80 85 90
 Ala Ala Lys Glu Gln Trp Lys Glu Leu Lys Ala Thr Tyr Arg Glu
 95 100 105
 His Val Glu Ala Ile Lys Ile Gly Leu Thr Lys Ala Leu Thr Gln
 110 115 120
 Met Glu Glu Ala Gln Arg Lys Arg Thr Gln Leu Arg Glu Ala Phe
 125 130 135
 Glu Gln Leu Gln Ala Lys Lys Gln Met Ala Met Glu Lys Arg Arg
 140 145 150
 Ala Val Gln Asn Gln Trp Gln Leu Gln Gln Glu Lys His Leu Gln
 155 160 165
 His Leu Ala Glu Val Ser Ala Glu Val Arg Glu Arg Lys Thr Gly
 170 175 180
 Thr Gln Gln Glu Leu Asp Gly Val Phe Gln Lys Leu Gly Asn Leu
 185 190 195
 Lys Gln Gln Ala Glu Gln Glu Arg Asp Lys Leu Gln Arg Tyr Gln
 200 205 210
 Thr Phe Leu Gln Leu Leu Tyr Thr Leu Gln Gly Lys Leu Leu Phe
 215 220 225
 Pro Glu Ala Glu Ala Glu Ala Glu Asn Leu Pro Asp Asp Lys Pro
 230 235 240
 Gln Gln Pro Thr Arg Pro Gln Glu Gln Ser Thr Gly Asp Thr Met
 245 250 255
 Gly Arg Asp Pro Gly Val Ser Phe Lys Phe Ser Lys Ala Val Gly
 260 265 270
 Leu Gln Pro Ala Gly Asp Val Asn Leu Pro
 275 280

<210> 21
 <211> 425
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2800717CD1

<400> 21
 Met Gly Glu Asp Ala Ala Gln Ala Glu Lys Phe Gln His Pro Gly
 1 5 10 15
 Ser Asp Met Arg Gln Glu Lys Pro Ser Ser Pro Ser Pro Met Pro
 20 25 30
 Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly Asn Thr Glu Glu

WO 01/07471

PCT/US00/19948

	35		40		45
Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr Val Leu Thr					
	50		55		60
Leu Leu Asp Lys Leu Val Asn Met Leu Asp Ala Val Gln Glu Asn					
	65		70		75
Gln His Lys Met Glu Gln Arg Gln Ile Ser Leu Glu Gly Ser Val					
	80		85		90
Lys Gly Ile Gln Asn Asp Leu Thr Lys Leu Ser Lys Tyr Gln Ala					
	95		100		105
Ser Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Ser Arg Lys					
	110		115		120
Val Ser Ala His Thr Arg Ala Val Lys Glu Arg Met Asp Arg Gln					
	125		130		135
Cys Ala Gln Val Lys Arg Leu Glu Asn Asn His Ala Gln Leu Leu					
	140		145		150
Arg Arg Asn His Phe Lys Val Leu Ile Phe Gln Glu Glu Asn Glu					
	155		160		165
Ile Pro Ala Ser Val Phe Val Lys Gln Pro Val Ser Gly Ala Val					
	170		175		180
Glu Gly Lys Glu Glu Leu Pro Asp Glu Asn Lys Ser Leu Glu Glu					
	185		190		195
Thr Leu His Thr Val Asp Leu Ser Ser Asp Asp Asp Leu Pro His					
	200		205		210
Asp Glu Glu Ala Leu Glu Asp Ser Ala Glu Glu Lys Val Glu Glu					
	215		220		225
Ser Arg Ala Glu Lys Ile Lys Arg Ser Ser Leu Lys Lys Val Asp					
	230		235		240
Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met					
	245		250		255
Asn Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys					
	260		265		270
Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly					
	275		280		285
Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys					
	290		295		300
Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser					
	305		310		315
Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu Glu					
	320		325		330
Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala					
	335		340		345
Leu Val Glu Gly Glu Ile Ala Glu Glu Ala Ala Glu Lys Ala Thr					
	350		355		360
Ser Arg Gly Ser Asn Ser Gly Met Asp Ser Asn Ile Asp Leu Thr					
	365		370		375
Ile Val Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala					
	380		385		390
Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu					
	395		400		405
Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln					
	410		415		420
Val His Gln Thr Ser					
	425				

<210> 22

<211> 128

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5664154CD1

<400> 22

WO 01/07471

PCT/US00/19948

Met Glu Ser Lys Glu Glu Arg Ala Leu Asn Asn Leu Ile Val Glu
 1 5 10 15
 Asn Val Asn Gln Glu Asn Asp Glu Lys Asp Glu Lys Glu Gln Val
 20 25 30
 Ala Asn Lys Gly Glu Pro Leu Ala Leu Pro Leu Asn Val Ser Glu
 35 40 45
 Tyr Cys Val Pro Arg Gly Asn Arg Arg Arg Phe Arg Val Arg Gln
 50 55 60
 Pro Ile Leu Gln Tyr Arg Trp Asp Ile Met His Arg Leu Gly Glu
 65 70 75
 Pro Gln Ala Arg Met Arg Glu Glu Asn Met Glu Arg Ile Gly Glu
 80 85 90
 Glu Val Arg Gln Leu Met Glu Lys Leu Arg Glu Lys Gln Leu Ser
 95 100 105
 His Ser Leu Arg Ala Val Ser Thr Asp Pro Pro His His Asp His
 110 115 120
 His Asp Glu Phe Cys Leu Met Pro
 125

<210> 23

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 017900CD1

<400> 23

Met Asp Gly Arg Val Gln Leu Ile Lys Ala Leu Leu Ala Leu Pro
 1 5 10 15
 Ile Arg Pro Ala Thr Arg Arg Trp Arg Asn Pro Ile Pro Phe Pro
 20 25 30
 Glu Thr Phe Asp Gly Asp Thr Asp Arg Leu Pro Glu Phe Ile Val
 35 40 45
 Gln Thr Gly Ser Tyr Met Phe Val Asp Glu Asn Thr Phe Ser Ser
 50 55 60
 Asp Ala Leu Lys Val Thr Phe Leu Ile Thr Arg Leu Thr Gly Pro
 65 70 75
 Ala Leu Gln Trp Val Ile Pro Tyr Ile Lys Lys Glu Ser Pro Leu
 80 85 90
 Leu Asn Asp Tyr Arg Gly Phe Leu Ala Glu Met Lys Arg Val Phe
 95 100 105
 Gly Trp Glu Glu Asp Glu Asp Phe
 110

<210> 24

<211> 308

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 035102CD1

<400> 24

Met Leu Gln Thr Pro Glu Ser Arg Gly Leu Pro Val Pro Gln Ala
 1 5 10 15
 Glu Gly Glu Lys Asp Gly Gly His Asp Gly Glu Thr Arg Ala Pro
 20 25 30
 Thr Ala Ser Gln Glu Arg Pro Lys Glu Glu Leu Gly Ala Gly Arg
 35 40 45
 Glu Glu Gly Ala Ala Glu Pro Ala Leu Thr Arg Lys Gly Ala Arg
 50 55 60
 Ala Leu Ala Ala Lys Ser Leu Ala Arg Arg Arg Ala Tyr Arg Arg

WO 01/07471

PCT/US00/19948

				65					70					75
Leu	Asn	Arg	Thr	Val	Ala	Glu	Leu	Val	Gln	Phe	Leu	Leu	Val	Lys
				80					85					90
Asp	Lys	Lys	Lys	Ser	Pro	Ile	Thr	Arg	Ser	Glu	Met	Val	Lys	Tyr
				95					100					105
Val	Ile	Gly	Asp	Leu	Lys	Ile	Leu	Phe	Pro	Asp	Ile	Ile	Ala	Arg
				110					115					120
Ala	Ala	Glu	His	Leu	Arg	Tyr	Val	Phe	Gly	Phe	Glu	Leu	Lys	Gln
				125					130					135
Phe	Asp	Arg	Lys	His	His	Thr	Tyr	Ile	Leu	Ile	Asn	Lys	Leu	Lys
				140					145					150
Pro	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Leu	Gly	Gly	Asp	Gly
				155					160					165
Pro	Arg	Leu	Gly	Leu	Leu	Met	Met	Ile	Leu	Gly	Leu	Ile	Tyr	Met
				170					175					180
Arg	Gly	Asn	Ser	Ala	Arg	Glu	Ala	Gln	Val	Trp	Glu	Met	Leu	Arg
				185					190					195
Arg	Leu	Gly	Val	Gln	Pro	Ser	Lys	Tyr	His	Phe	Leu	Phe	Gly	Tyr
				200					205					210
Pro	Lys	Arg	Leu	Ile	Met	Glu	Asp	Phe	Val	Gln	Gln	Arg	Tyr	Leu
				215					220					225
Ser	Tyr	Arg	Arg	Val	Pro	His	Thr	Asn	Pro	Pro	Ala	Tyr	Glu	Phe
				230					235					240
Ser	Trp	Gly	Pro	Arg	Ser	Asn	Leu	Glu	Ile	Ser	Lys	Met	Glu	Val
				245					250					255
Leu	Gly	Phe	Val	Ala	Lys	Leu	His	Lys	Lys	Glu	Pro	Gln	His	Trp
				260					265					270
Pro	Val	Gln	Tyr	Arg	Glu	Ala	Leu	Ala	Asp	Glu	Ala	Asp	Arg	Ala
				275					280					285
Arg	Ala	Lys	Ala	Arg	Ala	Glu	Ala	Ser	Met	Arg	Ala	Arg	Ala	Ser
				290					295					300
Ala	Arg	Ala	Gly	Ile	His	Leu	Trp							
				305										

<210> 25

<211> 221

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 259983CD1

<400> 25

Met	Phe	Gly	Phe	His	Lys	Pro	Lys	Met	Tyr	Arg	Ser	Ile	Glu	Gly
1				5					10					15
Cys	Cys	Ile	Cys	Arg	Ala	Lys	Ser	Ser	Ser	Ser	Arg	Phe	Thr	Asp
				20					25					30
Ser	Lys	Arg	Tyr	Glu	Lys	Asp	Phe	Gln	Ser	Cys	Phe	Gly	Leu	His
				35					40					45
Glu	Thr	Arg	Ser	Gly	Asp	Ile	Cys	Asn	Ala	Cys	Val	Leu	Leu	Val
				50					55					60
Lys	Arg	Trp	Lys	Lys	Leu	Pro	Ala	Gly	Ser	Lys	Lys	Asn	Trp	Asn
				65					70					75
His	Val	Val	Asp	Ala	Arg	Ala	Gly	Pro	Ser	Leu	Lys	Thr	Thr	Leu
				80					85					90
Lys	Pro	Lys	Lys	Val	Lys	Thr	Leu	Ser	Gly	Asn	Arg	Ile	Lys	Ser
				95					100					105
Asn	Gln	Ile	Ser	Lys	Leu	Gln	Lys	Glu	Phe	Lys	Arg	His	Asn	Ser
				110					115					120
Asp	Ala	His	Ser	Thr	Thr	Ser	Ser	Ala	Ser	Pro	Ala	Gln	Ser	Pro
				125					130					135
Cys	Tyr	Ser	Asn	Gln	Ser	Asp	Asp	Gly	Ser	Asp	Thr	Glu	Met	Ala
				140					145					150

WO 01/07471

PCT/US00/19948

Ser Gly Ser Asn Arg Thr Pro Val Phe Ser Phe Leu Asp Leu Thr	
	155 160 165
Tyr Trp Lys Arg Gln Lys Ile Cys Cys Gly Ile Ile Tyr Lys Gly	
	170 175 180
Arg Phe Gly Glu Val Leu Ile Asp Thr His Leu Phe Lys Pro Cys	
	185 190 195
Cys Ser Asn Lys Lys Ala Ala Ala Glu Lys Pro Glu Glu Gln Gly	
	200 205 210
Pro Glu Pro Leu Pro Ile Ser Thr Gln Glu Trp	
	215 220

<210> 26

<211> 402

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 926810CD1

<400> 26

Met Ala Ser Ile Ile Ala Arg Val Gly Asn Ser Arg Arg Leu Asn	
1 5 10 15	
Ala Pro Leu Pro Pro Trp Ala His Ser Met Leu Arg Ser Leu Gly	
	20 25 30
Arg Ser Leu Gly Pro Ile Met Ala Ser Met Ala Asp Arg Asn Met	
	35 40 45
Lys Leu Phe Ser Gly Arg Val Val Pro Ala Gln Gly Glu Glu Thr	
	50 55 60
Phe Glu Asn Trp Leu Thr Gln Val Asn Gly Val Leu Pro Asp Trp	
	65 70 75
Asn Met Ser Glu Glu Lys Leu Lys Arg Leu Met Lys Thr Leu	
	80 85 90
Arg Gly Pro Ala Arg Glu Val Met Arg Val Leu Gln Ala Thr Asn	
	95 100 105
Pro Asn Leu Ser Val Ala Asp Phe Leu Arg Ala Met Lys Leu Val	
	110 115 120
Phe Gly Glu Ser Glu Ser Ser Val Thr Ala His Gly Lys Phe Phe	
	125 130 135
Asn Thr Leu Gln Ala Gln Gly Glu Lys Ala Ser Leu Tyr Val Ile	
	140 145 150
Arg Leu Glu Val Gln Leu Gln Asn Ala Ile Gln Ala Gly Ile Ile	
	155 160 165
Ala Glu Lys Asp Ala Asn Arg Thr Arg Leu Gln Gln Leu Leu Leu	
	170 175 180
Gly Gly Glu Leu Ser Arg Asp Leu Arg Leu Arg Leu Lys Asp Phe	
	185 190 195
Leu Arg Met Tyr Ala Asn Glu Gln Glu Arg Leu Pro Asn Phe Leu	
	200 205 210
Glu Leu Ile Arg Met Val Arg Glu Glu Glu Asp Trp Asp Asp Ala	
	215 220 225
Phe Ile Lys Arg Lys Arg Pro Lys Arg Ser Glu Ser Met Val Glu	
	230 235 240
Arg Ala Val Ser Pro Val Ala Phe Gln Gly Ser Pro Pro Ile Val	
	245 250 255
Ile Gly Ser Ala Asp Cys Asn Val Ile Glu Ile Asp Asp Thr Leu	
	260 265 270
Asp Asp Ser Asp Glu Asp Val Ile Leu Val Glu Ser Gln Asp Pro	
	275 280 285
Pro Leu Pro Ser Trp Gly Ala Pro Pro Leu Arg Asp Arg Ala Arg	
	290 295 300
Pro Gln Asp Glu Val Leu Val Ile Asp Ser Pro His Asn Ser Arg	
	305 310 315
Ala Gln Phe Pro Ser Thr Ser Gly Gly Ser Gly Tyr Lys Asn Asn	

WO 01/07471

PCT/US00/19948

	320		325		330
Gly Pro Gly Glu Met Arg Arg Ala Arg Lys Arg Lys His Thr Ile					
	335		340		345
Arg Cys Ser Tyr Cys Gly Glu Glu Gly His Ser Lys Glu Thr Cys					
	350		355		360
Asp Asn Glu Ser Asp Lys Ala Gln Val Phe Glu Asn Leu Ile Ile					
	365		370		375
Thr Leu Gln Glu Leu Thr His Thr Glu Met Glu Arg Ser Arg Val					
	380		385		390
Ala Pro Gly Glu Tyr Asn Asp Phe Ser Glu Pro Leu					
	395		400		

<210> 27

<211> 93

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1398816CD1

<400> 27

Met Ser Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp					
1 5 10 15					
Gln Gly Ser Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val					
20 25 30					
Pro Val Gly Ile Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu					
35 40 45					
Tyr Lys Leu Lys Ser Arg Gly Asn Thr Lys Met Ser Ile His Leu					
50 55 60					
Ile His Met Arg Val Ala Ala Gln Gly Phe Val Val Gly Ala Met					
65 70 75					
Thr Val Gly Met Gly Tyr Ser Met Tyr Arg Glu Phe Trp Ala Lys					
80 85 90					
Pro Lys Pro					

<210> 28

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1496820CD1

<400> 28

Met Asn Arg Glu Asp Arg Asn Val Leu Arg Met Lys Glu Arg Glu					
1 5 10 15					
Arg Arg Asn Gln Glu Ile Gln Gln Gly Glu Asp Ala Phe Pro Pro					
20 25 30					
Ser Ser Pro Leu Phe Ala Glu Pro Tyr Lys Val Thr Ser Lys Glu					
35 40 45					
Asp Lys Leu Ser Ser Arg Ile Gln Ser Met Leu Gly Asn Tyr Asp					
50 55 60					
Glu Met Lys Asp Phe Ile Gly Asp Arg Ser Ile Pro Lys Leu Val					
65 70 75					
Ala Ile Pro Lys Pro Thr Val Pro Pro Ser Ala Asp Glu Lys Ser					
80 85 90					
Asn Pro Asn Phe Phe Glu Gln Arg His Gly Gly Ser His Gln Ser					
95 100 105					
Ser Lys Trp Thr Pro Val Gly Pro Ala Pro Ser Thr Ser Gln Ser					
110 115 120					
Gln Lys Arg Ser Ser Gly Leu Gln Ser Gly His Ser Ser Gln Arg					
125 130 135					

WO 01/07471

PCT/US00/19948

Thr	Ser	Ala	Gly	Ser	Ser	Ser	Gly	Thr	Asn	Ser	Ser	Gly	Gln	Arg	
				140					145					150	
His	Asp	Arg	Glu	Ser	Tyr	Asn	Asn	Ser	Gly	Ser	Ser	Ser	Arg	Lys	
				155					160					165	
Lys	Gly	Gln	His	Gly	Ser	Glu	His	Ser	Lys	Ser	Arg	Ser	Ser	Ser	
				170					175					180	
Pro	Gly	Lys	Pro	Gln	Ala	Val	Ser	Ser	Leu	Asn	Ser	Ser	His	Ser	
				185					190					195	
Arg	Ser	His	Gly	Asn	Asp	His	His	Ser	Lys	Glu	His	Gln	Arg	Ser	
				200					205					210	
Lys	Ser	Pro	Arg	Asp	Pro	Asp	Ala	Asn	Trp	Asp	Ser	Pro	Ser	Arg	
				215					220					225	
Val	Pro	Phe	Ser	Ser	Gly	Gln	His	Ser	Thr	Gln	Ser	Phe	Pro	Pro	
				230					235					240	
Ser	Leu	Met	Ser	Lys	Ser	Asn	Ser	Met	Leu	Gln	Lys	Pro	Thr	Ala	
				245					250					255	
Tyr	Val	Arg	Pro	Met	Asp	Gly	Gln	Glu	Ser	Met	Glu	Pro	Lys	Leu	
				260					265					270	
Ser	Ser	Glu	His	Tyr	Ser	Ser	Gln	Ser	His	Gly	Asn	Ser	Met	Thr	
				275					280					285	
Glu	Leu	Lys	Pro	Ser	Ser	Lys	Ala	His	Leu	Thr	Lys	Leu	Lys	Ile	
				290					295					300	
Pro	Ser	Gln	Pro	Leu	Asp	Ala	Ser	Ala	Ser	Gly	Asp	Val	Ser	Cys	
				305					310					315	
Val	Asp	Glu	Ile	Leu	Lys	Glu	Met	Thr	His	Ser	Trp	Pro	Pro	Pro	
				320					325					330	
Leu	Thr	Ala	Ile	His	Thr	Pro	Cys	Lys	Thr	Glu	Pro	Ser	Lys	Phe	
				335					340					345	
Pro	Phe	Pro	Thr	Lys	Val	Ser	Lys								
				350											

<210> 29

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1514559CD1

<400> 29

Met	Ser	Glu	Pro	Ala	Gly	Asp	Val	Arg	Gln	Asn	Pro	Cys	Gly	Ser	
1				5					10					15	
Lys	Ala	Cys	Arg	Arg	Leu	Phe	Gly	Pro	Val	Asp	Ser	Glu	Gln	Leu	
				20					25					30	
Ser	Arg	Asp	Cys	Asp	Ala	Leu	Met	Ala	Gly	Cys	Ile	Gln	Glu	Ala	
				35					40					45	
Arg	Glu	Arg	Trp	Asn	Phe	Asp	Phe	Val	Thr	Glu	Thr	Pro	Leu	Glu	
				50					55					60	
Gly	Asp	Phe	Ala	Trp	Glu	Arg	Val	Arg	Gly	Leu	Gly	Leu	Pro	Lys	
				65					70					75	
Leu	Tyr	Leu	Pro	Thr	Trp	Ser	Ala	Gly	Trp	Tyr	Pro	Leu	Glu	Gly	
				80					85					90	
Cys	Gly	Ser	Phe	Pro	Ser	Leu	Ser	Gln	Ala	Val	Met	Lys	Phe	Thr	
				95					100					105	
Pro	Phe	Pro	Gly	His	Ser	Asp	Leu	Asn	Ser	Phe	Ser	Phe	Glu	Lys	
				110					115					120	

<210> 30

<211> 144

<212> PRT

<213> Homo sapiens

<220>

WO 01/07471

PCT/US00/19948

	215		220		225
Asp Asp Lys Gly	Ala Gln Ala Ala Arg	Gly Ser Ser Asn Ala Ser			
	230		235		240
Leu Lys Glu Glu	Glu Cys Lys Glu Pro	Leu Leu Phe His Ser Gly			
	245		250		255
Asp His Tyr Pro	Leu Ser Asp Gly Asp	Trp Ser Pro Leu Glu Thr			
	260		265		270
Thr Tyr Pro Gln	Thr Ala Cys Pro Lys	Ser Asp Ser Glu Leu Glu			
	275		280		285
Val Lys Pro Ala	Glu Ser Leu Leu Arg	Ser Glu Tyr His Met Glu			
	290		295		300
Trp Thr Trp Gly	Gly Phe Pro Glu Ser	Thr Lys Val Ser Lys Arg			
	305		310		315
Glu Arg Ser Asp	His His Pro Arg Thr	Ala Thr Ile Thr Pro Ser			
	320		325		330
Glu Asn Thr His	Phe Arg Val Ile Pro	Ser Glu Asp Asn Leu Ile			
	335		340		345
Ser Glu Val Glu	Lys Asp Ala Ser Met	Glu Asp Thr Val Cys Thr			
	350		355		360
Ile Val Lys Pro	Lys Pro Arg Ala Leu	Gly Thr Gln Met Ser Asp			
	365		370		375
Pro Thr Ser Val	Ala Glu Leu Leu Glu	Pro Pro Leu Glu Ser Thr			
	380		385		390
Gln Ile Ser Ser	Met Leu Asp Ala Asp	His Leu Pro Asn Ala Ala			
	395		400		405
Leu Ala Glu Ala	Pro Ser Glu Ser Lys	Pro Ala Ala Lys Val Asp			
	410		415		420
Ser Pro Ser Lys	Lys Lys Gly Val His	Lys Arg Ile Gln His Gln			
	425		430		435
Gly Pro Asp Asp	Ile Tyr Leu Asp Asp	Leu Lys Gly Leu Glu Pro			
	440		445		450
Glu Val Ala Ala	Leu Tyr Phe Pro Lys	Ser Glu Ser Glu Pro Gly			
	455		460		465
Ser Arg Gln Trp	Pro Glu Ser Asp Thr	Leu Ser Gly Ser Gln Ser			
	470		475		480
Pro Gln Ser Val	Gly Ser Ala Ala Ala	Asp Ser Gly Thr Glu Cys			
	485		490		495
Leu Ser Asp Ser	Ala Met Asp Leu Pro	Asp Val Thr Leu Ser Leu			
	500		505		510
Cys Gly Gly Leu	Ser Glu Asn Gly Lys	Ile Ser Lys Glu Lys Phe			
	515		520		525
Met Glu His Ile	Ile Thr Tyr His Glu	Phe Ala Glu Asn Pro Gly			
	530		535		540
Leu Ile Asp Asn	Pro Asn Leu Val Ile	Arg Ile Tyr Asn Arg Tyr			
	545		550		555
Tyr Asn Trp Ala	Leu Ala Ala Pro Met	Ile Leu Ser Leu Gln Val			
	560		565		570
Phe Gln Lys Ser	Leu Pro Lys Ala Thr	Val Glu Ser Trp Val Lys			
	575		580		585
Asp Lys Met Pro	Lys Lys Ser Gly Arg	Trp Trp Phe Trp Arg Lys			
	590		595		600
Arg Glu Ser Met	Thr Lys Gln Leu Pro	Glu Ser Lys Glu Gly Lys			
	605		610		615
Ser Glu Ala Pro	Pro Ala Ser Asp Leu	Pro Ser Ser Ser Lys Glu			
	620		625		630
Pro Ala Gly Ala	Arg Pro Ala Glu Asn	Asp Ser Ser Ser Asp Glu			
	635		640		645
Gly Ser Gln Glu	Leu Glu Glu Ser Ile	Thr Val Asp Pro Ile Pro			
	650		655		660
Thr Glu Pro Leu	Ser His Gly Ser Thr	Thr Ser Tyr Lys Lys Ser			
	665		670		675
Leu Arg Leu Ser	Ser Asp Gln Ile Ala	Lys Leu Lys Leu His Asp			
	680		685		690

WO 01/07471

PCT/US00/19948

Gly	Pro	Asn	Asp	Val	Val	Phe	Ser	Ile	Thr	Thr	Gln	Tyr	Gln	Gly
				695					700					705
Thr	Cys	Arg	Cys	Ala	Gly	Thr	Ile	Tyr	Leu	Trp	Asn	Trp	Asn	Asp
				710					715					720
Lys	Ile	Ile	Ile	Ser	Asp	Ile	Asp	Gly	Thr	Ile	Thr	Lys	Ser	Asp
				725					730					735
Ala	Leu	Gly	Gln	Ile	Leu	Pro	Gln	Leu	Gly	Lys	Asp	Trp	Thr	His
				740					745					750
Gln	Gly	Ile	Ala	Lys	Leu	Tyr	His	Ser	Ile	Asn	Glu	Asn	Gly	Tyr
				755					760					765
Lys	Phe	Leu	Tyr	Cys	Ser	Ala	Arg	Ala	Ile	Gly	Met	Ala	Asp	Met
				770					775					780
Thr	Arg	Gly	Tyr	Leu	His	Trp	Val	Asn	Asp	Lys	Gly	Thr	Ile	Leu
				785					790					795
Pro	Arg	Gly	Pro	Leu	Met	Leu	Ser	Pro	Ser	Ser	Leu	Phe	Ser	Ala
				800					805					810
Phe	His	Arg	Glu	Val	Ile	Glu	Lys	Lys	Pro	Glu	Lys	Phe	Lys	Ile
				815					820					825
Glu	Cys	Leu	Asn	Asp	Ile	Lys	Asn	Leu	Phe	Ala	Pro	Ser	Lys	Gln
				830					835					840
Pro	Phe	Tyr	Ala	Ala	Phe	Gly	Asn	Arg	Pro	Asn	Asp	Val	Tyr	Ala
				845					850					855
Tyr	Thr	Gln	Val	Gly	Val	Pro	Asp	Cys	Arg	Ile	Phe	Thr	Val	Asn
				860					865					870
Pro	Lys	Gly	Glu	Leu	Ile	Gln	Glu	Arg	Thr	Lys	Gly	Asn	Lys	Ser
				875					880					885
Ser	Tyr	His	Arg	Leu	Ser	Glu	Leu	Val	Glu	His	Val	Phe	Pro	Leu
				890					895					900
Leu	Ser	Lys	Glu	Gln	Asn	Ser	Ala	Phe	Pro	Cys	Pro	Glu	Phe	Ser
				905					910					915
Ser	Phe	Cys	Tyr	Trp	Arg	Asp	Pro	Ile	Pro	Glu	Val	Asp	Leu	Asp
				920					925					930

Asp Leu Ser

<210> 32

<211> 268

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1708229CD1

<400> 32

Met	Leu	Gly	Asp	His	Cys	Ser	Leu	Pro	Glu	Asp	Gln	Ala	Arg	Pro
1				5					10					15
Gly	Gln	Ser	Leu	Gln	Ser	Gly	Leu	Cys	Cys	Lys	Met	Val	Leu	Gln
				20					25					30
Ala	Val	Ser	Lys	Val	Leu	Arg	Lys	Ser	Lys	Ala	Lys	Pro	Asn	Gly
				35					40					45
Lys	Lys	Pro	Ala	Ala	Glu	Glu	Arg	Lys	Ala	Tyr	Leu	Glu	Pro	Glu
				50					55					60
His	Thr	Lys	Ala	Arg	Ile	Thr	Asp	Phe	Gln	Phe	Lys	Glu	Leu	Val
				65					70					75
Val	Leu	Pro	Arg	Glu	Ile	Asp	Leu	Asn	Glu	Trp	Leu	Ala	Ser	Asn
				80					85					90
Thr	Thr	Thr	Phe	Phe	His	His	Ile	Asn	Leu	Gln	Tyr	Ser	Thr	Ile
				95					100					105
Ser	Glu	Phe	Cys	Thr	Gly	Glu	Thr	Cys	Gln	Thr	Met	Ala	Val	Cys
				110					115					120
Asn	Thr	Gln	Tyr	Tyr	Trp	Tyr	Asp	Glu	Arg	Gly	Lys	Lys	Val	Lys
				125					130					135
Cys	Thr	Ala	Pro	Gln	Tyr	Val	Asp	Phe	Val	Met	Ser	Ser	Val	Gln

WO 01/07471

PCT/US00/19948

	140		145		150
Lys Leu Val Thr	Asp Glu Asp Val Phe	Pro Thr Lys Tyr Gly	Arg		
	155		160		165
Glu Phe Pro Ser	Ser Phe Glu Ser Leu	Val Arg Lys Ile Cys	Arg		
	170		175		180
His Leu Phe His	Val Leu Ala His Ile	Tyr Trp Ala His Phe	Lys		
	185		190		195
Glu Thr Leu Ala	Leu Glu Leu His Gly	His Leu Asn Thr Leu	Tyr		
	200		205		210
Val His Phe Ile	Leu Phe Ala Arg Glu	Phe Asn Leu Leu Asp	Pro		
	215		220		225
Lys Glu Thr Ala	Ile Met Asp Asp Leu	Thr Glu Val Leu Cys	Ser		
	230		235		240
Gly Ala Gly Gly	Val His Ser Gly Gly	Ser Gly Asp Gly Ala	Gly		
	245		250		255
Ser Gly Gly Pro	Gly Ala Gln Asn His	Val Lys Glu Arg			
	260		265		

<210> 33'

<211> 337

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1806454CD1

<400> 33

Met Leu Leu Gly	Leu Ala Ala Met Glu	Leu Lys Val Trp Val	Asp		
1	5	10	15		
Gly Ile Gln Arg	Val Val Cys Gly Val	Ser Glu Gln Thr Thr	Cys		
	20	25	30		
Gln Glu Val Val	Ile Ala Leu Ala Gln	Ala Ile Gly Gln Thr	Gly		
	35	40	45		
Arg Phe Val Leu	Val Gln Arg Leu Arg	Glu Lys Glu Arg Gln	Leu		
	50	55	60		
Leu Pro Gln Glu	Cys Pro Val Gly Ala	Gln Ala Thr Cys Gly	Gln		
	65	70	75		
Phe Ala Ser Asp	Val Gln Phe Val Leu	Arg Arg Thr Gly Pro	Ser		
	80	85	90		
Leu Ala Gly Arg	Pro Ser Ser Asp Ser	Cys Pro Pro Pro Glu	Arg		
	95	100	105		
Cys Leu Ile Arg	Ala Ser Leu Pro Val	Lys Pro Arg Ala Ala	Leu		
	110	115	120		
Gly Cys Glu Pro	Arg Lys Thr Leu Thr	Pro Glu Pro Ala Pro	Ser		
	125	130	135		
Leu Ser Arg Pro	Gly Pro Ala Ala Pro	Val Thr Pro Thr Pro	Gly		
	140	145	150		
Cys Cys Thr Asp	Leu Arg Gly Leu Glu	Leu Arg Val Gln Arg	Asn		
	155	160	165		
Ala Glu Glu Leu	Gly His Glu Ala Phe	Trp Glu Gln Glu Leu	Arg		
	170	175	180		
Arg Glu Gln Ala	Arg Glu Arg Glu Gly	Gln Ala Arg Leu Gln	Ala		
	185	190	195		
Leu Ser Ala Ala	Thr Ala Glu His Ala	Ala Arg Leu Gln Ala	Leu		
	200	205	210		
Asp Ala Gln Ala	Arg Ala Leu Glu Ala	Glu Leu Gln Leu Ala	Ala		
	215	220	225		
Glu Ala Pro Gly	Pro Pro Ser Pro Met	Ala Ser Ala Thr Glu	Arg		
	230	235	240		
Leu His Gln Asp	Leu Ala Val Gln Glu	Arg Gln Ser Ala Glu	Val		
	245	250	255		
Gln Gly Ser Leu	Ala Leu Val Ser Arg	Ala Leu Glu Ala Ala	Glu		
	260	265	270		

WO 01/07471

PCT/US00/19948

Arg	Ala	Leu	Gln	Ala	Gln	Ala	Gln	Glu	Leu	Glu	Glu	Leu	Asn	Arg
				275					280					285
Glu	Leu	Arg	Gln	Cys	Asn	Leu	Gln	Gln	Phe	Ile	Gln	Gln	Thr	Gly
				290					295					300
Ala	Ala	Leu	Pro	Pro	Pro	Pro	Arg	Pro	Asp	Arg	Gly	Pro	Pro	Gly
				305					310					315
Thr	Gln	Val	Gly	Val	Val	Leu	Gly	Gly	Gly	Trp	Glu	Val	Arg	Thr
				320					325					330
Trp	Pro	Ser	Pro	Thr	Pro	Ser								
				335										

<210> 34

<211> 565

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1806850CD1

<400> 34

Met	Lys	Glu	Glu	Glu	Glu	Val	Phe	Gln	Pro	Met	Leu	Met	Glu	Tyr
1				5					10					15
Phe	Thr	Tyr	Glu	Glu	Leu	Lys	Tyr	Ile	Lys	Lys	Lys	Val	Ile	Ala
				20					25					30
Gln	His	Cys	Ser	Gln	Lys	Asp	Thr	Ala	Glu	Leu	Leu	Arg	Gly	Leu
				35					40					45
Ser	Leu	Trp	Asn	His	Ala	Glu	Glu	Arg	Gln	Lys	Phe	Phe	Lys	Tyr
				50					55					60
Ser	Val	Asp	Glu	Lys	Ser	Asp	Lys	Glu	Ala	Glu	Val	Ser	Glu	His
				65					70					75
Ser	Thr	Gly	Ile	Thr	His	Leu	Pro	Pro	Glu	Val	Met	Leu	Ser	Ile
				80					85					90
Phe	Ser	Tyr	Leu	Asn	Pro	Gln	Glu	Leu	Cys	Arg	Cys	Ser	Gln	Val
				95					100					105
Ser	Met	Lys	Trp	Ser	Gln	Leu	Thr	Lys	Thr	Gly	Ser	Leu	Trp	Lys
				110					115					120
His	Leu	Tyr	Pro	Val	His	Trp	Ala	Arg	Gly	Asp	Trp	Tyr	Ser	Gly
				125					130					135
Pro	Ala	Thr	Glu	Leu	Asp	Thr	Glu	Pro	Asp	Asp	Glu	Trp	Val	Lys
				140					145					150
Asn	Arg	Lys	Asp	Glu	Ser	Arg	Ala	Phe	His	Glu	Trp	Asp	Glu	Asp
				155					160					165
Ala	Asp	Ile	Asp	Glu	Ser	Glu	Glu	Ser	Ala	Glu	Glu	Ser	Ile	Ala
				170					175					180
Ile	Ser	Ile	Ala	Gln	Met	Glu	Lys	Arg	Leu	Leu	His	Gly	Leu	Ile
				185					190					195
His	Asn	Val	Leu	Pro	Tyr	Val	Gly	Thr	Ser	Val	Lys	Thr	Leu	Val
				200					205					210
Leu	Ala	Tyr	Ser	Ser	Ala	Val	Ser	Ser	Lys	Met	Val	Arg	Gln	Ile
				215					220					225
Leu	Glu	Leu	Cys	Pro	Asn	Leu	Glu	His	Leu	Asp	Leu	Thr	Gln	Thr
				230					235					240
Asp	Ile	Ser	Asp	Ser	Ala	Phe	Asp	Ser	Trp	Ser	Trp	Leu	Gly	Cys
				245					250					255
Cys	Gln	Ser	Leu	Arg	His	Leu	Asp	Leu	Ser	Gly	Cys	Glu	Lys	Ile
				260					265					270
Thr	Asp	Val	Ala	Leu	Glu	Lys	Ile	Ser	Arg	Ala	Leu	Gly	Ile	Leu
				275					280					285
Thr	Ser	His	Gln	Ser	Gly	Phe	Leu	Lys	Thr	Ser	Thr	Ser	Lys	Ile
				290					295					300
Thr	Ser	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Ile	Thr	Met	Gln	Ser	Thr
				305					310					315
Lys	Gln	Tyr	Ala	Cys	Leu	His	Asp	Leu	Thr	Asn	Lys	Gly	Ile	Gly

WO 01/07471

PCT/US00/19948

	320		325		330
Glu Glu Ile Asp	Asn Glu His Pro Trp	Thr Lys Pro Val Ser	Ser		
	335		340		345
Glu Asn Phe Thr	Ser Pro Tyr Val Trp	Met Leu Asp Ala Glu	Asp		
	350		355		360
Leu Ala Asp Ile	Glu Asp Thr Val Glu	Trp Arg His Arg Asn	Val		
	365		370		375
Glu Ser Leu Cys	Val Met Glu Thr Ala	Ser Asn Phe Ser Cys	Ser		
	380		385		390
Thr Ser Gly Cys	Phe Ser Lys Asp Ile	Val Gly Leu Arg Thr	Ser		
	395		400		405
Val Cys Trp Gln	Gln His Cys Ala Ser	Pro Ala Phe Ala Tyr	Cys		
	410		415		420
Gly His Ser Phe	Cys Cys Thr Gly Thr	Ala Leu Arg Thr Met	Ser		
	425		430		435
Ser Leu Pro Glu	Ser Ser Ala Met Cys	Arg Lys Ala Ala Arg	Thr		
	440		445		450
Arg Leu Pro Arg	Gly Lys Asp Leu Ile	Tyr Phe Gly Ser Glu	Lys		
	455		460		465
Ser Asp Gln Glu	Thr Gly Arg Val Leu	Leu Phe Leu Ser Leu	Ser		
	470		475		480
Gly Cys Tyr Gln	Ile Thr Asp His Gly	Leu Arg Val Leu Thr	Leu		
	485		490		495
Gly Gly Gly Leu	Pro Tyr Leu Glu His	Leu Asn Leu Ser Gly	Cys		
	500		505		510
Leu Thr Ile Thr	Gly Ala Gly Leu Gln	Asp Leu Val Ser Ala	Cys		
	515		520		525
Pro Ser Leu Asn	Asp Glu Tyr Phe Tyr	Tyr Cys Asp Asn Ile	Asn		
	530		535		540
Gly Pro His Ala	Asp Thr Ala Ser Gly	Cys Gln Asn Leu Gln	Cys		
	545		550		555
Gly Phe Arg Ala	Cys Cys Arg Ser Gly	Glu			
	560		565		

<210> 35

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1851534CD1

<400> 35

Met Asp Phe Ser	Phe Ser Phe Met Gln Gly	Ile Met Gly Asn Thr	
1	5	10	15
Ile Gln Gln Pro	Pro Gln Leu Ile Asp	Ser Ala Asn Ile Arg	Gln
	20	25	30
Glu Asp Ala Phe	Asp Asn Asn Ser Asp	Ile Ala Glu Asp Gly	Gly
	35	40	45
Gln Thr Pro Tyr	Glu Ala Thr Leu Gln	Gln Gly Phe Gln Tyr	Pro
	50	55	60
Ala Thr Thr Glu	Asp Leu Pro Pro Leu	Thr Asn Gly Tyr Pro	Ser
	65	70	75
Ser Ile Ser Val	Tyr Glu Thr Gln Thr	Lys Tyr Gln Ser Tyr	Asn
	80	85	90
Gln Tyr Pro Asn	Gly Ser Ala Asn Gly	Phe Gly Ala Val Arg	Asn
	95	100	105
Phe Ser Pro Thr	Asp Tyr Tyr His Ser	Glu Ile Pro Asn Thr	Arg
	110	115	120
Pro His Glu Ile	Leu Glu Lys Pro Ser	Pro Pro Gln Pro Pro	Pro
	125	130	135
Pro Pro Ser Val	Pro Gln Thr Val Ile	Pro Lys Lys Thr Gly	Ser
	140	145	150

WO 01/07471

PCT/US00/19948

Pro	Glu	Ile	Lys	Leu	Lys	Ile	Thr	Lys	Thr	Ile	Gln	Asn	Gly	Arg
				155					160					165
Glu	Leu	Phe	Glu	Ser	Ser	Leu	Cys	Gly	Asp	Leu	Leu	Asn	Glu	Val
				170					175					180
Gln	Ala	Ser	Glu	His	Thr	Lys	Ser	Lys	His	Glu	Ser	Arg	Lys	Glu
				185					190					195
Lys	Arg	Lys	Lys	Ser	Asn	Lys	His	Asp	Ser	Ser	Arg	Ser	Glu	Glu
				200					205					210
Arg	Lys	Ser	His	Lys	Ile	Pro	Lys	Leu	Glu	Pro	Glu	Glu	Gln	Asn
				215					220					225
Met	Thr	Lys												

<210> 36

<211> 495

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1868749CD1

<400> 36

Met	Lys	Gly	Met	Lys	Val	Glu	Val	Leu	Asn	Ser	Asp	Ala	Val	Leu
1				5					10					15
Pro	Ser	Arg	Val	Tyr	Trp	Ile	Ala	Ser	Val	Ile	Gln	Thr	Ala	Gly
				20					25					30
Tyr	Arg	Val	Leu	Leu	Arg	Tyr	Glu	Gly	Phe	Glu	Asn	Asp	Ala	Ser
				35					40					45
His	Asp	Phe	Trp	Cys	Asn	Leu	Gly	Thr	Val	Asp	Val	His	Pro	Ile
				50					55					60
Gly	Trp	Cys	Ala	Ile	Asn	Ser	Lys	Ile	Leu	Val	Pro	Pro	Arg	Thr
				65					70					75
Ile	His	Ala	Lys	Phe	Thr	Asp	Trp	Lys	Gly	Tyr	Leu	Met	Lys	Arg
				80					85					90
Leu	Val	Gly	Ser	Arg	Thr	Leu	Pro	Val	Asp	Phe	His	Ile	Lys	Met
				95					100					105
Val	Glu	Ser	Met	Lys	Tyr	Pro	Phe	Arg	Gln	Gly	Met	Arg	Leu	Glu
				110					115					120
Val	Val	Asp	Lys	Ser	Gln	Val	Ser	Arg	Thr	Arg	Met	Ala	Val	Val
				125					130					135
Asp	Thr	Val	Ile	Gly	Gly	Arg	Leu	Arg	Leu	Leu	Tyr	Glu	Asp	Gly
				140					145					150
Asp	Ser	Asp	Asp	Asp	Phe	Trp	Cys	His	Met	Trp	Ser	Pro	Leu	Ile
				155					160					165
His	Pro	Val	Gly	Trp	Ser	Arg	Arg	Val	Gly	His	Gly	Ile	Lys	Met
				170					175					180
Ser	Glu	Arg	Arg	Ser	Asp	Met	Ala	His	His	Pro	Thr	Phe	Arg	Lys
				185					190					195
Ile	Tyr	Cys	Asp	Ala	Val	Pro	Tyr	Leu	Phe	Lys	Lys	Val	Arg	Ala
				200					205					210
Val	Tyr	Thr	Glu	Gly	Gly	Trp	Phe	Glu	Glu	Gly	Met	Lys	Leu	Glu
				215					220					225
Ala	Ile	Asp	Pro	Leu	Asn	Leu	Gly	Asn	Ile	Cys	Val	Ala	Thr	Val
				230					235					240
Cys	Lys	Val	Leu	Leu	Asp	Gly	Tyr	Leu	Met	Ile	Cys	Val	Asp	Gly
				245					250					255
Gly	Pro	Ser	Thr	Asp	Gly	Leu	Asp	Trp	Phe	Cys	Tyr	His	Ala	Ser
				260					265					270
Ser	His	Ala	Ile	Phe	Pro	Ala	Thr	Phe	Cys	Gln	Lys	Asn	Asp	Ile
				275					280					285
Glu	Leu	Thr	Pro	Pro	Lys	Gly	Tyr	Glu	Ala	Gln	Thr	Phe	Asn	Trp
				290					295					300
Glu	Asn	Tyr	Leu	Glu	Lys	Thr	Lys	Ser	Lys	Ala	Ala	Pro	Ser	Arg

WO 01/07471

PCT/US00/19948

	305		310		315
Leu Phe Asn Met	Asp Cys Pro Asn His	Gly Phe Lys Val Gly	Met		
	320		325		330
Lys Leu Glu Ala	Val Asp Leu Met Glu	Pro Arg Leu Ile Cys	Val		
	335		340		345
Ala Thr Val Lys	Arg Val Val His Arg	Leu Leu Ser Ile His	Phe		
	350		355		360
Asp Gly Trp Asp	Ser Glu Tyr Asp Gln	Trp Val Asp Cys Glu	Ser		
	365		370		375
Pro Asp Ile Tyr	Pro Val Gly Trp Cys	Glu Leu Thr Gly Tyr	Gln		
	380		385		390
Leu Gln Pro Pro	Val Ala Ala Glu Pro	Ala Thr Pro Leu Lys	Ala		
	395		400		405
Lys Glu Ala Thr	Lys Lys Lys Lys Lys	Gln Phe Gly Lys Lys	Arg		
	410		415		420
Lys Arg Ile Pro	Pro Thr Lys Thr Arg	Pro Leu Arg Gln Gly	Ser		
	425		430		435
Lys Lys Pro Leu	Leu Glu Asp Asp Pro	Gln Gly Ala Arg Lys	Ile		
	440		445		450
Ser Ser Glu Pro	Val Pro Gly Glu Ile	Ile Ala Val Arg Val	Lys		
	455		460		465
Glu Glu His Leu	Asp Val Ala Ser Pro	Asp Lys Ala Ser Ser	Pro		
	470		475		480
Glu Leu Pro Val	Ser Val Glu Asn Ile	Lys Gln Glu Thr Asp	Asp		
	485		490		495

<210> 37

<211> 1336

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1980010CD1

<400> 37

Met Val Asp Gln Leu	Glu Gln Ile Leu	Ser Val Ser Glu Leu	Leu		
1	5	10	15		
Glu Lys His Gly Leu	Glu Lys Pro Ile	Ser Phe Val Lys Asn	Thr		
	20	25	30		
Gln Ser Ser Ser Glu	Glu Ala Arg Lys	Leu Met Val Arg Leu	Thr		
	35	40	45		
Arg His Thr Gly Arg	Lys Gln Pro Pro	Val Ser Glu Ser His	Trp		
	50	55	60		
Arg Thr Leu Leu Gln	Asp Met Leu Thr	Met Gln Gln Asn Val	Tyr		
	65	70	75		
Thr Cys Leu Asp Ser	Asp Ala Cys Tyr	Glu Ile Phe Thr Glu	Ser		
	80	85	90		
Leu Leu Cys Ser Ser	Arg Leu Glu Asn	Ile His Leu Ala Gly	Gln		
	95	100	105		
Met Met His Cys Ser	Ala Cys Ser Glu	Asn Pro Pro Ala Gly	Ile		
	110	115	120		
Ala His Lys Gly Asn	Pro His Tyr Arg	Val Ser Tyr Glu Lys	Ser		
	125	130	135		
Ile Asp Leu Val Leu	Ala Ala Ser Arg	Glu Tyr Phe Asn Ser	Ser		
	140	145	150		
Thr Asn Leu Thr Asp	Ser Cys Met Asp	Leu Ala Arg Cys Cys	Leu		
	155	160	165		
Gln Leu Ile Thr Asp	Arg Pro Pro Ala	Ile Gln Glu Glu Leu	Asp		
	170	175	180		
Leu Ile Gln Ala Val	Gly Cys Leu Glu	Glu Phe Gly Val Lys	Ile		
	185	190	195		
Leu Pro Leu Gln Val	Arg Leu Cys Pro	Asp Arg Ile Ser Leu	Ile		

WO 01/07471

PCT/US00/19948

	200		205		210
Lys Glu Cys Ile	Ser Gln Ser Pro Thr	Cys Tyr Lys Gln Ser Thr			
	215		220		225
Lys Leu Leu Gly	Leu Ala Glu Leu Leu	Arg Val Ala Gly Glu Asn			
	230		235		240
Pro Glu Glu Arg	Arg Gly Gln Val Leu	Ile Leu Leu Val Glu Gln			
	245		250		255
Ala Leu Arg Phe	His Asp Tyr Lys Ala	Ala Ser Met His Cys Gln			
	260		265		270
Glu Leu Met Ala	Thr Gly Tyr Pro Lys	Ser Trp Asp Val Cys Ser			
	275		280		285
Gln Leu Gly Gln	Ser Glu Gly Tyr Gln	Asp Leu Ala Thr Arg Gln			
	290		295		300
Glu Leu Met Ala	Phe Ala Leu Thr His	Cys Pro Pro Ser Ser Ile			
	305		310		315
Glu Leu Leu Leu	Ala Ala Ser Ser Ser	Leu Gln Thr Glu Ile Leu			
	320		325		330
Tyr Gln Arg Val	Asn Phe Gln Ile His	His Glu Gly Gly Glu Asn			
	335		340		345
Ile Ser Ala Ser	Pro Leu Thr Ser Lys	Ala Val Gln Glu Asp Glu			
	350		355		360
Val Gly Val Pro	Gly Ser Asn Ser Ala	Asp Leu Leu Arg Trp Thr			
	365		370		375
Thr Ala Thr Thr	Met Lys Val Leu Ser	Asn Thr Thr Thr Thr Thr			
	380		385		390
Lys Ala Val Leu	Gln Ala Val Ser Asp	Gly Gln Trp Trp Lys Lys			
	395		400		405
Ser Leu Thr Tyr	Leu Arg Pro Leu Gln	Gly Gln Lys Cys Gly Gly			
	410		415		420
Ala Tyr Gln Ile	Gly Thr Thr Ala Asn	Glu Asp Leu Glu Lys Gln			
	425		430		435
Gly Cys His Pro	Phe Tyr Glu Ser Val	Ile Ser Asn Pro Phe Val			
	440		445		450
Ala Glu Ser Glu	Gly Thr Tyr Asp Thr	Tyr Gln His Val Pro Val			
	455		460		465
Glu Ser Phe Ala	Glu Val Leu Leu Arg	Thr Gly Lys Leu Ala Glu			
	470		475		480
Ala Lys Asn Lys	Gly Glu Val Phe Pro	Thr Thr Glu Val Leu Leu			
	485		490		495
Gln Leu Ala Ser	Glu Ala Leu Pro Asn	Asp Met Thr Leu Ala Leu			
	500		505		510
Ala Tyr Leu Leu	Ala Leu Pro Gln Val	Leu Asp Ala Asn Arg Cys			
	515		520		525
Phe Glu Lys Gln	Ser Pro Ser Ala Leu	Ser Leu Gln Leu Ala Ala			
	530		535		540
Tyr Tyr Tyr Ser	Leu Gln Ile Tyr Ala	Arg Leu Ala Pro Cys Phe			
	545		550		555
Arg Asp Lys Cys	His Pro Leu Tyr Arg	Ala Asp Pro Lys Glu Leu			
	560		565		570
Ile Lys Met Val	Thr Arg His Val Thr	Arg His Glu His Glu Ala			
	575		580		585
Trp Pro Glu Asp	Leu Ile Ser Leu Thr	Lys Gln Leu His Cys Tyr			
	590		595		600
Asn Glu Arg Leu	Leu Asp Phe Thr Gln	Ala Gln Ile Leu Gln Gly			
	605		610		615
Leu Arg Lys Gly	Val Asp Val Gln Arg	Phe Thr Ala Asp Asp Gln			
	620		625		630
Tyr Lys Arg Glu	Thr Ile Leu Gly Leu	Ala Glu Thr Leu Glu Glu			
	635		640		645
Ser Val Tyr Ser	Ile Ala Ile Ser Leu	Ala Gln Arg Tyr Ser Val			
	650		655		660
Ser Arg Trp Glu	Val Phe Met Thr His	Leu Glu Phe Leu Phe Thr			
	665		670		675

WO 01/07471

PCT/US00/19948

Asp	Ser	Gly	Leu	Ser	Thr	Leu	Glu	Ile	Glu	Asn	Arg	Ala	Gln	Asp
				680					685					690
Leu	His	Leu	Phe	Glu	Thr	Leu	Lys	Thr	Asp	Pro	Glu	Ala	Phe	His
				695					700					705
Gln	His	Met	Val	Lys	Tyr	Ile	Tyr	Pro	Thr	Ile	Gly	Gly	Phe	Asp
				710					715					720
His	Glu	Arg	Leu	Gln	Tyr	Tyr	Phe	Thr	Leu	Leu	Glu	Asn	Cys	Gly
				725					730					735
Cys	Ala	Asp	Leu	Gly	Asn	Cys	Ala	Ile	Lys	Pro	Glu	Thr	His	Ile
				740					745					750
Arg	Leu	Leu	Lys	Lys	Phe	Lys	Val	Val	Ala	Ser	Gly	Leu	Asn	Tyr
				755					760					765
Lys	Lys	Leu	Thr	Asp	Glu	Asn	Met	Ser	Pro	Leu	Glu	Ala	Leu	Glu
				770					775					780
Pro	Val	Leu	Ser	Ser	Gln	Asn	Ile	Leu	Ser	Ile	Ser	Lys	Leu	Val
				785					790					795
Pro	Lys	Ile	Pro	Glu	Lys	Asp	Gly	Gln	Met	Leu	Ser	Pro	Ser	Ser
				800					805					810
Leu	Tyr	Thr	Ile	Trp	Leu	Gln	Lys	Leu	Phe	Trp	Thr	Gly	Asp	Pro
				815					820					825
His	Leu	Ile	Lys	Gln	Val	Pro	Gly	Ser	Ser	Pro	Glu	Trp	Leu	His
				830					835					840
Ala	Tyr	Asp	Val	Cys	Met	Lys	Tyr	Phe	Asp	Arg	Leu	His	Pro	Gly
				845					850					855
Asp	Leu	Ile	Thr	Val	Val	Asp	Ala	Val	Thr	Phe	Ser	Pro	Lys	Ala
				860					865					870
Val	Thr	Lys	Leu	Ser	Val	Glu	Ala	Arg	Lys	Glu	Met	Thr	Arg	Lys
				875					880					885
Ala	Ile	Lys	Thr	Val	Lys	His	Phe	Ile	Glu	Lys	Pro	Arg	Lys	Arg
				890					895					900
Asn	Ser	Glu	Asp	Glu	Ala	Gln	Glu	Ala	Lys	Asp	Ser	Lys	Val	Thr
				905					910					915
Tyr	Ala	Asp	Thr	Leu	Asn	His	Leu	Glu	Lys	Ser	Leu	Ala	His	Leu
				920					925					930
Glu	Thr	Leu	Ser	His	Ser	Phe	Ile	Leu	Ser	Leu	Lys	Asn	Ser	Glu
				935					940					945
Gln	Glu	Thr	Leu	Gln	Lys	Tyr	Ser	His	Leu	Tyr	Asp	Leu	Ser	Arg
				950					955					960
Ser	Glu	Lys	Glu	Lys	Leu	His	Asp	Glu	Ala	Val	Ala	Ile	Cys	Leu
				965					970					975
Asp	Gly	Gln	Pro	Leu	Ala	Met	Ile	Gln	Gln	Leu	Leu	Glu	Val	Ala
				980					985					990
Val	Gly	Pro	Leu	Asp	Ile	Ser	Pro	Lys	Asp	Ile	Val	Gln	Ser	Ala
				995					1000					1005
Ile	Met	Lys	Ile	Ile	Ser	Ala	Leu	Ser	Gly	Gly	Ser	Ala	Asp	Leu
				1010					1015					1020
Gly	Gly	Pro	Arg	Asp	Pro	Leu	Lys	Val	Leu	Glu	Gly	Val	Val	Ala
				1025					1030					1035
Ala	Val	His	Ala	Ser	Val	Asp	Lys	Gly	Glu	Glu	Leu	Val	Ser	Pro
				1040					1045					1050
Glu	Asp	Leu	Leu	Glu	Trp	Leu	Arg	Pro	Phe	Cys	Ala	Asp	Asp	Ala
				1055					1060					1065
Trp	Pro	Val	Arg	Pro	Arg	Ile	His	Val	Leu	Gln	Ile	Leu	Gly	Gln
				1070					1075					1080
Ser	Phe	His	Leu	Thr	Glu	Glu	Asp	Ser	Lys	Leu	Leu	Val	Phe	Phe
				1085					1090					1095
Arg	Thr	Glu	Ala	Ile	Leu	Lys	Ala	Ser	Trp	Pro	Gln	Arg	Gln	Val
				1100					1105					1110
Asp	Ile	Ala	Asp	Ile	Glu	Asn	Glu	Glu	Asn	Arg	Tyr	Cys	Leu	Phe
				1115					1120					1125
Met	Glu	Leu	Leu	Glu	Ser	Ser	His	His	Glu	Ala	Glu	Phe	Gln	His
				1130					1135					1140
Leu	Val	Leu	Leu	Leu	Gln	Ala	Trp	Pro	Pro	Met	Lys	Ser	Glu	Tyr

WO 01/07471

PCT/US00/19948

Val	Glu	Leu	Ile	His	Pro	Ser	Gln	Asp	Glu	Asp	Arg	Gln	Ser	Asn
				200					205					210
Ala	Ser	Gln	Thr	Leu	Cys	Asp	Ile	Val	Arg	Leu	Gly	Arg	Asp	Gln
				215					220					225
Gly	Ser	Gln	Leu	Gln	Glu	Ala	Leu	Glu	Pro	Asp	Pro	Leu	Leu	Thr
				230					235					240
Ala	Leu	Glu	Ser	Arg	Gln	Asp	Cys	Val	Glu	Gln	Leu	Leu	Lys	Asn
				245					250					255
Met	Phe	Asp	Gly	Asp	Arg	Thr	Glu	Ser	Cys	Leu	Val	Ser	Gly	Thr
				260					265					270
Gln	Val	Leu	Leu	Thr	Leu	Leu	Glu	Thr	Arg	Arg	Val	Gly	Thr	Glu
				275					280					285
Gly	Leu	Val	Asp	Ser	Phe	Ser	Gln	Gly	Leu	Glu	Arg	Ser	Tyr	Ala
				290					295					300
Val	Ser	Ser	Ser	Val	Leu	His	Gly	Ile	Glu	Pro	Arg	Leu	Lys	Asp
				305					310					315
Phe	His	Gln	Leu	Leu	Leu	Asn	Pro	Pro	Lys	Lys	Lys	Ala	Ile	Leu
				320					325					330
Thr	Thr	Ile	Gly	Val	Leu	Glu	Glu	Pro	Leu	Gly	Asn	Ala	Arg	Leu
				335					340					345
His	Gly	Ala	Arg	Leu	Met	Ala	Ala	Leu	Leu	His	Thr	Asn	Thr	Pro
				350					355					360
Ser	Ile	Asn	Gln	Glu	Leu	Cys	Arg	Leu	Asn	Thr	Met	Asp	Leu	Leu
				365					370					375
Leu	Asp	Leu	Phe	Phe	Lys	Tyr	Thr	Trp	Asn	Asn	Phe	Leu	His	Phe
				380					385					390
Gln	Val	Glu	Leu	Cys	Ile	Ala	Ala	Ile	Leu	Ser	His	Ala	Ala	Arg
				395					400					405
Glu	Glu	Arg	Thr	Glu	Ala	Ser	Gly	Ser	Glu	Ser	Arg	Val	Glu	Pro
				410					415					420
Pro	His	Glu	Asn	Gly	Asn	Arg	Ser	Leu	Glu	Thr	Pro	Gln	Pro	Ala
				425					430					435
Ala	Ser	Leu	Pro	Asp	Asn	Thr	Met	Val	Thr	His	Leu	Phe	Gln	Lys
				440					445					450
Cys	Cys	Leu	Val	Gln	Arg	Ile	Leu	Glu	Ala	Trp	Glu	Ala	Asn	Asp
				455					460					465
His	Thr	Gln	Ala	Ala	Gly	Gly	Met	Arg	Arg	Gly	Asn	Met	Gly	His
				470					475					480
Leu	Thr	Arg	Ile	Ala	Asn	Ala	Val	Val	Gln	Asn	Leu	Glu	Arg	Gly
				485					490					495
Pro	Val	Gln	Thr	His	Ile	Ser	Glu	Val	Ile	Arg	Gly	Leu	Pro	Ala
				500					505					510
Asp	Cys	Arg	Gly	Arg	Trp	Glu	Ser	Phe	Val	Glu	Glu	Thr	Leu	Thr
				515					520					525
Glu	Thr	Asn	Arg	Arg	Asn	Thr	Val	Asp	Leu	Ala	Phe	Ser	Asp	Tyr
				530					535					540
Gln	Ile	Gln	Gln	Met	Thr	Ala	Asn	Phe	Val	Asp	Gln	Phe	Gly	Phe
				545					550					555
Asn	Asp	Glu	Glu	Phe	Ala	Asp	Gln	Asp	Asp	Asn	Ile	Asn	Ala	Pro
				560					565					570
Phe	Asp	Arg	Ile	Ala	Glu	Ile	Asn	Phe	Asn	Ile	Asp	Ala	Asp	Glu
				575					580					585
Asp	Ser	Pro	Ser	Ala	Ala	Leu	Phe	Glu	Ala	Cys	Cys	Ser	Asp	Arg
				590					595					600
Ile	Gln	Pro	Phe	Asp	Asp	Asp	Glu	Asp	Glu	Asp	Ile	Trp	Glu	Asp
				605					610					615
Ser	Asp	Thr	Arg	Cys	Ala	Ala	Arg	Val	Met	Ala	Arg	Pro	Arg	Phe
				620					625					630
Gly	Ala	Pro	His	Ala	Ser	Glu	Ser	Cys	Ser	Lys	Asn	Gly	Pro	Glu
				635					640					645
Arg	Gly	Gly	Gln	Asp	Gly	Lys	Ala	Ser	Leu	Glu	Ala	His	Arg	Asp
				650					655					660
Ala	Pro	Gly	Ala	Gly	Ala	Pro	Pro	Ala	Pro	Gly	Lys	Lys	Glu	Ala

WO 01/07471

PCT/US00/19948

Pro	Pro	Val	Glu	665	Gly	Asp	Ser	Glu	Ala	670	Gly	Ala	Met	Trp	Thr	675	Ala
Val	Phe	Asp	Glu	680	Pro	Ala	Asn	Ser	Thr	685	Pro	Thr	Ala	Pro	Gly	690	Val
Val	Arg	Asp	Val	695	Gly	Ser	Ser	Val	Trp	700	Ala	Ala	Gly	Thr	Ser	705	Ala
Pro	Glu	Glu	Lys	710	Gly	Trp	Ala	Lys	Phe	715	Thr	Asp	Phe	Gln	Pro	720	Phe
Cys	Cys	Ser	Glu	725	Ser	Gly	Pro	Arg	Cys	730	Ser	Ser	Pro	Val	Asp	735	Thr
Glu	Cys	Ser	His	740	Ala	Glu	Gly	Ser	Arg	745	Ser	Gln	Gly	Pro	Glu	750	Lys
Ala	Phe	Ser	Pro	755	Ala	Ser	Pro	Cys	Ala	760	Trp	Asn	Val	Cys	Val	765	Thr
Arg	Lys	Ala	Pro	770	Leu	Ala	Ser	Asp	Pro	775	Ser	Ser	Ser	Ser	Gly	780	Gly
Ser	His	Ser	Glu	785	Asp	Gly	Asp	Gln	Lys	790	Ala	Ala	Ser	Ala	Met	795	Asp
Ala	Val	Ser	Arg	800	Gly	Pro	Gly	Arg	Glu	805	Ala	Pro	Pro	Leu	Pro	810	Thr
Val	Ala	Arg	Thr	815	Glu	Glu	Ala	Val	Gly	820	Arg	Val	Gly	Cys	Ala	825	Asp
Ser	Arg	Leu	Leu	830	Ser	Pro	Ala	Cys	Pro	835	Ala	Pro	Lys	Glu	Val	840	Thr
Ala	Ala	Pro	Ala	845	Val	Ala	Val	Pro	Pro	850	Glu	Ala	Thr	Val	Ala	855	Ile
Thr	Thr	Ala	Leu	860	Ser	Lys	Ala	Gly	Pro	865	Ala	Ile	Pro	Thr	Pro	870	Ala
Val	Ser	Ser	Ala	875	Leu	Ala	Val	Ala	Val	880	Pro	Leu	Gly	Pro	Ile	885	Met
Ala	Val	Thr	Ala	890	Ala	Pro	Ala	Met	Val	895	Ala	Thr	Leu	Gly	Thr	900	Val
Thr	Lys	Asp	Gly	905	Lys	Thr	Asp	Ala	Pro	910	Pro	Glu	Gly	Ala	Ala	915	Leu
Asn	Gly	Pro	Val	920						925						930	

<210> 39

<211> 515

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2359526CD1

<400> 39

Met	Ala	Ala	Asn	Met	Tyr	Arg	Val	Gly	Asp	Tyr	Val	Tyr	Phe	Glu	
1				5					10					15	
Asn	Ser	Ser	Ser	Asn	Pro	Tyr	Leu	Ile	Arg	Arg	Ile	Glu	Glu	Leu	
				20					25					30	
Asn	Lys	Thr	Ala	Ser	Gly	Asn	Val	Glu	Ala	Lys	Val	Val	Cys	Phe	
				35					40					45	
Tyr	Arg	Arg	Arg	Asp	Ile	Ser	Asn	Thr	Leu	Ile	Met	Leu	Ala	Asp	
				50					55					60	
Lys	His	Ala	Lys	Glu	Ile	Glu	Glu	Glu	Ser	Glu	Thr	Thr	Val	Glu	
				65					70					75	
Ala	Asp	Leu	Thr	Asp	Lys	Gln	Lys	His	Gln	Leu	Lys	His	Arg	Glu	
				80					85					90	
Leu	Phe	Leu	Ser	Arg	Gln	Tyr	Glu	Ser	Leu	Pro	Ala	Thr	His	Ile	
				95					100					105	
Arg	Gly	Lys	Cys	Ser	Val	Ala	Leu	Leu	Asn	Glu	Thr	Glu	Ser	Val	
				110					115					120	

WO 01/07471

PCT/US00/19948

Leu	Ser	Tyr	Leu	Asp	Lys	Glu	Asp	Thr	Phe	Phe	Tyr	Ser	Leu	Val
				125					130					135
Tyr	Asp	Pro	Ser	Leu	Lys	Thr	Leu	Leu	Ala	Asp	Lys	Gly	Glu	Ile
				140					145					150
Arg	Val	Gly	Pro	Arg	Tyr	Gln	Ala	Asp	Ile	Pro	Glu	Met	Leu	Leu
				155					160					165
Glu	Gly	Glu	Ser	Asp	Glu	Arg	Glu	Gln	Ser	Lys	Leu	Glu	Val	Lys
				170					175					180
Val	Trp	Asp	Pro	Asn	Ser	Pro	Leu	Thr	Asp	Arg	Gln	Ile	Asp	Gln
				185					190					195
Phe	Leu	Val	Val	Ala	Arg	Ala	Val	Gly	Thr	Phe	Ala	Arg	Ala	Leu
				200					205					210
Asp	Cys	Ser	Ser	Ser	Val	Arg	Gln	Pro	Ser	Leu	His	Met	Ser	Ala
				215					220					225
Ala	Ala	Ala	Ser	Arg	Asp	Ile	Thr	Leu	Phe	His	Ala	Met	Asp	Thr
				230					235					240
Leu	Tyr	Arg	His	Ser	Tyr	Asp	Leu	Ser	Ser	Ala	Ile	Ser	Val	Leu
				245					250					255
Val	Pro	Leu	Gly	Gly	Pro	Val	Leu	Cys	Arg	Asp	Glu	Met	Glu	Glu
				260					265					270
Trp	Ser	Ala	Ser	Glu	Ala	Ser	Leu	Phe	Glu	Glu	Ala	Leu	Glu	Lys
				275					280					285
Tyr	Gly	Lys	Asp	Phe	Asn	Asp	Ile	Arg	Gln	Asp	Phe	Leu	Pro	Trp
				290					295					300
Lys	Ser	Leu	Thr	Ser	Ile	Ile	Glu	Tyr	Tyr	Tyr	Met	Trp	Lys	Thr
				305					310					315
Thr	Asp	Arg	Tyr	Val	Gln	Gln	Lys	Arg	Leu	Lys	Ala	Ala	Glu	Ala
				320					325					330
Glu	Ser	Lys	Leu	Lys	Gln	Val	Tyr	Ile	Pro	Thr	Tyr	Ser	Lys	Pro
				335					340					345
Asn	Pro	Asn	Gln	Ile	Ser	Thr	Ser	Asn	Gly	Lys	Pro	Gly	Ala	Val
				350					355					360
Asn	Gly	Ala	Val	Gly	Thr	Thr	Phe	Gln	Pro	Gln	Asn	Pro	Leu	Leu
				365					370					375
Gly	Arg	Ala	Cys	Glu	Ser	Cys	Tyr	Ala	Thr	Gln	Ser	His	Gln	Trp
				380					385					390
Tyr	Ser	Trp	Gly	Pro	Pro	Asn	Met	Gln	Cys	Arg	Leu	Cys	Ala	Ile
				395					400					405
Cys	Trp	Leu	Tyr	Trp	Lys	Lys	Tyr	Gly	Gly	Leu	Lys	Met	Pro	Thr
				410					415					420
Gln	Ser	Glu	Glu	Glu	Lys	Leu	Ser	Pro	Ser	Pro	Thr	Thr	Glu	Asp
				425					430					435
Pro	Arg	Val	Arg	Ser	His	Val	Ser	Arg	Gln	Ala	Met	Gln	Gly	Met
				440					445					450
Pro	Val	Arg	Asn	Thr	Gly	Ser	Pro	Lys	Ser	Ala	Val	Lys	Thr	Arg
				455					460					465
Gln	Ala	Phe	Phe	Leu	His	Thr	Thr	Tyr	Phe	Thr	Lys	Phe	Ala	Arg
				470					475					480
Gln	Val	Cys	Lys	Asn	Thr	Leu	Arg	Leu	Arg	Gln	Ala	Ala	Arg	Arg
				485					490					495
Pro	Phe	Val	Ala	Ile	Asn	Tyr	Ala	Ala	Ile	Arg	Ala	Glu	Cys	Lys
				500					505					510
Met	Leu	Leu	Asn	Ser										
				515										

<210> 40

<211> 146

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2456494CD1

WO 01/07471

PCT/US00/19948

<400> 40

Met	Val	Asp	Glu	Leu	Val	Leu	Leu	Leu	His	Ala	Leu	Leu	Met	Arg
1				5					10					15
His	Arg	Ala	Leu	Ser	Ile	Glu	Asn	Ser	Gln	Leu	Met	Glu	Gln	Leu
				20					25					30
Arg	Leu	Leu	Val	Cys	Glu	Arg	Ala	Ser	Leu	Leu	Arg	Gln	Val	Arg
				35					40					45
Pro	Pro	Ser	Cys	Pro	Val	Pro	Phe	Pro	Glu	Thr	Phe	Asn	Gly	Glu
				50					55					60
Ser	Ser	Arg	Leu	Pro	Glu	Phe	Ile	Val	Gln	Thr	Ala	Ser	Tyr	Met
				65					70					75
Leu	Val	Asn	Glu	Asn	Arg	Phe	Cys	Asn	Asp	Ala	Met	Lys	Val	Ala
				80					85					90
Phe	Leu	Ile	Ser	Leu	Leu	Thr	Gly	Glu	Ala	Glu	Glu	Trp	Val	Val
				95					100					105
Pro	Tyr	Ile	Glu	Met	Asp	Ser	Pro	Ile	Leu	Gly	Asp	Tyr	Arg	Ala
				110					115					120
Phe	Leu	Asp	Glu	Met	Lys	Gln	Cys	Phe	Gly	Trp	Asp	Asp	Asp	Glu
				125					130					135
Asp	Asp	Asp	Asp	Glu	Glu	Glu	Glu	Asp	Asp	Tyr				
				140					145					

<210> 41

<211> 580

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2668536CD1

<400> 41

Met	Lys	Glu	Asn	Lys	Glu	Asn	Ser	Ser	Pro	Ser	Val	Thr	Ser	Ala
1				5					10					15
Asn	Leu	Asp	His	Thr	Lys	Pro	Cys	Trp	Tyr	Trp	Asp	Lys	Lys	Asp
				20					25					30
Leu	Ala	His	Thr	Pro	Ser	Gln	Leu	Glu	Gly	Leu	Asp	Pro	Ala	Thr
				35					40					45
Glu	Ala	Arg	Tyr	Arg	Arg	Glu	Gly	Ala	Arg	Phe	Ile	Phe	Asp	Val
				50					55					60
Gly	Thr	Arg	Leu	Gly	Leu	His	Tyr	Asp	Thr	Leu	Ala	Thr	Gly	Ile
				65					70					75
Ile	Tyr	Phe	His	Arg	Phe	Tyr	Met	Phe	His	Ser	Phe	Lys	Gln	Phe
				80					85					90
Pro	Arg	Tyr	Val	Thr	Gly	Ala	Cys	Cys	Leu	Phe	Leu	Ala	Gly	Lys
				95					100					105
Val	Glu	Glu	Thr	Pro	Lys	Lys	Cys	Lys	Asp	Ile	Ile	Lys	Thr	Ala
				110					115					120
Arg	Ser	Leu	Leu	Asn	Asp	Val	Gln	Phe	Gly	Gln	Phe	Gly	Asp	Asp
				125					130					135
Pro	Lys	Glu	Glu	Val	Met	Val	Leu	Glu	Arg	Ile	Leu	Leu	Gln	Thr
				140					145					150
Ile	Lys	Phe	Asp	Leu	Gln	Val	Glu	His	Pro	Tyr	Gln	Phe	Leu	Leu
				155					160					165
Lys	Tyr	Ala	Lys	Gln	Leu	Lys	Gly	Asp	Lys	Asn	Lys	Ile	Gln	Lys
				170					175					180
Leu	Val	Gln	Met	Ala	Trp	Thr	Phe	Val	Asn	Asp	Ser	Leu	Cys	Thr
				185					190					195
Thr	Leu	Ser	Leu	Gln	Trp	Glu	Pro	Glu	Ile	Ile	Ala	Val	Ala	Val
				200					205					210
Met	Tyr	Leu	Ala	Gly	Arg	Leu	Cys	Lys	Phe	Glu	Ile	Gln	Glu	Trp
				215					220					225
Thr	Ser	Lys	Pro	Met	Tyr	Arg	Arg	Trp	Trp	Glu	Gln	Phe	Val	Gln
				230					235					240

WO 01/07471

PCT/US00/19948

Asp	Val	Pro	Val	Asp	Val	Leu	Glu	Asp	Ile	Cys	His	Gln	Ile	Leu
				245					250					255
Asp	Leu	Tyr	Ser	Gln	Gly	Lys	Gln	Gln	Met	Pro	His	His	Thr	Pro
				260					265					270
His	Gln	Leu	Gln	Gln	Pro	Pro	Ser	Leu	Gln	Pro	Thr	Pro	Gln	Val
				275					280					285
Pro	Gln	Val	Gln	Gln	Ser	Gln	Pro	Ser	Gln	Ser	Ser	Glu	Pro	Ser
				290					295					300
Gln	Pro	Gln	Gln	Lys	Asp	Pro	Gln	Gln	Pro	Ala	Gln	Gln	Gln	Gln
				305					310					315
Pro	Ala	Gln	Gln	Pro	Lys	Lys	Pro	Ser	Pro	Gln	Pro	Ser	Ser	Pro
				320					325					330
Arg	Gln	Val	Lys	Arg	Ala	Val	Val	Val	Ser	Pro	Lys	Glu	Glu	Asn
				335					340					345
Lys	Ala	Ala	Glu	Pro	Pro	Pro	Pro	Lys	Ile	Pro	Lys	Ile	Glu	Thr
				350					355					360
Thr	His	Pro	Pro	Leu	Pro	Pro	Ala	His	Pro	Pro	Pro	Asp	Arg	Lys
				365					370					375
Pro	Pro	Leu	Ala	Ala	Ala	Leu	Gly	Glu	Ala	Glu	Pro	Pro	Gly	Pro
				380					385					390
Val	Asp	Ala	Thr	Asp	Leu	Pro	Lys	Val	Gln	Ile	Pro	Pro	Pro	Ala
				395					400					405
His	Pro	Ala	Pro	Val	His	Gln	Pro	Pro	Pro	Leu	Pro	His	Arg	Pro
				410					415					420
Pro	Pro	Pro	Pro	Pro	Ser	Ser	Tyr	Met	Thr	Gly	Met	Ser	Thr	Thr
				425					430					435
Ser	Ser	Tyr	Met	Ser	Gly	Glu	Gly	Tyr	Gln	Ser	Leu	Gln	Ser	Met
				440					445					450
Met	Lys	Thr	Glu	Gly	Pro	Ser	Tyr	Gly	Ala	Leu	Pro	Pro	Ala	Tyr
				455					460					465
Gly	Pro	Pro	Ala	His	Leu	Pro	Tyr	His	Pro	His	Val	Tyr	Pro	Pro
				470					475					480
Asn	Pro	Pro	Pro	Pro	Pro	Val	Pro	Pro	Pro	Pro	Ala	Ser	Phe	Pro
				485					490					495
His	Leu	Pro	Ser	His	Pro	Leu	Leu	Leu	Ala	Thr	Pro	Asn	Pro	His
				500					505					510
Pro	Pro	Thr	Thr	Pro	Thr	Ser	His	Pro	His	Pro	His	Ala	Ser	Arg
				515					520					525
Leu	Pro	Thr	Gln	Ser	Pro	Leu	Ile	Leu	Leu	Gln	Gly	Trp	Ala	Cys
				530					535					540
Arg	Gln	Pro	Ala	Thr	His	Leu	Leu	Pro	Ser	Pro	Leu	Glu	Asp	Ser
				545					550					555
Leu	Leu	Cys	Pro	Arg	Pro	Phe	Pro	His	Pro	Ala	Cys	Leu	Gln	Leu
				560					565					570
Glu	Gly	Leu	Gly	Arg	Ala	Ala	Trp	Met	Arg					
				575					580					

<210> 42

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2683225CD1

<400> 42

Met	Ala	Glu	Pro	Asp	Tyr	Ile	Glu	Asp	Asp	Asn	Pro	Glu	Leu	Ile
1				5					10					15
Arg	Pro	Gln	Lys	Leu	Ile	Asn	Pro	Val	Lys	Thr	Ser	Arg	Asn	His
				20					25					30
Gln	Asp	Leu	His	Arg	Glu	Leu	Leu	Met	Asn	Gln	Lys	Arg	Gly	Leu
				35					40					45
Ala	Pro	Gln	Asn	Lys	Pro	Glu	Leu	Gln	Lys	Val	Met	Glu	Lys	Arg

WO 01/07471

PCT/US00/19948

	50		55		60
Lys Arg Asp Gln Val Ile Lys Gln Lys Glu Glu Glu Ala Gln Lys					
	65		70		75
Lys Lys Ser Asp Leu Glu Ile Glu Leu Leu Lys Arg Gln Gln Lys					
	80		85		90
Leu Glu Gln Leu Glu Leu Glu Lys Gln Lys Leu Gln Glu Glu Gln					
	95		100		105
Glu Asn Ala Pro Glu Phe Val Lys Val Lys Gly Asn Leu Arg Arg					
	110		115		120
Thr Gly Gln Glu Val Ala Gln Ala Gln Glu Ser					
	125		130		

<210> 43

<211> 812

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2797839CD1

<400> 43

Met Gly Arg Lys Leu Asp Pro Thr Lys Glu Lys Arg Gly Pro Gly					
1	5		10		15
Arg Lys Ala Arg Lys Gln Lys Gly Ala Glu Thr Glu Leu Val Arg					
	20		25		30
Phe Leu Pro Ala Val Ser Asp Glu Asn Ser Lys Arg Leu Ser Ser					
	35		40		45
Arg Ala Arg Lys Arg Ala Ala Lys Arg Arg Leu Gly Ser Val Glu					
	50		55		60
Ala Pro Lys Thr Asn Lys Ser Pro Glu Ala Lys Pro Leu Pro Gly					
	65		70		75
Lys Leu Pro Lys Gly Ile Ser Ala Gly Ala Val Gln Thr Ala Gly					
	80		85		90
Lys Lys Gly Pro Gln Ser Leu Phe Asn Ala Pro Arg Gly Lys Lys					
	95		100		105
Arg Pro Ala Pro Gly Ser Asp Glu Glu Glu Glu Glu Asp Ser					
	110		115		120
Glu Glu Asp Gly Met Val Asn His Gly Asp Leu Trp Gly Ser Glu					
	125		130		135
Asp Asp Ala Asp Thr Val Asp Asp Tyr Gly Ala Asp Ser Asn Ser					
	140		145		150
Glu Asp Glu Glu Glu Gly Glu Ala Leu Leu Pro Ile Glu Arg Ala					
	155		160		165
Ala Arg Lys Gln Lys Ala Arg Glu Ala Ala Ala Gly Ile Gln Trp					
	170		175		180
Ser Glu Glu Glu Thr Glu Asp Glu Glu Glu Lys Glu Val Thr					
	185		190		195
Pro Glu Ser Gly Pro Pro Lys Val Glu Glu Ala Asp Gly Gly Leu					
	200		205		210
Gln Ile Asn Val Asp Glu Glu Pro Phe Val Leu Pro Pro Ala Gly					
	215		220		225
Glu Met Glu Gln Asp Ala Gln Ala Pro Asp Leu Gln Arg Val His					
	230		235		240
Lys Arg Ile Gln Asp Ile Val Gly Ile Leu Arg Asp Phe Gly Ala					
	245		250		255
Gln Arg Glu Glu Gly Arg Ser Arg Ser Glu Tyr Leu Asn Arg Leu					
	260		265		270
Lys Lys Asp Leu Ala Ile Tyr Tyr Ser Tyr Gly Asp Phe Leu Leu					
	275		280		285
Gly Lys Leu Met Asp Leu Phe Pro Leu Ser Glu Leu Val Glu Phe					
	290		295		300
Leu Glu Ala Asn Glu Val Pro Arg Pro Val Thr Leu Arg Thr Asn					
	305		310		315

WO 01/07471

PCT/US00/19948

Thr	Leu	Lys	Thr	Arg	Arg	Arg	Asp	Leu	Ala	Gln	Ala	Leu	Ile	Asn
				320					325					330
Arg	Gly	Val	Asn	Leu	Asp	Pro	Leu	Gly	Lys	Trp	Ser	Lys	Thr	Gly
				335					340					345
Leu	Val	Val	Tyr	Asp	Ser	Ser	Val	Pro	Ile	Gly	Ala	Thr	Pro	Glu
				350					355					360
Tyr	Leu	Ala	Gly	His	Tyr	Met	Leu	Gln	Gly	Ala	Ser	Ser	Met	Leu
				365					370					375
Pro	Val	Met	Ala	Leu	Ala	Pro	Gln	Glu	His	Glu	Arg	Ile	Leu	Asp
				380					385					390
Met	Cys	Cys	Ala	Pro	Gly	Gly	Lys	Thr	Ser	Tyr	Met	Ala	Gln	Leu
				395					400					405
Met	Lys	Asn	Thr	Gly	Val	Ile	Leu	Ala	Asn	Asp	Ala	Asn	Ala	Glu
				410					415					420
Arg	Leu	Lys	Ser	Val	Val	Gly	Asn	Leu	His	Arg	Leu	Gly	Val	Thr
				425					430					435
Asn	Thr	Ile	Ile	Ser	His	Tyr	Asp	Gly	Arg	Gln	Phe	Pro	Lys	Val
				440					445					450
Val	Gly	Gly	Phe	Asp	Arg	Val	Leu	Leu	Asp	Ala	Pro	Cys	Ser	Gly
				455					460					465
Thr	Gly	Val	Ile	Ser	Lys	Asp	Pro	Ala	Val	Lys	Thr	Asn	Lys	Asp
				470					475					480
Glu	Lys	Asp	Ile	Leu	Arg	Cys	Ala	His	Leu	Gln	Lys	Glu	Leu	Leu
				485					490					495
Leu	Ser	Ala	Ile	Asp	Ser	Val	Asn	Ala	Thr	Ser	Lys	Thr	Gly	Gly
				500					505					510
Tyr	Leu	Val	Tyr	Cys	Thr	Cys	Ser	Ile	Thr	Val	Glu	Glu	Asn	Glu
				515					520					525
Trp	Val	Val	Asp	Tyr	Ala	Leu	Lys	Lys	Arg	Asn	Val	Arg	Leu	Val
				530					535					540
Pro	Thr	Gly	Leu	Asp	Phe	Gly	Gln	Glu	Gly	Phe	Thr	Arg	Phe	Arg
				545					550					555
Glu	Arg	Arg	Phe	His	Pro	Ser	Leu	Arg	Ser	Thr	Arg	Arg	Phe	Tyr
				560					565					570
Pro	His	Thr	His	Asn	Met	Asp	Gly	Phe	Phe	Ile	Ala	Lys	Phe	Lys
				575					580					585
Lys	Phe	Ser	Asn	Ser	Ile	Pro	Gln	Ser	Gln	Thr	Gly	Asn	Ser	Glu
				590					595					600
Thr	Ala	Thr	Pro	Thr	Asn	Val	Asp	Leu	Pro	Gln	Val	Ile	Pro	Lys
				605					610					615
Ser	Glu	Asn	Ser	Ser	Gln	Pro	Ala	Lys	Lys	Ala	Lys	Gly	Ala	Ala
				620					625					630
Lys	Thr	Lys	Gln	Gln	Leu	Gln	Lys	Gln	Gln	His	Pro	Lys	Lys	Ala
				635					640					645
Ser	Phe	Gln	Lys	Leu	Asn	Gly	Ile	Ser	Lys	Gly	Ala	Asp	Ser	Glu
				650					655					660
Leu	Ser	Thr	Val	Pro	Ser	Val	Thr	Lys	Thr	Gln	Ala	Ser	Ser	Ser
				665					670					675
Phe	Gln	Asp	Ser	Ser	Gln	Pro	Ala	Gly	Lys	Ala	Glu	Gly	Ile	Arg
				680					685					690
Glu	Pro	Lys	Val	Thr	Gly	Lys	Leu	Lys	Gln	Arg	Ser	Pro	Lys	Leu
				695					700					705
Gln	Ser	Ser	Lys	Lys	Val	Ala	Phe	Leu	Arg	Gln	Asn	Ala	Pro	Pro
				710					715					720
Lys	Gly	Thr	Asp	Thr	Gln	Thr	Pro	Ala	Val	Leu	Ser	Pro	Ser	Lys
				725					730					735
Thr	Gln	Ala	Thr	Leu	Lys	Pro	Lys	Asp	His	His	Gln	Pro	Leu	Gly
				740					745					750
Arg	Ala	Lys	Gly	Val	Glu	Lys	Gln	Gln	Leu	Pro	Glu	Gln	Pro	Phe
				755					760					765
Glu	Lys	Ala	Ala	Phe	Gln	Lys	Gln	Asn	Asp	Thr	Pro	Lys	Gly	Pro
				770					775					780
Gln	Pro	Pro	Thr	Val	Ser	Pro	Ile	Arg	Ser	Ser	Arg	Pro	Pro	Pro

WO 01/07471

PCT/US00/19948

				785						790					795
Ala	Lys	Arg	Lys	Lys	Ser	Gln	Ser	Arg	Gly	Asn	Ser	Gln	Leu	Leu	
				800					805					810	
Leu	Ser														

<210> 44

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2959521CD1

<400> 44

Met	Arg	Gly	Val	Gly	Ala	Arg	Val	Tyr	Ala	Asp	Ala	Pro	Ala	Lys	
1				5					10					15	
Leu	Leu	Leu	Pro	Pro	Pro	Ala	Ala	Trp	Asp	Leu	Ala	Val	Arg	Leu	
				20					25					30	
Arg	Gly	Ala	Glu	Ala	Ala	Ser	Glu	Arg	Gln	Val	Tyr	Ser	Val	Thr	
				35					40					45	
Met	Lys	Leu	Leu	Leu	Leu	His	Pro	Ala	Phe	Gln	Ser	Cys	Leu	Leu	
				50					55					60	
Leu	Thr	Leu	Leu	Gly	Leu	Trp	Arg	Thr	Thr	Pro	Glu	Ala	His	Ala	
				65					70					75	
Ser	Ser	Leu	Gly	Ala	Pro	Ala	Ile	Ser	Ala	Ala	Ser	Phe	Leu	Gln	
				80					85					90	
Asp	Leu	Ile	His	Arg	Tyr	Gly	Glu	Gly	Asp	Ser	Leu	Thr	Leu	Gln	
				95					100					105	
Gln	Leu	Lys	Ala	Leu	Leu	Asn	His	Leu	Asp	Val	Gly	Val	Gly	Arg	
				110					115					120	
Gly	Asn	Val	Thr	Gln	His	Val	Gln	Gly	His	Arg	Asn	Leu	Ser	Thr	
				125					130					135	
Cys	Phe	Ser	Ser	Gly	Asp	Leu	Phe	Thr	Ala	His	Asn	Phe	Ser	Glu	
				140					145					150	
Gln	Ser	Arg	Ile	Gly	Ser	Ser	Glu	Leu	Gln	Glu	Phe	Cys	Pro	Thr	
				155					160					165	
Ile	Leu	Gln	Gln	Leu	Asp	Ser	Arg	Ala	Cys	Thr	Ser	Glu	Asn	Gln	
				170					175					180	
Glu	Asn	Glu	Glu	Asn	Glu	Gln	Thr	Glu	Glu	Gly	Arg	Pro	Ser	Ala	
				185					190					195	
Val	Glu	Val	Trp	Gly	Tyr	Gly	Leu	Leu	Cys	Val	Thr	Val	Ile	Ser	
				200					205					210	
Leu	Cys	Ser	Leu	Leu	Gly	Ala	Ser	Val	Val	Pro	Phe	Met	Lys	Lys	
				215					220					225	
Thr	Phe	Tyr	Lys	Arg	Leu	Leu	Leu	Tyr	Phe	Ile	Ala	Leu	Ala	Ile	
				230					235					240	
Gly	Thr	Leu	Tyr	Ser	Asn	Ala	Leu	Phe	Gln	Leu	Ile	Pro	Glu	Ala	
				245					250					255	
Phe	Gly	Phe	Asn	Pro	Leu	Glu	Asp	Tyr	Tyr	Val	Ser	Lys	Ser	Ala	
				260					265					270	
Val	Val	Phe	Gly	Gly	Phe	Tyr	Leu	Phe	Phe	Phe	Thr	Glu	Lys	Ile	
				275					280					285	
Leu	Lys	Ile	Leu	Leu	Lys	Gln	Lys	Asn	Glu	His	His	His	Gly	His	
				290					295					300	
Ser	His	Tyr	Ala	Ser	Glu	Ser	Leu	Pro	Ser	Lys	Lys	Asp	Gln	Glu	
				305					310					315	
Glu	Gly	Val	Met	Glu	Lys	Leu	Gln	Asn	Gly	Asp	Leu	Asp	His	Met	
				320					325					330	
Ile	Pro	Gln	His	Cys	Ser	Ser	Glu	Leu	Asp	Gly	Lys	Ala	Pro	Met	
				335					340					345	
Val	Asp	Glu	Lys	Val	Ile	Val	Gly	Ser	Leu	Ser	Val	Gln	Asp	Leu	
				350					355					360	

WO 01/07471

PCT/US00/19948

Gln	Ala	Ser	Gln	Ser	Ala	Cys	Tyr	Trp	Leu	Lys	Gly	Val	Arg	Tyr
				365					370					375
Ser	Asp	Ile	Gly	Thr	Leu	Ala	Trp	Met	Ile	Thr	Leu	Ser	Asp	Gly
				380					385					390
Leu	His	Asn	Phe	Ile	Asp	Gly	Leu	Ala	Ile	Gly	Ala	Ser	Phe	Thr
				395					400					405
Val	Ser	Val	Phe	Gln	Gly	Ile	Ser	Thr	Ser	Val	Ala	Ile	Leu	Cys
				410					415					420
Glu	Glu	Phe	Pro	His	Glu	Leu	Gly	Asp	Phe	Val	Ile	Leu	Leu	Asn
				425					430					435
Ala	Gly	Met	Ser	Ile	Gln	Gln	Ala	Leu	Phe	Phe	Asn	Phe	Leu	Ser
				440					445					450
Ala	Cys	Cys	Cys	Tyr	Leu	Gly	Leu	Ala	Phe	Gly	Ile	Leu	Ala	Gly
				455					460					465
Ser	His	Phe	Ser	Ala	Asn	Trp	Ile	Phe	Ala	Leu	Ala	Gly	Gly	Met
				470					475					480
Phe	Leu	Tyr	Ile	Ser	Leu	Ala	Asp	Met	Phe	Pro	Glu	Met	Asn	Glu
				485					490					495
Val	Cys	Gln	Glu	Asp	Glu	Arg	Lys	Gly	Ser	Ile	Leu	Ile	Pro	Phe
				500					505					510
Ile	Ile	Gln	Asn	Leu	Gly	Leu	Leu	Thr	Gly	Phe	Thr	Ile	Met	Val
				515					520					525
Val	Leu	Thr	Met	Tyr	Ser	Gly	Gln	Ile	Gln	Ile	Gly			
				530					535					

<210> 45

<211> 584

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3082014CD1

<400> 45

Met	Leu	Trp	Gly	Gly	Arg	Val	Gly	Leu	Thr	Gly	Val	Phe	Gln	Ser
1				5					10					15
Leu	Ser	Tyr	Arg	Gly	Lys	Cys	Ser	Val	Thr	Leu	Leu	Asn	Glu	Thr
				20					25					30
Asp	Ile	Leu	Ser	Gln	Tyr	Leu	Glu	Lys	Glu	Asp	Cys	Phe	Phe	Tyr
				35					40					45
Ser	Leu	Val	Phe	Asp	Pro	Val	Gln	Lys	Thr	Leu	Leu	Ala	Asp	Gln
				50					55					60
Gly	Glu	Ile	Arg	Val	Gly	Cys	Lys	Tyr	Gln	Ala	Glu	Ile	Pro	Asp
				65					70					75
Arg	Leu	Val	Glu	Gly	Glu	Ser	Asp	Asn	Arg	Asn	Gln	Gln	Lys	Met
				80					85					90
Glu	Met	Lys	Val	Trp	Asp	Pro	Asp	Asn	Pro	Leu	Thr	Asp	Arg	Gln
				95					100					105
Ile	Asp	Gln	Phe	Leu	Val	Val	Ala	Arg	Ala	Val	Gly	Thr	Phe	Ala
				110					115					120
Arg	Ala	Leu	Asp	Cys	Ser	Ser	Ser	Ile	Arg	Gln	Pro	Ser	Leu	His
				125					130					135
Met	Ser	Ala	Ala	Ala	Ala	Ser	Arg	Asp	Ile	Thr	Leu	Phe	His	Ala
				140					145					150
Met	Asp	Thr	Leu	Gln	Arg	Asn	Gly	Tyr	Asp	Leu	Ala	Lys	Ala	Met
				155					160					165
Ser	Thr	Leu	Val	Pro	Gln	Gly	Gly	Pro	Val	Leu	Cys	Arg	Asp	Glu
				170					175					180
Met	Glu	Glu	Trp	Ser	Ala	Ser	Glu	Ala	Met	Leu	Phe	Glu	Glu	Ala
				185					190					195
Leu	Glu	Lys	Tyr	Gly	Lys	Asp	Phe	Asn	Asp	Ile	Arg	Gln	Asp	Phe
				200					205					210
Leu	Pro	Trp	Lys	Ser	Leu	Ala	Ser	Ile	Val	Gln	Phe	Tyr	Tyr	Met

WO 01/07471

PCT/US00/19948

Glu	Asn	Glu	Ala	Cys	Ala	Val	Leu	Gly	Gly	Ser	Asp	Ser	Glu	Lys
				35					40					45
Cys	Ser	Tyr	Ser	Gln	Gly	Ser	Val	Lys	Arg	Gln	Ala	Leu	Tyr	Ala
				50					55					60
Cys	Ser	Thr	Cys	Thr	Pro	Glu	Gly	Glu	Glu	Pro	Ala	Gly	Ile	Cys
				65					70					75
Leu	Ala	Cys	Ser	Tyr	Glu	Cys	His	Gly	Ser	His	Lys	Leu	Phe	Glu
				80					85					90
Leu	Tyr	Thr	Lys	Arg	Asn	Phe	Arg	Cys	Asp	Cys	Gly	Asn	Ser	Lys
				95					100					105
Phe	Lys	Asn	Leu	Glu	Cys	Lys	Leu	Leu	Pro	Asp	Lys	Ala	Lys	Val
				110					115					120
Asn	Ser	Gly	Asn	Lys	Tyr	Asn	Asp	Asn	Phe	Phe	Gly	Leu	Tyr	Cys
				125					130					135
Ile	Cys	Lys	Arg	Pro	Tyr	Pro	Asp	Pro	Glu	Asp	Glu	Ile	Pro	Asp
				140					145					150
Glu	Met	Ile	Gln	Cys	Val	Val	Cys	Glu	Asp	Trp	Phe	His	Gly	Arg
				155					160					165
His	Leu	Gly	Ala	Ile	Pro	Pro	Glu	Ser	Gly	Asp	Phe	Gln	Glu	Met
				170					175					180
Val	Cys	Gln	Ala	Cys	Met	Lys	Arg	Cys	Ser	Phe	Leu	Trp	Ala	Tyr
				185					190					195
Ala	Ala	Gln	Leu	Ala	Val	Thr	Lys	Ile	Ser	Thr	Glu	Asp	Asp	Gly
				200					205					210
Leu	Val	Arg	Asn	Ile	Asp	Gly	Ile	Gly	Asp	Gln	Glu	Val	Ile	Lys
				215					220					225
Pro	Glu	Asn	Gly	Glu	His	Gln	Asp	Ser	Thr	Leu	Lys	Glu	Asp	Val
				230					235					240
Pro	Glu	Gln	Gly	Lys	Asp	Asp	Val	Arg	Glu	Val	Lys	Val	Glu	Gln
				245					250					255
Asn	Ser	Glu	Pro	Cys	Ala	Gly	Ser	Ser	Ser	Glu	Ser	Asp	Leu	Gln
				260					265					270
Thr	Val	Phe	Lys	Asn	Glu	Ser	Leu	Asn	Ala	Glu	Ser	Lys	Ser	Gly
				275					280					285
Cys	Lys	Leu	Gln	Glu	Leu	Lys	Ala	Lys	Gln	Leu	Ile	Lys	Lys	Asp
				290					295					300
Thr	Ala	Thr	Tyr	Trp	Pro	Leu	Asn	Trp	Arg	Ser	Lys	Leu	Cys	Thr
				305					310					315
Cys	Gln	Asp	Cys	Met	Lys	Met	Tyr	Gly	Asp	Leu	Asp	Val	Leu	Phe
				320					325					330
Leu	Thr	Asp	Glu	Tyr	Asp	Thr	Val	Leu	Ala	Tyr	Glu	Asn	Lys	Gly
				335					340					345
Lys	Ile	Ala	Gln	Ala	Thr	Asp	Arg	Ser	Asp	Pro	Leu	Met	Asp	Thr
				350					355					360
Leu	Ser	Ser	Met	Asn	Arg	Val	Gln	Gln	Val	Glu	Leu	Ile	Cys	Glu
				365					370					375
Tyr	Asn	Asp	Leu	Lys	Thr	Glu	Leu	Lys	Asp	Tyr	Leu	Lys	Arg	Phe
				380					385					390
Ala	Asp	Glu	Gly	Thr	Val	Val	Lys	Arg	Glu	Asp	Ile	Gln	Gln	Phe
				395					400					405
Phe	Glu	Glu	Phe	Gln	Ser	Lys	Lys	Arg	Arg	Arg	Val	Asp	Gly	Met
				410					415					420
Gln	Tyr	Tyr	Cys	Ser										
				425										

<210> 47

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4184320CD1

WO 01/07471

PCT/US00/19948

<400> 47

Met	Tyr	Val	Arg	Val	Ser	Phe	Asp	Thr	Lys	Pro	Asp	Leu	Leu	Leu
1				5					10					15
His	Leu	Met	Thr	Lys	Glu	Trp	Gln	Leu	Glu	Leu	Pro	Lys	Leu	Leu
				20					25					30
Ile	Ser	Val	His	Gly	Gly	Leu	Gln	Asn	Phe	Glu	Leu	Gln	Pro	Lys
				35					40					45
Leu	Lys	Gln	Val	Phe	Gly	Lys	Gly	Leu	Ile	Lys	Ala	Ala	Met	Thr
				50					55					60
Thr	Gly	Ala	Trp	Ile	Phe	Thr	Gly	Gly	Val	Asn	Thr	Gly	Val	Ile
				65					70					75
Arg	His	Val	Gly	Asp	Ala	Leu	Lys	Asp	His	Ala	Ser	Lys	Ser	Arg
				80					85					90
Gly	Lys	Ile	Cys	Thr	Ile	Gly	Ile	Ala	Pro	Trp	Gly	Ile	Val	Glu
				95					100					105
Asn	Gln	Glu	Asp	Leu	Ile	Gly	Arg	Asp	Val	Val	Arg	Pro	Tyr	Gln
				110					115					120
Thr	Met	Ser	Asn	Pro	Met	Ser	Lys	Leu	Thr	Val	Leu	Asn	Ser	Met
				125					130					135
His	Ser	His	Phe	Ile	Leu	Ala	Asp	Asn	Gly	Thr	Thr	Gly	Lys	Tyr
				140					145					150
Gly	Ala	Glu	Val	Lys	Leu	Arg	Arg	Gln	Leu	Glu	Lys	His	Ile	Ser
				155					160					165
Leu	Gln	Lys	Ile	Asn	Thr	Arg	Cys	Leu	Pro	Phe	Phe	Ser	Leu	Asp
				170					175					180
Ser	Arg	Leu	Phe	Tyr	Ser	Phe	Trp	Gly	Ser	Cys	Gln	Leu	Asp	Ser
				185					190					195
Val	Gly	Ile	Gly	Gln	Gly	Val	Pro	Val	Val	Ala	Leu	Ile	Val	Glu
				200					205					210
Gly	Gly	Pro	Asn	Val	Ile	Ser	Ile	Val	Leu	Glu	Tyr	Leu	Arg	Asp
				215					220					225
Thr	Pro	Pro	Val	Pro	Val	Val	Val	Cys	Asp	Gly	Ser	Gly	Arg	Ala
				230					235					240
Ser	Asp	Ile	Leu	Ala	Phe	Gly	His	Lys	Tyr	Ser	Glu	Glu	Gly	Gly
				245					250					255

<210> 48

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4764233CD1

<400> 48

Met	Ser	Trp	Arg	Gly	Arg	Ser	Thr	Tyr	Arg	Pro	Arg	Pro	Arg	Arg
1				5					10					15
Ser	Leu	Gln	Pro	Pro	Glu	Leu	Ile	Gly	Ala	Met	Leu	Glu	Pro	Thr
				20					25					30
Asp	Glu	Glu	Pro	Lys	Glu	Glu	Lys	Pro	Pro	Thr	Lys	Ser	Arg	Asn
				35					40					45
Pro	Thr	Pro	Asp	Gln	Lys	Arg	Glu	Asp	Asp	Gln	Gly	Ala	Ala	Glu
				50					55					60
Ile	Gln	Val	Pro	Asp	Leu	Glu	Ala	Asp	Leu	Gln	Glu	Leu	Cys	Gln
				65					70					75
Thr	Lys	Thr	Gly	Asp	Gly	Cys	Glu	Gly	Gly	Thr	Asp	Val	Lys	Gly
				80					85					90
Lys	Ile	Leu	Pro	Lys	Ala	Glu	His	Phe	Lys	Met	Pro	Glu	Ala	Gly
				95					100					105
Glu	Gly	Lys	Ser	Gln	Val									
				110										

<210> 49

WO 01/07471

PCT/US00/19948

<211> 422
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 4817352CD1

<400> 49
Met Gly Lys Ala Lys Val Pro Ala Ser Lys Arg Ala Pro Ser Ser
1 5 10 15
Pro Val Ala Lys Pro Gly Pro Val Lys Thr Leu Thr Arg Lys Lys
20 25 30
Asn Lys Lys Lys Lys Arg Phe Trp Lys Ser Lys Ala Arg Glu Val
35 40 45
Ser Lys Lys Pro Ala Ser Gly Pro Gly Ala Val Val Arg Pro Pro
50 55 60
Lys Ala Pro Glu Asp Phe Ser Gln Asn Trp Lys Ala Leu Gln Glu
65 70 75
Trp Leu Leu Lys Gln Lys Ser Gln Ala Pro Glu Lys Pro Leu Val
80 85 90
Ile Ser Gln Met Gly Ser Lys Lys Lys Pro Lys Ile Ile Gln Gln
95 100 105
Asn Lys Lys Glu Thr Ser Pro Gln Val Lys Gly Glu Glu Met Pro
110 115 120
Ala Gly Lys Asp Gln Glu Ala Ser Arg Gly Ser Val Pro Ser Gly
125 130 135
Ser Lys Met Asp Arg Arg Ala Pro Val Pro Arg Thr Lys Ala Ser
140 145 150
Gly Thr Glu His Asn Lys Lys Gly Thr Lys Glu Arg Thr Asn Gly
155 160 165
Asp Ile Val Pro Glu Arg Gly Asp Ile Glu His Lys Lys Arg Lys
170 175 180
Ala Lys Glu Ala Ala Pro Ala Pro Pro Thr Glu Glu Asp Ile Trp
185 190 195
Phe Asp Asp Val Asp Pro Ala Asp Ile Glu Ala Ala Ile Gly Pro
200 205 210
Glu Ala Ala Lys Ile Ala Arg Lys Gln Leu Gly Gln Ser Glu Gly
215 220 225
Ser Val Ser Leu Ser Leu Val Lys Glu Gln Ala Phe Gly Gly Leu
230 235 240
Thr Arg Ala Leu Ala Leu Asp Cys Glu Met Val Gly Val Gly Pro
245 250 255
Lys Gly Glu Glu Ser Met Ala Ala Arg Val Ser Ile Val Asn Gln
260 265 270
Tyr Gly Lys Cys Val Tyr Asp Lys Tyr Val Lys Pro Thr Glu Pro
275 280 285
Val Thr Asp Tyr Arg Thr Ala Val Ser Gly Ile Arg Pro Glu Asn
290 295 300
Leu Lys Gln Gly Glu Glu Leu Glu Val Val Gln Lys Glu Val Ala
305 310 315
Glu Met Leu Lys Gly Arg Ile Leu Val Gly His Ala Leu His Asn
320 325 330
Asp Leu Lys Val Leu Phe Leu Asp His Pro Lys Lys Lys Ile Arg
335 340 345
Asp Thr Gln Lys Tyr Lys Pro Phe Lys Ser Gln Val Lys Ser Gly
350 355 360
Arg Pro Ser Leu Arg Leu Leu Ser Glu Lys Ile Leu Gly Leu Gln
365 370 375
Val Gln Gln Ala Glu His Cys Ser Ile Gln Asp Ala Gln Ala Ala
380 385 390
Met Arg Leu Tyr Val Met Val Lys Lys Glu Trp Glu Ser Met Ala
395 400 405

WO 01/07471

PCT/US00/19948

Arg Asp Arg Arg Pro Leu Leu Thr Ala Pro Asp His Cys Ser Asp
410 415 420

Asp Ala

<210> 50

<211> 397

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5040573CD1

<400> 50

Met	Ala	Met	Ile	Glu	Leu	Gly	Phe	Gly	Arg	Gln	Asn	Phe	His	Pro
1				5					10					15
Leu	Lys	Arg	Lys	Ser	Ser	Leu	Leu	Leu	Lys	Leu	Ile	Ala	Val	Val
				20					25					30
Phe	Ala	Val	Leu	Leu	Phe	Cys	Glu	Phe	Leu	Ile	Tyr	Tyr	Leu	Ala
				35					40					45
Ile	Phe	Gln	Cys	Asn	Trp	Pro	Glu	Val	Lys	Thr	Thr	Ala	Ser	Asp
				50					55					60
Gly	Glu	Gln	Thr	Thr	Arg	Glu	Pro	Val	Leu	Lys	Ala	Met	Phe	Leu
				65					70					75
Ala	Asp	Thr	His	Leu	Leu	Gly	Glu	Phe	Leu	Gly	His	Trp	Leu	Asp
				80					85					90
Lys	Leu	Arg	Arg	Glu	Trp	Gln	Met	Glu	Arg	Ala	Phe	Gln	Thr	Ala
				95					100					105
Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val	Val	Phe	Ile	Leu	Gly	Asp	Ile
				110					115					120
Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro	Glu	Ala	Trp	Ala	Asp	Asp
				125					130					135
Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His	Pro	Ser	His	Val	Gln
				140					145					150
Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly	Phe	His	Tyr	Glu
				155					160					165
Met	Asn	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Glu	Lys	Val	Phe	Ser	Ser
				170					175					180
Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met	Val	Asn
				185					190					195
Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu	Thr
				200					205					210
Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg
				215					220					225
Glu	Gln	Ala	Arg	Gly	Ser	Ser	Arg	Cys	Gly	Pro	Gly	Pro	Leu	Leu
				230					235					240
Pro	Thr	Ser	Ala	Pro	Val	Leu	Leu	Gln	His	Tyr	Pro	Leu	Tyr	Arg
				245					250					255
Arg	Ser	Asp	Ala	Asn	Cys	Ser	Gly	Glu	Asp	Ala	Ala	Pro	Pro	Glu
				260					265					270
Glu	Arg	Asp	Ile	Pro	Phe	Lys	Glu	Asn	Tyr	Asp	Val	Leu	Ser	Arg
				275					280					285
Glu	Ala	Ser	Gln	Lys	Leu	Leu	Trp	Trp	Leu	Gln	Pro	Arg	Leu	Val
				290					295					300
Leu	Ser	Gly	His	Thr	His	Ser	Ala	Cys	Glu	Val	His	His	Gly	Gly
				305					310					315
Arg	Val	Pro	Glu	Leu	Ser	Val	Pro	Ser	Phe	Ser	Trp	Arg	Asn	Arg
				320					325					330
Asn	Asn	Pro	Ser	Phe	Ile	Met	Gly	Ser	Ile	Thr	Pro	Thr	Asp	Tyr
				335					340					345
Thr	Leu	Ser	Lys	Cys	Tyr	Leu	Pro	Arg	Glu	Asp	Val	Val	Leu	Ile
				350					355					360
Ile	Tyr	Cys	Gly	Val	Val	Gly	Phe	Leu	Val	Val	Leu	Thr	Leu	Thr

WO 01/07471

PCT/US00/19948

	365		370		375
His Phe Gly Leu	Leu Ala Ser Pro Phe	Leu Ser Gly Leu Asn	Leu		
	380		385		390
Leu Gly Lys Arg	Lys Thr Arg				
	395				

<210> 51

<211> 800

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5627029CD1

<400> 51

Met Gly Ser Ser Lys	Lys His Arg Gly Glu	Lys Glu Ala Ala Gly	
1	5	10	15
Thr Thr Ala Ala Ala	Gly Thr Gly Gly Ala	Thr Glu Gln Pro Pro	
	20	25	30
Arg His Arg Glu His	Lys Lys His Lys	His Arg Ser Gly Gly Ser	
	35	40	45
Gly Gly Ser Gly Gly	Glu Arg Arg Lys Arg	Ser Arg Glu Arg Gly	
	50	55	60
Gly Glu Arg Gly Ser	Gly Arg Arg Gly Ala	Glu Ala Glu Ala Arg	
	65	70	75
Ser Ser Thr His Gly	Arg Glu Arg Ser Gln	Ala Glu Pro Ser Glu	
	80	85	90
Arg Arg Val Lys Arg	Glu Lys Arg Asp Asp	Gly Tyr Glu Ala Ala	
	95	100	105
Ala Ser Ser Lys Thr	Ser Ser Gly Asp Ala	Ser Ser Leu Ser Ile	
	110	115	120
Glu Glu Thr Asn Lys	Leu Arg Ala Lys Leu	Gly Leu Lys Pro Leu	
	125	130	135
Glu Val Asn Ala Ile	Lys Lys Glu Ala Gly	Thr Lys Glu Glu Pro	
	140	145	150
Val Thr Ala Asp Val	Ile Asn Pro Met Ala	Leu Arg Gln Arg Glu	
	155	160	165
Glu Leu Arg Glu Lys	Leu Ala Ala Ala Lys	Glu Lys Arg Leu Leu	
	170	175	180
Asn Gln Lys Leu Gly	Lys Ile Lys Thr Leu	Gly Glu Asp Asp Pro	
	185	190	195
Trp Leu Asp Asp Thr	Ala Ala Trp Ile Glu	Arg Ser Arg Gln Leu	
	200	205	210
Gln Lys Glu Lys Asp	Leu Ala Glu Lys Arg	Ala Lys Leu Leu Glu	
	215	220	225
Glu Met Asp Gln Glu	Phe Gly Val Ser Thr	Leu Val Glu Glu Glu	
	230	235	240
Phe Gly Gln Arg Arg	Gln Asp Leu Tyr Ser	Ala Arg Asp Leu Gln	
	245	250	255
Gly Leu Thr Val Glu	His Ala Ile Asp Ser	Phe Arg Glu Gly Glu	
	260	265	270
Thr Met Ile Leu Thr	Leu Lys Asp Lys Gly	Val Leu Gln Glu Glu	
	275	280	285
Glu Asp Val Leu Val	Asn Val Asn Leu Val	Asp Lys Glu Arg Ala	
	290	295	300
Glu Lys Asn Val Glu	Leu Arg Lys Lys Lys	Pro Asp Tyr Leu Pro	
	305	310	315
Tyr Ala Glu Asp Glu	Ser Val Asp Asp Leu	Ala Gln Gln Lys Pro	
	320	325	330
Arg Ser Ile Leu Ser	Lys Tyr Asp Glu Glu	Leu Glu Gly Glu Arg	
	335	340	345
Pro His Ser Phe Arg	Leu Glu Gln Gly Gly	Thr Ala Asp Gly Leu	
	350	355	360

WO 01/07471

PCT/US00/19948

Arg	Glu	Arg	Glu	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Leu	Arg	Leu	Gln
				365					370					375
Ala	Gln	Ser	Leu	Ser	Thr	Val	Gly	Pro	Arg	Leu	Ala	Ser	Glu	Tyr
				380					385					390
Leu	Thr	Pro	Glu	Glu	Met	Val	Thr	Phe	Lys	Lys	Thr	Lys	Arg	Arg
				395					400					405
Val	Lys	Lys	Ile	Arg	Lys	Lys	Glu	Lys	Glu	Val	Val	Val	Arg	Ala
				410					415					420
Asp	Asp	Leu	Leu	Pro	Leu	Gly	Asp	Gln	Thr	Gln	Asp	Gly	Asp	Phe
				425					430					435
Gly	Ser	Arg	Leu	Arg	Gly	Arg	Gly	Arg	Arg	Arg	Val	Ser	Glu	Val
				440					445					450
Glu	Glu	Glu	Lys	Glu	Pro	Val	Pro	Gln	Pro	Leu	Pro	Ser	Asp	Asp
				455					460					465
Thr	Arg	Val	Glu	Asn	Met	Asp	Ile	Ser	Asp	Glu	Glu	Glu	Gly	Gly
				470					475					480
Ala	Pro	Pro	Pro	Ala	Ser	Pro	Gln	Val	Leu	Glu	Glu	Asp	Glu	Ala
				485					490					495
Glu	Leu	Glu	Leu	Gln	Lys	Gln	Leu	Glu	Lys	Gly	Arg	Arg	Leu	Arg
				500					505					510
Gln	Leu	Gln	Gln	Leu	Gln	Gln	Leu	Arg	Asp	Ser	Gly	Glu	Lys	Val
				515					520					525
Val	Glu	Ile	Val	Lys	Lys	Leu	Glu	Ser	Arg	Gln	Arg	Gly	Trp	Glu
				530					535					540
Glu	Asp	Glu	Asp	Pro	Glu	Arg	Lys	Gly	Ala	Ile	Val	Phe	Asn	Ala
				545					550					555
Thr	Ser	Glu	Phe	Cys	Arg	Thr	Leu	Gly	Glu	Ile	Pro	Thr	Tyr	Gly
				560					565					570
Leu	Ala	Gly	Asn	Arg	Glu	Glu	Gln	Glu	Glu	Leu	Met	Asp	Phe	Glu
				575					580					585
Arg	Asp	Glu	Glu	Arg	Ser	Ala	Asn	Gly	Gly	Ser	Glu	Ser	Asp	Gly
				590					595					600
Glu	Glu	Asn	Ile	Gly	Trp	Ser	Thr	Val	Asn	Leu	Asp	Glu	Glu	Lys
				605					610					615
Gln	Gln	Gln	Asp	Phe	Ser	Ala	Ser	Ser	Thr	Thr	Ile	Leu	Asp	Glu
				620					625					630
Glu	Pro	Ile	Val	Asn	Arg	Gly	Leu	Ala	Ala	Ala	Leu	Leu	Leu	Cys
				635					640					645
Gln	Asn	Lys	Gly	Leu	Leu	Glu	Thr	Thr	Val	Gln	Lys	Val	Ala	Arg
				650					655					660
Val	Lys	Ala	Pro	Asn	Lys	Ser	Leu	Pro	Ser	Ala	Val	Tyr	Cys	Ile
				665					670					675
Glu	Asp	Lys	Met	Ala	Ile	Asp	Asp	Lys	Tyr	Ser	Arg	Arg	Glu	Glu
				680					685					690
Tyr	Arg	Gly	Phe	Thr	Gln	Asp	Phe	Lys	Glu	Lys	Asp	Gly	Tyr	Lys
				695					700					705
Pro	Asp	Val	Lys	Ile	Glu	Tyr	Val	Asp	Glu	Thr	Gly	Arg	Lys	Leu
				710					715					720
Thr	Pro	Lys	Glu	Ala	Phe	Arg	Gln	Leu	Ser	His	Arg	Phe	His	Gly
				725					730					735
Lys	Gly	Ser	Gly	Lys	Met	Lys	Thr	Glu	Arg	Arg	Met	Lys	Lys	Leu
				740					745					750
Asp	Glu	Glu	Ala	Leu	Leu	Lys	Lys	Met	Ser	Ser	Ser	Asp	Thr	Pro
				755					760					765
Leu	Gly	Thr	Val	Ala	Leu	Leu	Gln	Glu	Lys	Gln	Lys	Ala	Gln	Lys
				770					775					780
Thr	Pro	Tyr	Ile	Val	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Met	Asn	Ala
				785					790					795
Asn	Thr	Ile	Thr	Lys										
				800										

<210> 52

<211> 713

<212> PRT

WO 01/07471

PCT/US00/19948

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5678487CD1

<400> 52

Met	Ala	Lys	Ser	Pro	Glu	Asn	Ser	Thr	Leu	Glu	Glu	Ile	Leu	Gly
1				5					10					15
Gln	Tyr	Gln	Arg	Ser	Leu	Arg	Glu	His	Ala	Ser	Arg	Ser	Ile	His
				20					25					30
Gln	Leu	Thr	Cys	Ala	Leu	Lys	Glu	Gly	Asp	Val	Thr	Ile	Gly	Glu
				35					40					45
Asp	Ala	Pro	Asn	Leu	Ser	Phe	Ser	Thr	Ser	Val	Gly	Asn	Glu	Asp
				50					55					60
Ala	Arg	Thr	Ala	Trp	Pro	Glu	Leu	Gln	Gln	Ser	His	Ala	Val	Asn
				65					70					75
Gln	Leu	Lys	Asp	Leu	Leu	Arg	Gln	Gln	Ala	Asp	Lys	Glu	Ser	Glu
				80					85					90
Val	Ser	Pro	Ser	Arg	Arg	Arg	Lys	Met	Ser	Pro	Leu	Arg	Ser	Leu
				95					100					105
Glu	His	Glu	Glu	Thr	Asn	Met	Pro	Thr	Met	His	Asp	Leu	Val	His
				110					115					120
Thr	Ile	Asn	Asp	Gln	Ser	Gln	Tyr	Ile	His	His	Leu	Glu	Ala	Glu
				125					130					135
Val	Lys	Phe	Cys	Lys	Glu	Glu	Leu	Ser	Gly	Met	Lys	Asn	Lys	Ile
				140					145					150
Gln	Val	Val	Val	Leu	Glu	Asn	Glu	Gly	Leu	Gln	Gln	Gln	Leu	Lys
				155					160					165
Ser	Gln	Arg	Gln	Glu	Glu	Thr	Leu	Arg	Glu	Gln	Thr	Leu	Leu	Asp
				170					175					180
Ala	Ser	Gly	Asn	Met	His	Asn	Ser	Trp	Ile	Thr	Thr	Gly	Glu	Asp
				185					190					195
Ser	Gly	Val	Gly	Glu	Thr	Ser	Lys	Arg	Pro	Phe	Ser	His	Asp	Asn
				200					205					210
Ala	Asp	Phe	Gly	Lys	Ala	Ala	Ser	Ala	Gly	Glu	Gln	Leu	Glu	Leu
				215					220					225
Glu	Lys	Leu	Lys	Leu	Thr	Tyr	Glu	Glu	Lys	Cys	Glu	Ile	Glu	Glu
				230					235					240
Ser	Gln	Leu	Lys	Phe	Leu	Arg	Asn	Asp	Leu	Ala	Glu	Tyr	Gln	Arg
				245					250					255
Thr	Cys	Glu	Asp	Leu	Lys	Glu	Gln	Leu	Lys	His	Lys	Glu	Phe	Leu
				260					265					270
Leu	Ala	Ala	Asn	Thr	Cys	Asn	Arg	Val	Gly	Gly	Leu	Cys	Leu	Lys
				275					280					285
Cys	Ala	Gln	His	Glu	Ala	Val	Leu	Ser	Gln	Thr	His	Thr	Asn	Val
				290					295					300
His	Met	Gln	Thr	Ile	Glu	Arg	Leu	Val	Lys	Glu	Arg	Asp	Asp	Leu
				305					310					315
Met	Ser	Ala	Leu	Val	Ser	Val	Arg	Ser	Ser	Leu	Ala	Asp	Thr	Gln
				320					325					330
Gln	Arg	Glu	Ala	Ser	Ala	Tyr	Glu	Gln	Val	Lys	Gln	Val	Leu	Gln
				335					340					345
Ile	Ser	Glu	Glu	Ala	Asn	Phe	Glu	Lys	Thr	Lys	Ala	Leu	Ile	Gln
				350					355					360
Cys	Asp	Gln	Leu	Arg	Lys	Glu	Leu	Glu	Arg	Gln	Ala	Glu	Arg	Leu
				365					370					375
Glu	Lys	Asp	Leu	Ala	Ser	Gln	Gln	Glu	Lys	Arg	Ala	Ile	Glu	Lys
				380					385					390
Asp	Met	Met	Lys	Lys	Glu	Ile	Thr	Lys	Glu	Arg	Glu	Tyr	Met	Gly
				395					400					405
Ser	Lys	Met	Leu	Ile	Leu	Ser	Gln	Asn	Ile	Ala	Gln	Leu	Glu	Ala
				410					415					420

WO 01/07471

PCT/US00/19948

Gln	Val	Glu	Lys	Val	Thr	Lys	Glu	Lys	Ile	Ser	Ala	Ile	Asn	Gln
				425					430					435
Leu	Glu	Glu	Ile	Gln	Ser	Gln	Leu	Ala	Ser	Arg	Glu	Met	Asp	Val
				440					445					450
Thr	Lys	Val	Cys	Gly	Glu	Met	Arg	Tyr	Gln	Leu	Asn	Lys	Thr	Asn
				455					460					465
Met	Glu	Lys	Asp	Glu	Ala	Glu	Lys	Glu	His	Arg	Glu	Phe	Arg	Ala
				470					475					480
Lys	Thr	Asn	Arg	Asp	Leu	Glu	Ile	Lys	Asp	Gln	Glu	Ile	Glu	Lys
				485					490					495
Leu	Arg	Ile	Glu	Leu	Asp	Glu	Ser	Lys	Gln	His	Leu	Glu	Gln	Glu
				500					505					510
Gln	Gln	Lys	Ala	Ala	Leu	Ala	Arg	Glu	Glu	Cys	Leu	Arg	Leu	Thr
				515					520					525
Glu	Leu	Leu	Gly	Glu	Ser	Glu	His	Gln	Leu	His	Leu	Thr	Arg	Gln
				530					535					540
Glu	Lys	Asp	Ser	Ile	Gln	Gln	Ser	Phe	Ser	Lys	Glu	Ala	Lys	Ala
				545					550					555
Gln	Ala	Leu	Gln	Ala	Gln	Gln	Arg	Glu	Gln	Glu	Leu	Thr	Gln	Lys
				560					565					570
Ile	Gln	Gln	Met	Glu	Ala	Gln	His	Asp	Lys	Thr	Glu	Asn	Glu	Gln
				575					580					585
Tyr	Leu	Leu	Leu	Thr	Ser	Gln	Asn	Thr	Phe	Leu	Thr	Lys	Leu	Lys
				590					595					600
Glu	Glu	Cys	Cys	Thr	Leu	Ala	Lys	Lys	Leu	Glu	Gln	Ile	Ser	Gln
				605					610					615
Lys	Thr	Arg	Ser	Glu	Ile	Ala	Gln	Leu	Ser	Gln	Glu	Lys	Arg	Tyr
				620					625					630
Thr	Tyr	Asp	Lys	Leu	Gly	Lys	Leu	Gln	Arg	Arg	Asn	Glu	Glu	Leu
				635					640					645
Glu	Glu	Gln	Cys	Val	Gln	His	Gly	Arg	Val	His	Glu	Thr	Met	Lys
				650					655					660
Gln	Arg	Leu	Arg	Gln	Leu	Asp	Lys	His	Ser	Gln	Ala	Thr	Ala	Gln
				665					670					675
Gln	Leu	Val	Gln	Leu	Leu	Ser	Lys	Gln	Asn	Gln	Leu	Leu	Leu	Glu
				680					685					690
Arg	Gln	Ser	Leu	Ser	Glu	Glu	Val	Asp	Arg	Leu	Arg	Thr	Gln	Leu
				695					700					705
Pro	Ser	Met	Pro	Gln	Ser	Asp	Cys							
				710										

<210> 53

<211> 880

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5682976CD1

<400> 53

Met	Ser	Arg	Gly	Gly	Ser	Cys	Pro	His	Leu	Leu	Trp	Asp	Val	Arg
1				5					10					15
Lys	Arg	Ser	Leu	Gly	Leu	Glu	Asp	Pro	Ser	Arg	Leu	Arg	Ser	Arg
				20					25					30
Tyr	Leu	Gly	Arg	Arg	Glu	Phe	Ile	Gln	Arg	Leu	Lys	Leu	Glu	Ala
				35					40					45
Thr	Leu	Asn	Val	His	Asp	Gly	Cys	Val	Asn	Thr	Ile	Cys	Trp	Asn
				50					55					60
Asp	Thr	Gly	Glu	Tyr	Ile	Leu	Ser	Gly	Ser	Asp	Asp	Thr	Lys	Leu
				65					70					75
Val	Ile	Ser	Asn	Pro	Tyr	Ser	Arg	Lys	Val	Leu	Thr	Thr	Ile	Arg
				80					85					90
Ser	Gly	His	Arg	Ala	Asn	Ile	Phe	Ser	Ala	Lys	Phe	Leu	Pro	Cys

WO 01/07471

PCT/US00/19948

	95		100		105
Thr Asn Asp Lys	Gln Ile Val Ser Cys	Ser Gly Asp Gly Val	Ile		
	110		115		120
Phe Tyr Thr Asn	Val Glu Gln Asp Ala	Glu Thr Asn Arg Gln	Cys		
	125		130		135
Gln Phe Thr Cys	His Tyr Gly Thr Thr	Tyr Glu Ile Met Thr	Val		
	140		145		150
Pro Asn Asp Pro	Tyr Thr Phe Leu Ser	Cys Gly Glu Asp Gly	Thr		
	155		160		165
Val Arg Trp Phe	Asp Thr Arg Ile Lys	Thr Ser Cys Thr Lys	Glu		
	170		175		180
Asp Cys Lys Asp	Asp Ile Leu Ile Asn	Cys Arg Arg Ala Ala	Thr		
	185		190		195
Ser Val Ala Ile	Cys Pro Pro Ile Pro	Tyr Tyr Leu Ala Val	Gly		
	200		205		210
Cys Ser Asp Ser	Ser Val Arg Ile Tyr	Asp Arg Arg Met Leu	Gly		
	215		220		225
Thr Arg Ala Thr	Gly Asn Tyr Ala Gly	Arg Gly Thr Thr Gly	Met		
	230		235		240
Val Ala Arg Phe	Ile Pro Ser His Leu	Asn Asn Lys Ser Cys	Arg		
	245		250		255
Val Thr Ser Leu	Cys Tyr Ser Glu Asp	Gly Gln Glu Ile Leu	Val		
	260		265		270
Ser Tyr Ser Ser	Asp Tyr Ile Tyr Leu	Phe Asp Pro Lys Asp	Asp		
	275		280		285
Thr Ala Arg Glu	Leu Lys Thr Pro Ser	Ala Glu Glu Arg Arg	Glu		
	290		295		300
Glu Leu Arg Gln	Pro Pro Val Lys Arg	Leu Arg Leu Arg Gly	Asp		
	305		310		315
Trp Ser Asp Thr	Gly Pro Arg Ala Arg	Pro Glu Ser Glu Arg	Glu		
	320		325		330
Arg Asp Gly Glu	Gln Ser Pro Asn Val	Ser Leu Met Gln Arg	Met		
	335		340		345
Ser Asp Met Leu	Ser Arg Trp Phe Glu	Glu Ala Ser Glu Val	Ala		
	350		355		360
Gln Ser Asn Arg	Gly Arg Gly Arg Ser	Arg Pro Arg Gly Gly	Thr		
	365		370		375
Ser Gln Ser Asp	Ile Ser Thr Leu Pro	Thr Val Pro Ser Ser	Pro		
	380		385		390
Asp Leu Glu Val	Ser Glu Thr Ala Met	Glu Val Asp Thr Pro	Ala		
	395		400		405
Glu Gln Phe Leu	Gln Pro Ser Thr Ser	Ser Thr Met Ser Ala	Gln		
	410		415		420
Ala His Ser Thr	Ser Ser Pro Thr Glu	Ser Pro His Ser Thr	Pro		
	425		430		435
Leu Leu Ser Ser	Pro Asp Ser Glu Gln	Arg Gln Ser Val Glu	Ala		
	440		445		450
Ser Gly His His	Thr His His Gln Ser	Asp Ser Pro Ser Ser	Val		
	455		460		465
Val Asn Lys Gln	Leu Gly Ser Met Ser	Leu Asp Glu Gln Gln	Asp		
	470		475		480
Asn Asn Asn Glu	Lys Leu Ser Pro Lys	Pro Gly Thr Gly Glu	Pro		
	485		490		495
Val Leu Ser Leu	His Tyr Ser Thr Glu	Gly Thr Thr Thr Ser	Thr		
	500		505		510
Ile Lys Leu Asn	Phe Thr Asp Glu Trp	Ser Ser Ile Ala Ser	Ser		
	515		520		525
Ser Arg Gly Ile	Gly Ser His Cys Lys	Ser Glu Gly Gln Glu	Glu		
	530		535		540
Ser Phe Val Pro	Gln Ser Ser Val Gln	Pro Pro Glu Gly Asp	Ser		
	545		550		555
Glu Thr Lys Ala	Pro Glu Glu Ser Ser	Glu Asp Val Thr Lys	Tyr		
	560		565		570

WO 01/07471

PCT/US00/19948

Gln Glu Gly Val Ser Ala Glu Asn Pro Val Glu Asn His Ile Asn
 575 580 585
 Ile Thr Gln Ser Asp Lys Phe Thr Ala Lys Pro Leu Asp Ser Asn
 590 595 600
 Ser Gly Glu Arg Asn Asp Leu Asn Leu Asp Arg Ser Cys Gly Val
 605 610 615
 Pro Glu Glu Ser Ala Ser Ser Glu Lys Ala Lys Glu Pro Glu Thr
 620 625 630
 Ser Asp Gln Thr Ser Thr Glu Ser Ala Thr Asn Glu Asn Asn Thr
 635 640 645
 Asn Pro Glu Pro Gln Phe Gln Thr Glu Ala Thr Gly Pro Ser Ala
 650 655 660
 His Glu Glu Thr Ser Thr Arg Asp Ser Ala Leu Gln Asp Thr Asp
 665 670 675
 Asp Ser Asp Asp Asp Pro Val Leu Ile Pro Gly Ala Arg Tyr Arg
 680 685 690
 Ala Gly Pro Gly Asp Arg Arg Ser Ala Val Ala Arg Ile Gln Glu
 695 700 705
 Phe Phe Arg Arg Arg Lys Glu Arg Lys Glu Met Glu Glu Leu Asp
 710 715 720
 Thr Leu Asn Ile Arg Arg Pro Leu Val Lys Met Val Tyr Lys Gly
 725 730 735
 His Arg Asn Ser Arg Thr Met Ile Lys Glu Ala Asn Phe Trp Gly
 740 745 750
 Ala Asn Phe Val Met Ser Gly Ser Asp Cys Gly His Ile Phe Ile
 755 760 765
 Trp Asp Arg His Thr Ala Glu His Leu Met Leu Leu Glu Ala Asp
 770 775 780
 Asn His Val Val Asn Cys Leu Gln Pro His Pro Phe Asp Pro Ile
 785 790 795
 Leu Ala Ser Ser Gly Ile Asp Tyr Asp Ile Lys Ile Trp Ser Pro
 800 805 810
 Leu Glu Glu Ser Arg Ile Phe Asn Arg Lys Leu Ala Asp Glu Val
 815 820 825
 Ile Thr Arg Asn Glu Leu Met Leu Glu Glu Thr Arg Asn Thr Ile
 830 835 840
 Thr Val Pro Ala Ser Phe Met Leu Arg Met Leu Ala Ser Leu Asn
 845 850 855
 His Ile Arg Ala Asp Arg Leu Glu Gly Asp Arg Ser Glu Gly Ser
 860 865 870
 Gly Gln Glu Asn Glu Asn Glu Asp Glu Glu
 875 880

<210> 54

<211> 855

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5992432CD1

<400> 54

Met Val Val Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu
 1 5 10 15
 Val Phe Glu Glu Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg
 20 25 30
 Asn Gln Phe Ser Val Lys Cys Trp Leu Arg Tyr Ile Glu Phe Lys
 35 40 45
 Gln Gly Ala Pro Lys Pro Arg Leu Asn Gln Leu Tyr Glu Arg Ala
 50 55 60
 Leu Lys Leu Leu Pro Cys Ser Tyr Lys Leu Trp Tyr Arg Tyr Leu
 65 70 75
 Lys Ala Arg Arg Ala Gln Val Lys His Arg Cys Val Thr Asp Pro

WO 01/07471

PCT/US00/19948

80	85	90
Ala Tyr Glu Asp Val	Asn Asn Cys His Glu Arg Ala Phe Val	Phe
95	100	105
Met His Lys Met Pro	Arg Leu Trp Leu Asp Tyr Cys Gln Phe	Leu
110	115	120
Met Asp Gln Gly Arg	Val Thr His Thr Arg Arg Thr Phe Asp	Arg
125	130	135
Ala Leu Arg Ala Leu	Pro Ile Thr Gln His Ser Arg Ile Trp	Pro
140	145	150
Leu Tyr Leu Arg Phe	Leu Arg Ser His Pro Leu Pro Glu Thr	Ala
155	160	165
Val Arg Gly Tyr Arg	Arg Phe Leu Lys Leu Ser Pro Glu Ser	Ala
170	175	180
Glu Glu Tyr Ile Glu	Tyr Leu Lys Ser Ser Asp Arg Leu Asp	Glu
185	190	195
Ala Ala Gln Arg Leu	Ala Thr Val Val Asn Asp Glu Arg Phe	Val
200	205	210
Ser Lys Ala Gly Lys	Ser Asn Tyr Gln Leu Trp His Glu Leu	Cys
215	220	225
Asp Leu Ile Ser Gln	Asn Pro Asp Lys Val Gln Ser Leu Asn	Val
230	235	240
Asp Ala Ile Ile Arg	Gly Gly Leu Thr Arg Phe Thr Asp	Gln Leu
245	250	255
Gly Lys Leu Trp Cys	Ser Leu Ala Asp Tyr Tyr Ile Arg Ser	Gly
260	265	270
His Phe Glu Lys Ala	Arg Asp Val Tyr Glu Glu Ala Ile Arg	Thr
275	280	285
Val Met Thr Val Arg	Asp Phe Thr Gln Val Phe Asp Ser Tyr	Ala
290	295	300
Gln Phe Glu Glu Ser	Met Ile Ala Ala Lys Met Glu Thr Ala	Ser
305	310	315
Glu Leu Gly Arg Glu	Glu Glu Glu Asp Asp Val Asp Leu Glu Leu	Arg
320	325	330
Leu Ala Arg Phe Glu	Gln Leu Ile Ser Arg Arg Pro Leu Leu	Leu
335	340	345
Asn Ser Val Leu Leu	Arg Gln Asn Pro His His Val His Glu	Trp
350	355	360
His Lys Arg Val Ala	Leu His Gln Gly Arg Pro Arg Glu Ile	Ile
365	370	375
Asn Thr Tyr Thr Glu	Ala Val Gln Thr Val Asp Pro Phe Lys	Ala
380	385	390
Thr Gly Lys Pro His	Thr Leu Trp Val Ala Phe Ala Lys Phe	Tyr
395	400	405
Glu Asp Asn Gly Gln	Leu Asp Asp Ala Arg Val Ile Leu Glu	Lys
410	415	420
Ala Thr Lys Val Asn	Phe Lys Gln Val Asp Asp Leu Ala Ser	Val
425	430	435
Trp Cys Gln Cys Gly	Glu Leu Glu Leu Arg His Glu Asn Tyr	Asp
440	445	450
Glu Ala Leu Arg Leu	Leu Arg Lys Ala Thr Ala Leu Pro Ala	Arg
455	460	465
Arg Ala Glu Tyr Phe	Asp Gly Ser Glu Pro Val Gln Asn Arg	Val
470	475	480
Tyr Lys Ser Leu Lys	Val Trp Ser Met Leu Ala Asp Leu Glu	Glu
485	490	495
Ser Leu Gly Thr Phe	Gln Ser Thr Lys Ala Val Tyr Asp Arg	Ile
500	505	510
Leu Asp Leu Arg Ile	Ala Thr Pro Gln Ile Val Ile Asn Tyr	Ala
515	520	525
Met Phe Leu Glu Glu	His Lys Tyr Phe Glu Glu Ser Phe Lys	Ala
530	535	540
Tyr Glu Arg Gly Ile	Ser Leu Phe Lys Trp Pro Asn Val Ser	Asp
545	550	555

WO 01/07471

PCT/US00/19948

Ile	Trp	Ser	Thr	Tyr	Leu	Thr	Lys	Phe	Ile	Ala	Arg	Tyr	Gly	Gly
				560					565					570
Arg	Lys	Leu	Glu	Arg	Ala	Arg	Asp	Leu	Phe	Glu	Gln	Ala	Leu	Asp
				575					580					585
Gly	Cys	Pro	Pro	Lys	Tyr	Ala	Lys	Thr	Leu	Tyr	Leu	Leu	Tyr	Ala
				590					595					600
Gln	Leu	Glu	Glu	Glu	Trp	Gly	Leu	Ala	Arg	His	Ala	Met	Ala	Val
				605					610					615
Tyr	Glu	Arg	Ala	Thr	Arg	Ala	Val	Glu	Pro	Ala	Gln	Gln	Tyr	Asp
				620					625					630
Met	Phe	Asn	Ile	Tyr	Ile	Lys	Arg	Ala	Ala	Glu	Ile	Tyr	Gly	Val
				635					640					645
Thr	His	Thr	Arg	Gly	Ile	Tyr	Gln	Lys	Ala	Ile	Glu	Val	Leu	Ser
				650					655					660
Asp	Glu	His	Ala	Arg	Glu	Met	Cys	Leu	Arg	Phe	Ala	Asp	Met	Glu
				665					670					675
Cys	Lys	Leu	Gly	Glu	Ile	Asp	Arg	Ala	Arg	Ala	Ile	Tyr	Ser	Phe
				680					685					690
Cys	Ser	Gln	Ile	Cys	Asp	Pro	Arg	Thr	Thr	Gly	Ala	Phe	Trp	Gln
				695					700					705
Thr	Trp	Lys	Asp	Phe	Glu	Val	Arg	His	Gly	Asn	Glu	Asp	Thr	Ile
				710					715					720
Lys	Glu	Met	Leu	Arg	Ile	Arg	Arg	Ser	Val	Gln	Ala	Thr	Tyr	Asn
				725					730					735
Thr	Gln	Val	Asn	Phe	Met	Ala	Ser	Gln	Met	Leu	Lys	Val	Ser	Gly
				740					745					750
Ser	Ala	Thr	Gly	Thr	Val	Ser	Asp	Leu	Ala	Pro	Gly	Gln	Ser	Gly
				755					760					765
Met	Asp	Asp	Met	Lys	Leu	Leu	Glu	Gln	Arg	Ala	Glu	Gln	Leu	Ala
				770					775					780
Ala	Glu	Ala	Glu	Arg	Asp	Gln	Pro	Leu	Arg	Ala	Gln	Ser	Lys	Ile
				785					790					795
Leu	Phe	Val	Arg	Ser	Asp	Ala	Ser	Arg	Glu	Glu	Leu	Ala	Glu	Leu
				800					805					810
Ala	Gln	Gln	Val	Asn	Pro	Glu	Glu	Ile	Gln	Leu	Gly	Glu	Asp	Glu
				815					820					825
Asp	Glu	Asp	Glu	Met	Asp	Leu	Glu	Pro	Asn	Glu	Val	Arg	Leu	Glu
				830					835					840
Gln	Gln	Ser	Val	Pro	Ala	Ala	Val	Phe	Gly	Ser	Leu	Lys	Glu	Asp
				845					850					855

<210> 55

<211> 1598

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 116462CB1

<400> 55

atttatttag	gtcccttact	tttactagcc	accccttcc	cacttgcttc	taatggcaaa	60
ttagaatggt	aacttgcccc	ttgctcacct	catgcttggc	tttggaacc	ggtgagaaac	120
tgcaatccat	tggcggtagg	aaccacgatt	cccggcattc	ccagtgtccc	gagtccttcg	180
ggcttccctt	tccgggtctc	gaggctgctg	aaaccgaaac	cgctgtgctg	tgggcgcagc	240
gccgagattg	attcaccttc	acctgtgctg	cactccagct	gacccaagta	ggaagccaga	300
cgagctgtaa	aacatgaacg	gaagagtggg	ttatttggtc	actgaggaag	agatcaatct	360
taccagaggg	ccctcagggc	tgggcttcaa	catcgctcgg	gggacagatc	agcagtatgt	420
ctccaacgac	agtggcatct	acgtcagccg	catcaaagaa	aatggggctg	cggccctgga	480
tgggcggctc	caggagggtg	ataagatcct	ttcggtaaat	ggccaagacc	taaagaacct	540
gctgcaccag	gatgctgtag	acctctttcg	taatgcaggc	tatgctgtgt	ctctgagagt	600
gcagcacagg	ttacaggtgc	agaatggacc	tataggacat	cgaggtgaag	gggacccaag	660
tggtattccc	atatttatgg	tgctggtgcc	agtgtttgcc	ctcaccatgg	tagcagcctg	720

WO 01/07471

PCT/US00/19948

```

ggctttcatg agataccggc aacaactttg aaaaacttgc tctctttcaa tactcccaat 780
gaagatacat ttcactcacc ctccaccctt gctattctgc catgtctttc cctctctctg 840
catagccaga tttgaagtga ctgataccca ccccaaacct tgctgttcac agtctccaat 900
tcttcatatt ctaatgggaa agtaaaggta ttgtttgaag gaaaactgaa gaaaagactt 960
ggcttagaac aaatgaggag ttatatattt tactaggact tttgatagaa attcagctac 1020
aaccctaaaga gagaaagatt gagtcttctt gtcaccatag gcaatacctt ttttcttagc 1080
tggcatgcca taaaggccag ctatgtgata ttagaggaag aaaggatttt tctttttaat 1140
gatcttctct gggaaattat tgtggccttt atttaatttc taactacgta cctgggtgac 1200
tatatcgaca aagagtgaga agagcatttt tactttttta aaaaagcaaa tacatatata 1260
cacatacgta tgcaaatatt atagtataat agttagccct atggagaatt aaaggtgaga 1320
aagctacttt gtggtgtcta ggtttctgat aaaagggatg atcttaactg aagaatttaa 1380
agagatactt aaacagagca aatgtagtag gaacaaggga gtgagcctta taagaggacg 1440
ttcagtctca tttattaaaa taataactga gactgggaga ggtggctcat gcctgtaaat 1500
cccagcactt tggtagcctg aagtgggaga ttgcttgagt ccaggagacc agcctgggca 1560
acatagcaaa acctcatctc tatttaaaaa aaaaaaaaaa 1598

```

<210> 56

<211> 1432

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1210462CB1

<400> 56

```

tgagaatgaa agtggatgcc cgcgaatccc ggaagtcaga ctgttttttt cagttccctg 60
gaggcttttt gatactgatt cgcgtacacc tgttgtttga aagctctcag cgggacaatg 120
ctgacccagc tgaaagcaaa atcagagggg aagcttgcaa aacagatttg caaagtgtgt 180
ttggatcatt ttgaaaaaca gtattccaaa gaactcggag atgcctggaa tacagtaagg 240
gagatactaa catctccatc atgctggcaa tatgtgtcc tgcttaaccg attcaattat 300
ccttttgaac tggaaaagga tttacatttg aagggtctatc acacactctc tcagggatct 360
ttacccaact atcctaaatc agtgaagtgt taccttagca gaactccggg ccgaatccct 420
tcagaaagac accaaatttg aaacctgaaa aaatattatc tcctaaatgc tgcttctctt 480
ctcccagttg ttgctctgga attaagggat ggggagaagg ttctggatct ctgtgctgct 540
cctggaggga aatcaatagc tctgctgcag tgtgcttgtc caggttatct tcattgtaat 600
gaatatgata gtctgagatt gaggtggcta aggcagacgt tggaaatctt catccacag 660
cctttgataa atgtaattaa agtgtctgaa ttggatggca gaaaaatggg agatgcacag 720
cctgaaatgt ttgacaaggt gttagtggat gctccgtgtt caaatgatcg aagctggttg 780
ttttcttctg actctcagaa ggcacctctg aggataagtc aaaggaggaa tttgectctt 840
ctacagatag agctgttaag gtctgcaatt aaggccttac gtectggagg gatacttgta 900
tactctacat gcacgctttc caaggcagaa aatcaagatg tgatcagtga aattttaaac 960
tcccacggta acatcatgcc tatggacatt aaaggaatag caaggacttg ctcccacgac 1020
ttcacatttg ctcccactgg ccaggaatgt gggctcttag tgattccaga taagggcaaa 1080
gcctggggcc caatgtatgt agccaaattg aagaaatcat ggagcacagg aaaatggtga 1140
catgaatttg taaactgtgt ttatgtgtta ttatatttat atttctgaac tcagtacatg 1200
ttaatattta aataattatg cagtaacttt ctctgggtct gtttggaaac ctatttagtt 1260
aatactttag catcttagaa tctaggcttg agaattgttc aggtgtatct ttttcttaga 1320
aatatatctg taacaatgat ttaagggtgt gcagatggtg tttgttctat attataaatc 1380
tgctgtcttt gcttggcatt ttatagttaa attaattaga atatgtggtt tt 1432

```

<210> 57

<211> 2317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1305252CB1

<400> 57

```

gcgggtgctg ctacggagg cgccatattg gaggggacaa aactccggcg acacgagtga 60
cacaaataaa cccctggacc cccttgttcc ctacgtctta agggccgcga tgttgtaact 120

```


WO 01/07471

PCT/US00/19948

```

aacttggaca gcaggcttct gatcttccct ttatatatct gctgtaactt cttgtatata 960
tcaccagaaa aaaagaattg aaaataatcg tcaccagaaa aatccagaaa actgaagatt 1020
tcactgattg gaaacagtag cactttgaaa acttttttagg ccagctttta tttaatggcc 1080
ctactgatat tcacatcgaa ggtgactaac aatgacaaag gccttatgaa ctgtacagac 1140
aatacagaag attattctta tcttcattgc atttctatgc atatgcgtaa gaacatttta 1200
aagccaagaa aatatctgtc aaaccatttc tgttagaacg atgtcaattc atgcttttaa 1260
tttagcatca atagaaaatt gctgtaggta aatctcacat ttatctgcaa caaaatatag 1320
atttaatttt tagcttaaac tttgtttcta ccttatgtta gtggacctca gttatccatc 1380
tgtaaatctt tttttatttg gctaaaataa tctaaaagaa taatttggtt ggccaattag 1440
aaatgccttt ttcagttggt gtattgaaag ctttcttcta acattttcac ctgctcattg 1500
tgattcctcc ttttagtcta atatctttcc aggtcatact tgtttttaac cattaatat 1560
tttcttctcg gttttggaga ctaagctgat aaactttttt taaaacttaa gcattgtcat 1620
tgctattttt ttttaattga ctttcctagg agtttaagaa cagtgaaggt tagcttcgca 1680
ccttcaaatt atcttgaatt agggaaaaat cagtttgatt ccaaggatat ttcttgcctt 1740
acatgggtctt ttctttgaca gtctgtacac cttt

```

<210> 59

<211> 1268

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1558289CB1

<400> 59

```

taagtgaagc ttctccattc tgtaagcttt ccgggaacat ccaaggcaag actggcaccc 60
agcacagcag tgactgacca catacccccac tctccaggac ccatggagtc cttcagctca 120
aagagccttg cactgcaagc agagaagaag ctactgagta agatggcggg tcgctctgtg 180
gctcatctct tcatagatga gacaagcagt gaggtgctag atgagctcta ccgtgtgtcc 240
aaggagtaca cgcacagccg gccccaggcc cagcgcgtga tcaaggacct gatcaaagtg 300
gccatcaagg tggctgtgct gcaccgcaat ggctcctttg gccccagtga gctggccctg 360
gctacccgct ttccgccagaa gctgcggcag ggtgccatga cggcacttag ctttggtgag 420
gtagacttca ccttcgaggc tgctgttctg gctggcctgc tgaccgagtg ccgggatgtg 480
ctgctagagt tgggtggaaca ccacctcacg cccaagtcac atggccgcac ccgccacgtg 540
tttgatcact tctctgaccc aggtctgctc acggccctct atgggcctga cttcactcag 600
caccttggca agatctgtga cggactcagg aagctgctag acgaaggga gctctgagag 660
ccctgagcct agcacattcc accttgacaa aatggttgac tgagaaaaca cagataatgg 720
gcttcctaac cctgctcacc tggcactaac acttttcaat cttcaggctt cattccttcc 780
caagagtgtt tttgactctg agaccagccc acccccaaac agctagtgga gaaggagcaa 840
tgctgagggg tgaggcctct ctcccactcc agccccagga caggaaacag aactgcctga 900
aaaaggtgaa gtgaaacttg gatctctatt tctcccataa gggacttctg aaacagggaa 960
gccccctccc atgtgaacca aggaaaggag gcacagccca gagaaccctt ttggggatac 1020
taaagacaga agaggggaag gtggccctta gagacagagc ttggacagat gccagaggct 1080
ctgttccaga gtgcaggaag aaggggctag ggcaggggag attctcatag gggaaataaa 1140
actactaaaa tatgagaaaa aaaaaggacc cagcgaaacc ccaaggaagc gcaacaggca 1200
agggaaaaga gaacgaggag gggagccggc cccaagacac aaagcagcaa aaaaagaggg 1260
ggggccgc

```

<210> 60

<211> 1331

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1577739CB1

<400> 60

```

gacatcttga ggcccacgtg gacctgagtt ctgggtgcagg atttaataca ctgaggagtt 60
cagccacccc gtggagagcc tggcgctgac tgtggaagag gtgatggacg tgcgccgtgt 120
gctgggtgaag gccgagatgg aaaagttttt gcagaacaag gagctcttca gcagtctgaa 180
gaaggggaag atttgctgct gctgccgggc caagttcccg ctgttctcgt ggccgcccag 240

```

WO 01/07471

PCT/US00/19948

```

ctgtctcttc tgcaagagag ccgtctgcac ttctctgtag ataaagatga agatgccttc 300
taagaaatth ggacacatcc ctgtctacac actgggcttt gagagtcttc agagggtatc 360
agctgccaaa accgcgccaa tccagagaag agacatcttt cagtctctgc aagggccaca 420
gtggcagagc gtggaggagg cgttccccc catctactcc cacggctgtg tcctgaagga 480
tgtctgcagt gagtgcacca gctttgtggc agacgtgggt cgttccagcc gcaagagcgt 540
ggacgtcttc aacactacgc cagcagcgag tcgccagacc caatccctct acatccctaa 600
caccaggact cttgacttca agtgacagcc ccagggtggcc aggcctccag gaggcaccag 660
gcaggccctg tatcaggcta ggacgtctct agctgtgcat gtacatatat acatatatag 720
atacatttat aatatataca cacagtctat atatttatat acactgtttc ctggccccag 780
agctcatttg ggttcaggcg cacttcaaaa cctccctggg gggaggctgt ttcttctcag 840
gattccttgc cagggaggaa ggggagggaa caggggtggg tttctcactg aagagagaaa 900
gcagaagggt ctagatcctg gcacagactg catcccatgt tcccatgctc ttctccgtcc 960
ccagggaatgc gaacggcagt ttcccttccc cagtggacgt ctagggtggg acagggtatc 1020
ttggctcccc gctggaccag agtgccctgc ttgcctctgc tctccctttg tggggactca 1080
ggcagcagag gcatctggga agtctctgag taggcagggt cctcctggga ggcaccccca 1140
cctgtttgaa aggtctggcc aggcgtgggt gttcaggcct gtaattccag cactttggga 1200
ggccgaggag ggaggatcac ctgaggtcag gagtgtgaga ccagcctggc caacatgatg 1260
aaatgttgct tctactgaaa atgcaaaaat tagccaggta tagtggcagg aacctgtaat 1320
cccagctaca g

```

1331

<210> 61

<211> 3227

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1752768CB1

<400> 61

```

tgcgagtacc tccatgggtcc cgggtggctgt gacggcgcca gtggcgcttg tctgtccat 60
aaacagcgat ttctcagatt tgcgggaaat taaaaagcaa ctgctgctta ttgcgggct 120
taccggggag cggggcctac tacacagtag caaatggteg gcggagtggg ctttctctct 180
ccctgcattg cctctggccg agctgcaacc gcctccgcct attacagagg aagatgcccc 240
ggatatggat gcctataccc tggccaaggc ctactttgac gttaaagagt atgatcgggc 300
agcacatttc ctgcatggct gcaatagcaa gaaagcctat tttctgtata tgtattccag 360
atatctgtct ggagaaaaaa agaaggacga tgaacagtt gatagcttag gccccctgga 420
aaaaggacaa gtgaaaaatg aggcgcttag agaattgaga gtggagctca gcaaaaaaca 480
ccaagctcga gaacttgatg gatttggact ttatctgtat ggtgtgggtg ttcgaaaact 540
ggacttgggt aaagaggcca ttgatgtgtt tgtggaagct actcatgttt tgccttgca 600
ttggggagcc tggttagaac tctgtaacct gatcacagc aaagagatgc tgaagttcct 660
gtctttgcca gacacctgga tgaagagtt tttctggct catatataca cagagtgtga 720
gttgatagag gaggccctgc aaaagtatca gaatctcatt gatgtgggct tctctaagag 780
ctcgtatatt gtttcccaa ttgcagttgc ctatcacaa atcagagata ttgacaaagc 840
cctctccatt tttaatgagc taaggaaaca agacccttac aggattgaaa atatggacac 900
attctccaac cttctttatg tcaggagcat gaaatcggag ttgagttatc tggctcataa 960
cctctgtgag attgataaat atcgtgtaga aacgtgctgt gtaattggca attattacag 1020
tttacgttct cagcatgaga aagcagcctt atatttccag agagccctga aattaaatcc 1080
tcggtatctt ggtgcctgga cactaatggg acatgagtac atggagatga agaacacgtc 1140
tgctgctatc caggcttata gacatgccat tgagggtcaac aaacgggact acagagcttg 1200
gtatggcctc gggcagacct atgaaatcct taagatgcca ttttactgcc ttattatttg 1260
tagacggggc caccagcttc tagtggaagc caaaaagtgt tattggagag cttacgccgt 1380
ttacgagaaa ctcaatcaac tagtggaagc actggcaaaag cttcatgaac agttgactga 1440
gggagatgtg gctgcccagt gttacatcaa atatatccaa gatattctatt cctgtgggga 1500
aatagtagaa cacttgaggg cttcaacttg tgcacaaaag tgttgtgcat ttaatgatac 1620
gtgcaaaactg tgggatgaag tactccggca aatcctacag cttcggaacc aaggcgagac 1680
ccgggaagaa ggtaaggcct ctcccttttt cctacctgct tcaactctct ctaacaatac 1740
tccatccacc agagttttct cactcaactt gtcttctgtc acgccatagt tggctactct 1800
caagccagca cattgttaga cccatcttaa ttaagcctta cctccatgta aagaacagca 1860
cgtctgttcc aaggacctca gctcttcttg tttctacaga tggcaacagc tccataggga 1920
cagcttgtat aattaccttc agaggccaac tgacagaatc ctggcaggaa cagacattat 1980

```

WO 01/07471

PCT/US00/19948

```

cttgccagtt agaagtactt ctgtctcact tatgtccaaa gagtggctat agatcttggc 2040
cttcttcctt gaatgctttt ttttttttgg cccccaagaa agtccctttt atagcacttt 2100
agcacaggca atgctacagg aacaaagttt caatgctgct gagagtgaag gaaaggagga 2160
aagtctgcca ctctaccctg agctggcagt agggcactga gtaccctagg aagaagtcag 2220
agcaatggat acaaatgacc ttgctcttgg atttcttgag catgatccct attctgatgt 2280
cagagattag gtttaaatgg aatagagcta tccatttggt cttactctct agggagacaa 2340
tcttccaaaa cagttttggg ggggtcttct aaagctttca aattggaagt aactttattc 2400
aactagagtt gaataaaaaga agggcaaaaa taatctcaca gagcttggaa ctgctgatag 2460
cccttactga gggcaaaaaga tggctatatt gttagctata ctccctacca agcaagcaag 2520
gagataggat tatagataat ttcacggaca tttggaaata acattggtga ttatacagac 2580
aagaataaac tcacttcaag ctggctctgt ttaataaatt ttcaacgtaa ttgtctattt 2640
ttttccctcc catctgcaac agaatacatt tttttcagcc tttatctaga tgaggtaaag 2700
ggaatcattc ttatggtgct cttggagagt ttcaggcctg tgcattgtgtg tacagcagga 2760
ggtaatatgc tataatgtct gctgtaatat atttgcacag tagatgctat ggatcattct 2820
gagctcaggg tccagacttt attcttattc ccagaatttt gtgttacgtt tttacctcct 2880
aacatatgac acttcatctt atattaagga aggttttagaa tatctaatac gacttgaatt 2940
catttggttac taagccttct caggcaagct gtatactagt tactggcttc cactggcatg 3000
ccttttcaag gttcccatgg tccagaatga tgtttgatcc ttaatttttc tgtccctttt 3060
ataatttggt ttaatgattt tgctacattt ggaattcaat aaaaaatgtg aacaataata 3120
tctttaatat aactgttttt gtgtgcatag aaatcatata agtaataaaa aaaaaacaac 3180
aacatgagat tacataggtg gttataatac aaaagtgaga aaaaagc 3227

```

<210> 62

<211> 1865

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1887228CB1

<400> 62

```

gttctagatc gcgagcggcc gcctcccggg ggtcctcctg atgccctagg aagacgcgac 60
tcagaatttg gccagggagt gaaggccaag aagcccatcc agactaagtt ccgaatgcca 120
ctcttgaact ggggtggcatt gaaacccagc cagatcaccc gcactgtctt cacagagctc 180
aatgatgaga aggtgctgca ggagctagac atgagtgttt ttgaggaaca gttcaagacc 240
aagtcccaag gccccagcct ggacctcagc gctctcaaga gtaaggcagc ccagaaggcc 300
cccagcaagg cgacactcat tgaggccaac cgggccaaga acttggccat caccctgcgg 360
aagggcaacc tgggggcccga gcgcatctgc caagccattg aggcgtacga cctgcaggct 420
ctgggcccgtg acttccctgga gctgctgatg cgcttccctg ccacagagta tgagcgcagc 480
ctcatcaccg gctttgagcg ggagcagcgg ccaattggagg agctgtcaga ggaggaccgc 540
ttcatgctat gcttcagcgg catcccgcgc ctgcggagc gcattgaccac actcaccttc 600
ctgggcaact tcccggacac agcccagctg ctcatgccgc aactgaatgc catcattgca 660
gcctcaatgt ccatcaagtc ctctgacaaa ctccgccaga tcctggagat tgtcctggcc 720
tttggcaact acatgaacag tagcaagcgt ggggcagcct atggcttccg gctccagagc 780
ctggatgcgc tgttggagat gaagtcgact gatcgcaagc agacgtgtgt gcactacctg 840
gtgaaggtea ttgctgagaa gtacccgcaa ctcacaggct tccacagcga cctgcacttc 900
ctggacaagg cgggctcagt gtccctggac agtgtcctgg cggacgtgcg ctccctgcag 960
cgaggccctag agttgacaca gagagagttt gtgcggcagg atgactgcat ggtgtctcaag 1020
gagttcctga gggccaactc gccaccatg gacaagctgc tggcagacag caagacggct 1080
caggaggcct ttgagctctgt ggtggagtag ttcggagaga accccaagac cacatcccca 1140
ggcctgttct tctccctctt tagccgcttc attaaaggct acaagaaagc tgagcaggag 1200
gtggaacagt ggaaaaaaga agccgctgcc caggaggcag gcgctgatac cccgggcaaa 1260
ggggagcccc cagcacccaa gtcaccgcca aaggcccggc ggccacagat ggacctcatc 1320
tctgagctga aacggaggca gcagaaggag ccactcattt atgagagcga ccgtgatggg 1380
gccattgaag acatcatcac agatctgcgg aaccagccct acatccgcgc agacacaggc 1440
cgccgcagtg cccgtcggcg tccccgggc ccccactgc aggtcacctc cgacctctcg 1500
ctgtagccgc tatttctgca ggtggattct gcagggtgtg ggggcccgtg acaggctgag 1560
gctcaaggaa ggtggctctc agctcggctg gccgggcagc cctcctcccg ctgtggcccg 1620
cctcaaaccg gctgggtgat cctcctcttg gccacagagg gcagcatcgc ccgccccttc 1680
ccccaaatgc tgcttgagc acccacccta aagccccctc caaatagcca tacttagcct 1740
cagcaggagc ctggcctgta acttataaag tgcacctcgc ccccgcaagc cccagccccg 1800
aggaccgtcc atggacctta tttttatatg agattaataa agatgtttgc aaaaaaaaaa 1860

```

WO 01/07471

PCT/US00/19948

aaaaa

1865

<210> 63
<211> 1924
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1988468CB1

<400> 63
agctgccggg cggtcctgcc gagctgtgag ggcaacggag gggaaataaa agggaaacggc 60
tccgaatctg ccccgagcggc cgctgcgaga cctcggcgcc gacatcgcg cagagcgctt 120
tgcacgccag gaaggtcccc tctatgtgct gctgagccgg tectggacgc gacgagcccg 180
ccctcggtct tcggagcaga aatcgcaaaa acggaaggac tggaaatggc agaccatatg 240
atggccatga accacgggcg ctccccgac ggacccaatg ggctgcacca tcacctgcc 300
caccgcatgg gcatggggca gttcccgagc ccccatcacc accagcagca gcagccccag 360
cacgccttca acgcccctaat gggcgagcac atacactacg gcgcgggcaa catgaatgcc 420
acgagcggca tcaggcatgc gatggggccg gggactgtga acggagggca ccccccgagc 480
gcgctggccc ccgcggccag gtttaacaac tcccagttca tgggtcccc gggtggccagc 540
cagggaggct cctgcggcg cagcatgcag ctgcagaagc tcaacaacca gtatttcaac 600
catcaccctt acccccacaa ccactacatg ccggatttgc accctgctgc agggccaccag 660
atgaacggga caaaccagca ctcccgagat tgcaacccca agcacagcgg cggcagcagc 720
acccccggcg gctcggggcg cagcagcacc cccggcggtc ctggcagcag ctcggggcg 780
ggcgcgggca gcagcaacag cggcgggcg agcggcagc gcaacatgcc cgctcccg 840
ccccacgtcc ccgctgcaat gctgcgccc aatgtcatag acactgattt catcgacgag 900
gaagtcttta tgtccttggg gatagaaatg ggtttggacc gcatcaagga gctgcccga 960
ctctggctgg ggcaaaacga gtttgatttt atgacggact tcgtgtgcaa acagcagccc 1020
agcagagtga gctgttgact cgatcgaaac cccggcgaaa gaaatcaaac ccccaacttc 1080
ttcggcgtag attaaaagaa acattccctt agacacagta tctcactttt cagatcttga 1140
aaggtttgag aacttggaia caaagtaaac tataaacttg tacaattgg ttttaaaaaa 1200
aattgctgcc actttttttt cctgtttttt tttcgttttt gtagccttga cattcaccca 1260
cctcccttat gtagttgaaa tatctagcta acttggctct tttcgtttgt tgtttttact 1320
cctttccctc actttctcca gtgctcaact gttagatatt aatcttggca aactgcttaa 1380
tcttgtggat tttgtagatg gtttcaaact actgaactgc attcagattt acgagtga 1440
ggaaaaattg cattagtgg ttgcatgaac ttcgaaaggc agatattact gcacaaactg 1500
ccatctcgct tcattttttt aactatgcat ttgagtacag actaattttt aaaatatgct 1560
aaactggaag attaaacaga tgtggggcaa actgttctgg atcaggaaag tcatactgtt 1620
cactttcaag ttggctgtcc ccccgccgc cccccccacc cccatagtga cagatgataa 1680
taggggtgtg aatgtcgtca gtggcaaaac tttcacagat ttttattttg tttctgtctt 1740
caacattttt gacactgtgc taatagttat attcagtaca tgaaaagata ctactgtgtt 1800
gaaagctttt taggaaattt tgacagtatt tttgtacaaa acattttttt gaaaaaatac 1860
ttgttaattt attctatttt aatttgccaa tgtcaataaa aagttaagaa ataaaaaaa 1920
aaaa 1924

<210> 64
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 2049176CB1

<400> 64
ggcctggtcc gcagcgccct gcgcccacc gcccgagac tggggcccaa gccccgtga 60
agatggtgtc ctggatgac tccagagccg tgggtgctgt gtttggaatg ctttatcctg 120
catattattc atacaaagct gtgaaaacaa aaaacgtgaa ggaatatgtt cgatggatga 180
tgtactggat tgtttttgct ctctatactg tgattgaaac agtagccgat caaacagttg 240
cttggtttcc cctgtactat gagctgaaga ttgcttttgt catatggctg ctttctccct 300
ataccaaagg agcaagttta atatatagaa aattccctca tccacttctt tcttcaaagg 360
aaagggagat tgatgattat attgtacaag caaaggaacg aggttatgaa accatggtaa 420

WO 01/07471

PCT/US00/19948

```

actttggacg gcaagggttta aaccttgcag ctactgctgc tgttactgca gcagtaaaga 480
gccaaggagc aataactgaa cgtttaagaa gcttcagtat gcatgattta acaactatcc 540
aagggtgatga gcctgtggga caaagaccat accaacctct accagaagca aaaaagaaaa 600
gtaaaccagc cccagtgaa tcagcagggt atggaattcc actgaaagac ggagatgaga 660
aaacagatga agaagcagag gggccatatt cagataatga gatgttaaca cacaaagggc 720
ttcgaagatc gcaaagcatg aaatctgtga aaaccaccaa aggccgcaaa gaggtgcggt 780
acgggtcact aaaatacaaa gtgaagaaac gaccacaagt gtatttttag tcatctacac 840
gtcaaatatc ccaagacaga ttatgctaaa tacatcgact tcatcttcta acatgatata 900
ttcaggattt acacattaaa atgattattt aaattgtggc agtgatgg 948

```

<210> 65
 <211> 2035
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2686765CB1

```

<400> 65
gaccgtggcc ctgaccgcca aacccccgct tgcccccaag ccgggaacca cagtggcctc 60
aggagtgact gcacggagtg atgcaggaca agtgacaggt gggcatggag ctgccgcagc 120
aacatcagca tcagcaggac aggcctcctga ggacccctca ggccctggca caggccctc 180
tgggacttgt gaggtccgg tagctgtcgt gaccgtgacc ccagctccgg agcctgctga 240
aaactctcaa gacctgggct ccacgtccag cctgggacct ggcattctctg ggcctcgagg 300
gcaggccccg gacacgctga gttacttgga ctccgtgagc ctcatgtctg ggaccttga 360
gtccttggcg gatgatgtga gctccatggg ctacgattca gagataaacg ggctggccct 420
gcgcaagacg gacaagtatg gcttccttgg gggcagccag tactcgggca gcctagagag 480
ctccattccc gtggacgtgg ctccggcagcg ggagctcaaa tggctggaca tgttcagtaa 540
ctgggataag tggctgtcac ggcgattcca gaaggtgaag ctgctgctgc ggaaggggat 600
ccctcctct ctccagagcca aagcctggca gtacctgtct aatagcaagg aacttctgga 660
gcagaaccca ggaaagtgtg aggagctgga acgggctcct ggggacccca agtggctgga 720
tgtgattgag aaggacctgc accgccagtt ccttttccac gagatgtttg ctgctcgagg 780
ggggcatggg caacaggacc tgtaccgaat cctgaaggcc tacaccatct accggcctga 840
cgagggttac tgccaggccc agggccccgt ggctgcggtc ctgctcatgc acatgcctgc 900
ggagaagcct tttggtgcct ggggtgcagat ctgcgacaag tacctcccag gttactacag 960
tgcagggtcg gaggccattc agctggacgg ggagatcttt tttgcactcc tgcgccgggc 1020
ctcccgcgtg gcgcatcgcc acctgcagcg gcagcgcatt gacctgtgc tctacatgac 1080
ggagtggttc atgtgcatct tcgccgcac cctgccctgg gcgtcggtgc tgcgtgtctg 1140
ggacatgttt ttctgtgaag gcgttaagat catcttccgg gtggccctgg tcctgctgcg 1200
ccacacgctg ggtcagtgag agaagctgcg ctctgcca aaaggatgat agaccatgga 1260
gcagctgcgt aacctgcccc agcagtgcat gcaggaagac ttctggtgc atgaggtgac 1320
caatctgccg gtgacagaag cactgattga gcgggagaat gcagcccagc tcaagaagt 1380
gcgggaaacg cggggggagc tgcaagtatc gccctcacgg cgactgcatg ggtcccgggc 1440
catccacgag ggcgcgggc ggcaacagcc acccctgggc cctcctcca gcctcctcag 1500
cctccctggc ctcaagagcc gaggtcccc ggcagctgga ggggccccgt ccccgccgcc 1560
ccccgtccgc agagccagtg ctgggcctgc cccaggccct gtgggtcactg ctgagggact 1620
gcatccatcc ctccctcac ccactggcaa tagcaccccc ttgggttcca gcaaggagac 1680
ccggaagcag gagaaggagc ggcagaaaca ggagaaggag cggcagaaac aggagaagga 1740
gcgggagaag gagcggcaga agcaggagaa agagcgagag aagcaggaaa aggagcgaga 1800
gaagcaggag aaggagcggc agaagcagga gaagaaggct caaggccgga agctttcgtc 1860
gcgtcgaaaag gcagatgggc ccccaggccc ccatgatggt ggggacaggc cctcagccga 1920
ggccccggcag gacgcttact tctgacctct gccctggggc tggactgcat ggccccctc 1980
tttccctcag ccaagaacag gcctggccca aggtgccacc ccctagcacc ttgtc 2035

```

<210> 66
 <211> 766
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3215187CB1

WO 01/07471

PCT/US00/19948

```
<400> 66
cttggaggga gtgcggtcct ctagggaggc atcgggctcc taggggcttc ttggcgtgtg 60
tgggtgggatt ggggtccgcc ggccatggcc ttcacttttcg ctgcgttctg ctacatgctg 120
tctctgggtgc tgtgcgctgc gctcatcttc ttcgccatct ggcacataat tgcctttgat 180
gagttaagga cagattttta gagcccata gaccagtgc aacctgttca tgcgagggaa 240
cggttgagga acatcgagcg catctgcttc cttctgcgaa agctgggtgct gccagaatac 300
tccatccata gcctcttctg cattatgttc ctgtgtgcgc aagagtggct cagcgtgggg 360
ctgaatgtcc ctctactttt ctatcacttc tggaggtatt tccactgtcc agcagatagc 420
tcagaactag cctacgaccc accggtgggtc atgaatgccg acacttttag ttactgtcag 480
aaggaggcct ggtgtaagct ggcttctat ctctctctct tcttctacta cctttactgc 540
atgatctaca ctttagtgag ctcttaacgc aaagaccatg cacatcatca gagactgaga 600
tgggagagggc ctgagacgga gaggtgcatt tctgctgggt actggaggag ggaccagaat 660
gaggatacgt gagatataga cccggcaggc agtcagactg aatgggagct ggaatcacgc 720
agcagctggg agccgagtta accctgcgtg tctgtgtcac cctgtt 766
```

```
<210> 67
<211> 2503
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<223> Incyte ID No: 3500375CB1
```

```
<400> 67
tgtcctcggc ggccctgggtg gctactgccc ctgctgctgt cgtaggcgag gacggctgtt 60
agtgtgctgt ctgttggttc gtcgcggcgg cgaaggagga ggaggaagag ggcgaggcga 120
caagagaaga aggaggcagg cgcggcggca gcggcggcgc cccgagccgg cggaggcgag 180
ggggggggaag atggcggacg tgcttagcgt cctgcgcacg tacaacatcc agaagaagga 240
gatttggtgt aaggagagac aagtgtatct cggggagttc tcctggccca agaattgtga 300
gaccaactat gttgtttggg ggactggaaa gacactttct catcctgttt atgtccgacg 360
ggattccatt ttattttctac ttaataacgt ggaaggccaa cccagagagt actacacatt 420
tgcagctact gaaaatatct ctgtggttag aagacctgat cgaaaagatc tacttgata 480
tctcaatggt gaagcgtcaa catcggcaag tatagacaga agcgtccct tagaaatagg 540
tcttcagcga tctactcaag tcaaacgagc tgcagatgaa gtttttagcag aagcaaagaa 600
accacgaatt gaggatgaag agtgtgtgcg ccttgataaa gagagattgg ctgccggttt 660
ggagggtcac aaagaaggga ttgtacagac tgaacagatt aggtccttgt ctgaagctat 720
gtcagtgga aaaaattgctg caatcaaagc caaaattatg gctaagaaaa gatctactat 780
caagactgat ctagatgatg acataactgc ccttaaacag aggagttttg tggatgctga 840
ggtagatgtg acccgagata ttgtcagcag agagagagta tggaggacac gaacaactat 900
cttacaaagc acaggaaaga atttttccaa gaacattttt gcaattcttc aatctgtaaa 960
agccagagaa gaaggcgctg cacctgaaca gcacctgccc ccaaagtcag cacctgtgga 1020
tcccactttg cgcaccaaac agcctatccc agctgcctat aacagatacg atcaggaaaag 1080
attcaaagga aaagaagaaa cgggaaggctt caaaattgac actatgggaa cctaccatgg 1140
tatgacactg aaatctgtaa cggagggtgc atctgcccgg aagactcaga ctctgcagc 1200
ccagccagta ccaagaccag tttctcaagc aagacctccc ccaaatacga agaaaggatc 1260
tcgaacaccc attatcataa ttcttcagc taccacctct ttaataacca tgcttaatgc 1320
aaaagacctt ctacaggacc tgaaatttgt cccatcagat gaaaagaaga aacaaggttg 1380
tcaacgagaa aatgaaactc taatacaaag aagaaaagac cagatgcaac cagggggcac 1440
tgcaattagt gttacagtac cttatagagt agtagaccag ccccttaaac ttatgcctca 1500
agactgggac cgcgttgtag ccgtttttgt gcagggtcct gcatggcagt tcaaaggttg 1560
gccatggctt ttgcctgatg gatcaccagt tgatatattt gctaaaatta aagccttcca 1620
tctgaagtat gatgaagttc gtctggatcc aaatgttcag aaatgggatg taacagtatt 1680
agaactcagc tatcacaac gtcatttgga tagaccagtg ttcttacggt tttgggaaac 1740
attggacagg tacatggtaa agcataaatc gcacttgaga ttctgaatta tttggctcct 1800
ccattttctg aaattgagac tcaagcttta tgaatttatc aagaacttaa aaatgaagaa 1860
ggtcacagat tgatctttta taagacctta tttgatgctt tgtgcttcaa ggagatgata 1920
cctgtcatcc atataagcaa actttttggc ttacaactat ttttttaata tttagcctct 1980
agtctgtaat ggaaattgta tattttgata gaagtttttt ctccattggg taaattagca 2040
ttacttaaaa tttgtttctt tagaaaataa atgcaggtta taaatgtgtg tatatttaga 2100
gattataagg ctctctgagc catcttctga tttttcattg ctctataatt ctttttactg 2160
aaaatactat gttatgaatg gtattaaatt ttagtctctg gaacatccaa aaccaagcaa 2220
agggatgtga ctattttgaa tgaatcagaa tgtcaacttg tatgtacac atattctacac 2280
```


WO 01/07471

PCT/US00/19948

```

cccatcacgg cgtagtgcaa gctaaaatta accctcacta aaggggaataa gcttgcgggc 60
gccgggcgaa tggtcggcag ctgcgaggcc aagagagacc ccaggacaca cacagctgcc 120
tcccgggtgcg agaagaagac cccgggttga gagtgagatg gcgtttaatg attgcttcag 180
tttgaactac cctggcaacc cctgcccagg ggacttgatc gaagtgttcc gtcctggcta 240
tcagcactgg gccctgtact tgggtgatgg ttacgttatc aacatagcac ctgtagatgg 300
cattcctgcg tcctttacaa gcgccaagtc tgtattcagc agtaaggccc tggtgaaaat 360
gcagctcttg aaggatgttg tgggaaatga cacatacaga ataaacaata aatacgatga 420
aacgtacccc cctctccctg tgggaagaaat cataaagcgg tcagagtttg taattggaca 480
ggagggtggc tataacttac ttgtcaacaa ctgtgaacat tttgtgacat tgcttcgcta 540
tggagaagga gtttcagagc aggccaaacc agcgataagt accgttgagt ttgtgacagc 600
tgctgttggg gtctttctcat tccctgggctt gtttccaaaa ggacaaagag caaaatacta 660
ttaacaattt accaaagaga tattgatatt gaaggaattt gggaggagga aaagaaacct 720
ggggtgaata cttattttca gtgcattcatt actgttccag attcctatga tggatggcag 780
actctttaat aaattgctta ctgatattat cttaaaaaaa aaa 823

```

<210> 71

<211> 1033

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1511488CB1

<400> 71

```

gcgccagggg ttccagctgc acgtcccagg ctctccagcg cgcggcaggc cggggcgggg 60
cgaggagagc tgccggggaca acgcctgtgg ctgggtccgg aggtgcgggt gcggcgcggg 120
acaagcgggc agcatgctca gggcggtcgg gagcctactg cgccttggcc gcgggctaac 180
agtcgcgtgc ggccccgggg cgctctcga ggccacgcga cggcccgcac cggtcttcc 240
gccccgggg ctcccctgct actccagcgg cggggccccc agcaattctg ggccccaagg 300
tcacggggag attcacggag tccccacgca gcgcaggcct tcgcagttcg acaagaaaaat 360
cctgctgtgg acagggcgtt tcaaatcgat ggaggagatc ccgcctcgga tcccgccaga 420
aatgatagac accgcaagaa acaaagctcg agtgaaagct tgttacataa tgattggact 480
cacaattatc gcctgctttg ctgtgatagt gtcagccaaa agggctgtag aacgacatga 540
atccttaaca agttggaact tggcaaagaa agctaagtgg cgtgaagaag ctgcattggc 600
tgcacaggct aaagctaaat gatattctaa gtgacaaagt gttcacctga ataccatccc 660
tgtcatcagc aacagtagaa gatgggaaaa atagaatatt taccaaaata tctgccatgg 720
ttttattttg gtaacaagaa gcacaatgtc ttttttattt ttatttttta gtaaaactttt 780
actgaagtat accatgcatt caaaaagtgg acaaaactgt atacagtctg atagatattt 840
atgtcgtgaa cacctgtgta accactgcc aagtgaagat gtagaatatt ggcaaacactt 900
cacagcctca ttctgcctt ttctcagcca ttacctccca aacatagcag tttttctgag 960
tttcatcacc tttgattcat tttgcctgtt tttgaacttt atataaatgg atttatacat 1020
taaaaaaaaa aaa 1033

```

<210> 72

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1638819CB1

<400> 72

```

ggcacttccg gcggcgcgct gcaggcgcg ggaacaccaa tggcggggta cttgaagctg 60
gtgtgtgttt cttttcagcg tcaagggttc cacactgttg ggagtgcgtg caagaatcgg 120
acaggcgctg agcacctgtg gctgaccgga catctcaggg acccatttgt gaaggctgcg 180
aagggtggaga gttaccgggtg tcgaagcgcc ttcaagctcc tggagggtgaa cgagaggcac 240
cagattctgc ggccccggcct tcgggtgtta gactgtgggg cagctcctgg ggctggagt 300
cagggtggcg tgcagaaggt caacgcgcga ggcacagatc ccagctctcc tgttggtctc 360
gtgcttgggg tagatcttct tcacatatc cccctggaag gagcaacttt tctgtgccct 420
gctgacgtga ctgaccgga aacctcacag agaatectcg aggtgcttcc tggcaggaga 480
gcagatgtga ttctgagcga catggcgccc aatgccacag ggttccggga ctcgatcat 540

```

WO 01/07471

PCT/US00/19948

```

gacaggctca tcagcctgtg cctgaccctt ctgagcgtga cccagacat cctgcaacct 600
ggggggacat tcctttgtaa aacctgggct ggaagtcaaa gccgtcggtt acagaggaga 660
ctgacagagg aattccagaa tgtaaggatc atcaaacctg aagccagcag gaaagagtca 720
tcagaagtgt acttcttggc cacacagtac cacggaagga agggcactgt gaagcagtga 780
ggatttcttg tgccattttc ataatggtca ttagctcctt ttaagctaga aacgtagcct 840
gagctcctga agagttcctg ggagatttga gctgattttg gagatggagc aggacaagtg 900
gggagtctct ctctctcttt ctctctctct ctttttaacc aaaaagagat gacaaaacta 960
agttcagggg ccatggaaaa tgaaaaagtc cgctatatgt tgatttggga agagaaagtt 1020
atcaagagaa agaggtgagg atggaaggat ggagaaaaac agactgtggg aaggatcaga 1080
aggaatccgc cgaggcagg atgggtgtgc ccatgtgtgc cttgacggga cttcatctta 1140
tagactgtta aactgtcaca cacaaacagg ctttccaccc ctgctctgag agcaccacgc 1200
acagatttcc agttcttagt gtggctgttt aaagtagaaa atctgggggc tgggtgaggc 1260
cactcatgcc tgtaaaccca gggctttaga aggcagaggc tgggggattg cttgaagtca 1320
ggagttcaag accaacctgg gcaacatagc aacaccccc atgtctacaa aaatgaaaaa 1380
ccaaaaagca aacccaaaaga aaaatctgaa atttccatct ggggattaac ttctgtcttt 1440
ctgggtgaaca atatagcaat tcacgcattc ttcaagcagc aaaagttccc ggaacaatta 1500
gggaagacgt atgggtctgaa tttatccagg cagtgggtct gctttggttt ttgctggaaa 1560
tttatatcag tgtctgggct cccaagaaca taaatgtaat tgccaaagca aaaaaaaaaa 1620
aa

```

<210> 73

<211> 2449

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1655123CB1

<400> 73

```

cgttgccggg ctctccggaa ggagacgtgg cggcggttgg gccggtgata cccgggcgct 60
ttatagtcct gccgctctct cctccaccct cccctcctcc tcctctctct ctggagcaga 120
ggaggttgtg gcggtggctg gagaaagcgg cggcgaggga tggaggaagg aggcggcggc 180
gtacggagtc tgggtccggg cgggcgggtg ttactggtcc tctgcccct cctggaggcg 240
tccggcggcg gccgagccct tctcaactc agcgatgaca tccctttccg agtcaactgg 300
cccggcaccg agttctctct gccacaact ggagttttat ataaagaaga taattatgtc 360
atcatgacaa ctgcacataa agaaaaatat aaatgcatac ttccccctgt gacaagtggg 420
gatgaggaag aagaaaagga ttataaaggc cctaatacaa gagagctttt ggagccacta 480
tttaaacaaa gcagttgttc ctacagaatt gagtcttatt ggacttacga agtatgtcat 540
ggaaaacaca ttcggcagta ccatgaagag aaagaaactg gtcagaaaat aaatattcac 600
gagtactacc ttgggaatat gttggccaag aaccttctat ttgaaaaaga acgagaagca 660
gaagaaaagg aaaaatcaaa tgagattccc actaaaaata tcgaagggtc gatgacacca 720
tactatcctg tgggaatggg aaatgggtaca ccttgtagtt tgaaacagaa ccggcccaga 780
tcaagtactg tgatgtacat atgtcatect gaatctaagc atgaaattct ttcagtagct 840
gaagttacaa cttgtgaata tgaagttgtc attttgacac cactcttgtg cagtcatect 900
aaatataggt tcagagcatc tctgtgaat gacataattt gtcaatcact gccaggatct 960
ccatttaagc cctcaccct gaggcagctg gagcagcagg aagaaatact aagggtgcct 1020
tttaggagaa ataaagagga agatttgcaa tcaactaaag aagagagatt tccagcgatc 1080
cacaagtcga ttgctatttg ctctcagcca gtgctcactg ttgggacaac ccacatatcc 1140
aaattgacag atgaccaact cataaaagag ttctttagtg gttcttactg ctttcgtggg 1200
ggtgtcggtt ggtggaaata tgaattctgc tatggcaaac atgtacatca ataccatgag 1260
gacaaggata gtgggaaaac ctctgtggtt gtcgggacat ggaaccaaga agagcatatt 1320
gaatgggcta agaagaatac tgctagagct tatcatcttc aagacgatgg taccagaca 1380
gtcaggatgg tgtcacattt ttatggaaat ggagatattt gtgatataac tgacaaacca 1440
agacagggtg ctgtaaaact aaagtgcata gaatcagatt cacctcatgc tgttactgta 1500
tatatgctag agcctcactc ctgtcaatat attcttggg ttgaatctcc agtgatectt 1560
aaaatcttag atacagcaga tgaaaatgga cttctttctc tccccaacta aaggatatta 1620
aagttagggg aaagaaaaga tcattgaaag tcatgataat ttctgtccca ctgtgtctca 1680
ttatagagtt ctgagccatt ggacctcttc taaaggatgg tataaaatga ctctcaacca 1740
ctttgtgaat acatatgtgt atataagagc ttattgataa acttctgagg cagacatttg 1800
ctcgctttt ttctattttt gttgtgtctt ataaactgac tgtttttctt tgcctggata 1860
ctgtgattcc aaaataaatc tcatccaagc aagttagagt ccagcctaata caaatgtcat 1920
aattgttgta cctattgaaa gtttttaaat aatagattta ttatgtaaat tatagtatat 1980

```

WO 01/07471

PCT/US00/19948

```

gtaagtagct aatgaagtaa agatcatgaa gaaagaaatt gataggtgta aatgagagac 2040
catgtaaaat atgtaaattc tagtacctga aatcctttca acagattttt atatagcaac 2100
tgctctctgc aagtagttaa actagaaact gggcacatgg tagaggctca catgggagtt 2160
gtcctcacc cttgtaatct caagaaactc ttatttataa taggttgctt ctctctcaga 2220
acttttatct attacttttt tcttcttatg agtatgttta ctctcagagt atctatctga 2280
tgtagacagt tgggtgatgct tctgagactc agaattggttt actctaacaa aacactgtgc 2340
tgtctatccc ttgtacttgc ctactgtaat atggatttca cttctgaaca gtttacagca 2400
caatatttat tttaaagtga ataaaatgtc cacaagcaaa aaaaaaaaaa 2449

```

<210> 74
 <211> 1689
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2553926CB1

```

<400> 74
aagtaatctt agggattgtg ggaaggcagc tgaactcggc gcctggaaag atggaggcag 60
cggagacaga ggcggaagct gcagccctag aggtcctggc tgagggtggca ggcattcttg 120
aacctgtagg cctgcaggag gaggcagaac tgccagccaa gatcctgggt gagtttgtgg 180
tggaactctc gaagaaagac aagctgctct gcagccagct tcaggtagcg gatttctctg 240
agaacatcct ggctcaggag gacactgcta aggtctcga ccccttggt tctgaagaca 300
cgagccgaca gaaggcaatt gcagctaagg aacaatggaa agagctgaag gccacctaca 360
gggagcacgt agaggccatc aaaattggcc tcaccaaggc cctgactcag atggagggaag 420
cccagaggaa acggacacaa ctccgggaag cctttgagca gctccaggcc aagaaacaaa 480
tggccatgga gaaacgcaga gcagtccaga accagtggca gctacaacag gagaagcatc 540
tgcagcatct ggccggaggt tctgcagagg tgaggagcg taagacaggg actcagcagg 600
agcttgacgg ggtgtttcag aaacttggaa acctgaagca gcaggcagaa caggagcggg 660
acaagctgca gaggtatcag accttctcc agcttctgta taccctgcag ggtaagctgt 720
tgttccctga ggctgaggct gaggcagaga atcttccaga tgataaacc cagcagccga 780
ctcgacccca ggagcagagt acaggagaca ccatggggag agacctggt gtgtccttca 840
agtcttccaa ggctgttggt ctacaacctg ctggagatgt aaatttgcca tgacttctctg 900
gaggacagca gcatggagaa agatcctaga aaaggcctct gacttccctc acctcccaac 960
catcattaca ggaaagactg tgaactcctg agttcagctt gatttctgac tacatcccag 1020
caagctctgg catctgtgga ttaaaatccc tggaactctc tcagttgtgt atttgttcat 1080
cttcatatgc tggcaggaac aactattaat acagatactc agaagccaat aacatgacag 1140
gagctgggac tggtttgaac acaggtgtgt cagatgggga gggggtactg gccttggggc 1200
tcttatgatg cagacatggt gaattttaat caaggaggag gagaatgttt taggcaggtg 1260
gttatatgtg ggaagataat tttattcatg gatccaaatg tttgttgagt ctttctttg 1320
tgctaagggt cttgcggtga accagaatta taacagtggc ctcatctgac tgttttagga 1380
tgtacagcct agtggttaaca ttcttggtat ctttttgtgc cttatctaaa acatttctcg 1440
atcactgggt tcagatgttc atttattata ttcttttcaa agattcagag attggctttt 1500
gtcatccact attgtatgtt ttgtttcatt gacctctagt gataccttga tctttccac 1560
tttctgtttt cggattggag aagatgtacc ttttttgtca actcttactt ttatcagatg 1620
atcaactcac gtatttggat ctttatttgt ttctcaaat aaatatttaa ggttaaaaaa 1680
aaaaaaaaa

```

<210> 75
 <211> 2489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2800717CB1

```

<400> 75
tgtgcccaga acgcgggttag gaagtgtgtg catacgtctg aaccctaaat ggttctcagt 60
tctgtaaaact tctcctccca ctgggtggag tagggccttt aagagcagct ggaatgcagt 120
tccctgatac agcgtaccag ttgttgctg tctgaacctc tgccagtcct ggagactggt 180
gccctgagct ccaaccagcg ggcctcatcc tacacctca ccaccgaac ttctcaccg 240

```

WO 01/07471

PCT/US00/19948

agcaagaagc	agctcccaga	gagaaagaac	gttcccacct	gcctagccat	gggagaggac	300
gctgcacagg	ccgaaaagtt	ccagcaccct	gggtctgaca	tgccggcagga	aaagccctcg	360
agccccagcc	cgatgccttc	ctccacacca	agccccagcc	tgaacctagg	gaacacagag	420
gaggccatcc	gggacaactc	acaggtgaac	gcagtcacgg	tgctcacgct	cctggacaag	480
ctggtgaaca	tgctagacgc	tgtgcaggag	aaccagcaca	agatggagca	gcgacagatc	540
agttttggagg	gctccgtgaa	gggcatccag	aatgacctca	ccaagctctc	caagtaccag	600
gcctccacca	gcaacacggt	gagcaagctg	ctggagaagt	cccgaagggt	cagcgccccac	660
acgcgcgcgg	tcaaagagcg	catggatagg	cagtgcgcac	aggtgaagcg	gctggagaac	720
aaccacgccc	agctcctccg	acgcaaccat	ttcaaagtgc	tcattcttcca	ggaggaaaaat	780
gagatccctg	ccagcgtggt	tgtgaaacag	cccgtttccg	gtgccgtgga	agggaaggag	840
gagcttcccg	atgaaaacaa	atccctggag	gaaaccctgc	acaccgtgga	cctctctcca	900
gatgatgatt	tgccccacga	tgaggaggcc	ctggaagaca	gtgccgagga	aaaggtggaa	960
gaaagtaggg	cagagaaaaat	aaaaagatcc	agcctgaaga	aagtggatag	cctcaagaaa	1020
gcattttctc	gccagaacat	cgagaaaaag	atgaacaagc	tggggacaaa	gatcgtatct	1080
gtagagagga	gagagaagat	taagaaatct	ctcacgtcaa	atcaccagaa	aatatcctca	1140
ggaaaaagct	cccccttcaa	ggtttctccc	ctcactttcg	ggcggaagaa	agtcgagag	1200
ggagaaagcc	atgcagaaaa	tgagaccaag	tcagaagacc	tgccatagcag	tgagcagatg	1260
ccaaatgacc	aggaagagga	gtcctttgca	gaggggtcatt	ccgaagcgtc	cctcgccagc	1320
gctctgggtg	aaggggaaat	tgcagaggag	gctgctgaga	aggcgacctc	cagggggagt	1380
aactcggggg	tggaacagca	catcgacttg	actattgtgg	aagatgaaga	ggaggagtca	1440
gtggccctgg	aacaggcaca	gaagggtacg	tatgagggtg	gctacgcgct	aacatccgag	1500
gaggcggagc	gctccgatgg	ggacccccgtg	cagccccg	tgctccaggt	gcaccagacc	1560
tcctgagctt	agagccaccg	tgccatcctg	tgctgtgctc	aagcgggcag	ccagggctga	1620
agaacaaact	cttgcacatc	tccagcacga	ctcaccact	cctgcgttcc	tgtccaggca	1680
gtaatcattg	accatatagt	catagtaaga	cacacgagac	caggctttac	catgaaagcg	1740
acctgtcacg	gactccactt	ttaatttctg	cttaggttct	atctctgtag	aatgtctcca	1800
agattgaaga	agaaactgag	cagttgaaaa	atgctaactc	ctttgactta	gtcagaaaaa	1860
aacagaggat	aattaagata	ctagtcatga	aaagtgatcc	attctttttt	gtcattccat	1920
aagcttgctg	aatagtgtac	cggtaatata	ttgtatttcc	accgtactct	gtgaatctaa	1980
ttattattct	ttaagtgttg	atatataata	tacataaata	tgtaagctaa	acataataact	2040
atatgttttta	agaagaaaaa	atctacgaaa	ggtaaaaaa	gatgatcagt	tggttgttta	2100
cttgctagaa	accattgttt	tattgcaaac	gaaggaaaaa	tgaagagatt	ataaaagtca	2160
gctaataaag	taagatacgt	agtaaagtca	ggactattca	aaaagtaaga	aagaaaaattt	2220
ggaaaaatgag	agaaacagga	aacaaagaat	gccgaaaaa	atgaaaaacag	agaaaaaatg	2280
tatgtgcttg	aaagtaaaat	acttacaata	gtagcttaac	tatttcactc	tttaaataaaa	2340
aatactaaag	aagttcgtat	atcctggaat	aacatgtcat	cttcaaaaata	tttttatttt	2400
ctaataatttt	taataataaaa	catttttatag	tgttaaagct	gtatttttct	taataataaa	2460
aggacattac	aaatattttct	ttaaaaaaa				2489

<210> 76

<211> 898

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5664154CB1

<400> 76

cctctggcga	tgacaacagc	cacacgtgat	cggccaacac	tgagtcttac	ctcgttggtg	60
cgtcagaacc	gccgtcgctc	gtcccttctc	cggcagtggt	acctgttccc	gggtgtccctg	120
aggacgtgcg	ggccaggtag	ggccccgaaa	gtaggaagcg	gagggggagc	aggtttgcgg	180
ggccaagtgt	tgccggcgacg	cacctcacgt	cgagaatcgg	gaggaggaga	ctgcaaggat	240
aggcccagga	gtaatggagt	ccaaagagga	acgagcgtta	aacaatctca	tcgtggaaaa	300
tgtcaaccag	gaaaaatgat	aaaaagatga	aaaggagcaa	gttgctaata	aaggggagcc	360
cttggcccta	cctttgaatg	ttagtgaaata	ctgtgtgcct	agaggaaacc	gtaggcggtt	420
ccgcgttagg	cagcccatcc	tgcagtatat	atgggacata	atgcataggc	ttggagagcc	480
acaggcaagg	atgagagagg	agaatatgga	aaggattggg	gaggaggtga	gacagctgat	540
ggaaaagctg	agggaaaagc	agttgagtca	tagtctgcgg	gcagtcagca	ctgatcccc	600
tcaccatgac	catcacgatg	agttttgcct	tatgccctga	atcctgatgg	ttccctgaa	660
gttaatatgg	agacccctgc	ttcctaaact	tacacatttg	tggtgtacct	ttgtcgtaaa	720
cgttttgatg	ttacctatct	cttggtgggtc	tcctattacc	agcttctaaa	tgaatgttgt	780
ttttgaccca	gtttgtgaagt	ttctgtcagc	aggagagttt	tacctattgc	atggaaagat	840

WO 01/07471

PCT/US00/19948

```

gtcctgagtc ataagtaata tgggtggggc gaggggtctta tttctgtaga aatcgtgtga 1200
ctttaaggat ttagattttg tatcttatgt tttgtaacat ttaataatta ctgttaaaat 1260
gctgttttga aatgagattg gtctactttt tcctgtagga ttttattgta gagttttgct 1320
ggttttgtaa aatggatgga agaactttgt atttatactg tgattttgaa cagattatgc 1380
aacattggaa ggaaggctgt actttgatgg tttgaaggaa ctgagcagta tgatgatctg 1440
gttccagggg aaaaaaatag ctggttggtg tctagcccc caacactttt gtctgttgtg 1500
tataaaagaa gaaagactgg catgtacctt catttgctta gctatttgag tatctagaga 1560
aaaattaaaa tgcaatgagt tagcagtata ccctggcaca ctttaataat taaacatttg 1620
tggaaaaaaa aaaa                                     1634

```

<210> 79
 <211> 1258
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 259983CB1

```

<400> 79
tccccggccag cggtagcaac tgcagaactg caggagacta tctttctaga caaggcagtt 60
gaggaggagg gagcgcttga gggggactgg cctggcgtgc actccgcacc tcggggacat 120
tattgcgcgt ggaacggctg cttttggaag gcacaacttc ctgaatggac catgactccc 180
accaaagatc cctgtctctg attcaccaaa cagcttcaac cctgaaacca ggacgagaag 240
ttgacaacat ctgagtggac agctaattga cctaagactt cagaccaggc ctactattgc 300
ccagaagaaa agatgtttgg ttttcacaag ccaaagatgt accgaagtat agagggctgc 360
tgtattttgca gagctaagtc ctccagttct cgattcactg acagtaaacy ctatgaaaag 420
gacttccaga gctgttttgg attgcatgag actcgttcag gagacatctg caatgcctgt 480
gtcctgcttg tgaaaagatg gaagaagttg ccagcaggat caaaaaaaaaa ctggaatcat 540
gtggtagatg caagggtctg acccagtcta aagactacat tgaaaccaa gaaagtgaag 600
actctatctg ggaacaggat aaaaagcaac cagatcagta aactgcagaa ggaatttaaa 660
cgtcataatt ctgatgctca cagtaccacc tcaagtgcct cccagctca atctccttgt 720
tacagtaacc agtcagatga cggctcagat acagagatgg cttctgggtc taacagaaca 780
ccagtttttt cttttttaga tctcacttac tggaaaagac agaagatatg ttgtgggac 840
atctataaag gccgttttgg ggaagtcctc attgacacac atctcttcaa gccttgctgc 900
agcaataaga aagcagctgc tgagaagcca gaggagcagg ggccagagcc tctgcccac 960
tccactcagg agtggtgact gaggttttta tgtagaaggg gaacaaaaaa aaaaatatct 1020
gaattttgaa aaaccacaaa gctacaaact gaccctcttt tttttttgag acggagtttt 1080
gctcttgtaa cccaggctgg agtgagtggt cgtgatcttg gctcactgca acttccgtct 1140
cccgggggtc aggtgattct cctgcctcag cctcccaagt agctgggttt ataggtgccc 1200
gctacagacc cggctaattt tttagtttta gtagagacgg ggttcacca cgttgggc 1258

```

<210> 80
 <211> 2223
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 926810CB1

```

<400> 80
aaaagccgcc gcggtgcct taggaacggc gctgcctcgt ctctgctacc cctgggtggg 60
cggccctgcg aagcagctcc ttcgggcagc cccgggtcgc ttagcggcca aggaggcttc 120
agttctttgc cgctgcaag gcggagacca gaaggcggaa tccacagctg gcgacgagg 180
agcatctgct gtccaccagc ggagcacagg ccatacaagc cgcactctgaa cttgaattct 240
gtgcagctga ttgcagagc ggaccggat ctgcgacccc ctgtggacag aggttgaccg 300
taccgccggag aggagctttc tcacggaggg cactgggttg agaggctgga agtgaaataa 360
agacgcgctc ttgtttcaga gttcgtcccc tgctgagata ggaaggcaga gccacctcct 420
ctcctctccc acctgcagat taagcttttc taaaaagcct aggcactctc ttatattcag 480
ataccctatc gtcgtcagtc atggctagca tcattgcacg tgtcggtaac agccggcggc 540
tgaattgacc cttgcgcct tgggccatt ccattgctgag gtccctgggg agaagtctcg 600
gtcctataat ggccagcatg gcagacagaa acatgaagtt gttctcgggg aggggtggtgc 660

```

WO 01/07471

PCT/US00/19948

```

cagcccaagg ggaagaaacc tttgaaaact ggctgaccca agtcaatggc gtcctgccag 720
attggaatat gtctgaggag gaaaagctca agcgcttgat gaaaaccctt agggggccctg 780
cccgcgaggt catgcgtgtg cttcaggcga ccaaccctaa cctaagtgtg gcagatttct 840
tgcgagccat gaaattgggtg tttggggagt ctgaaagcag tgtgactgcc catggtaaat 900
tttttaacac cctacaagct caaggggaga aagcctccct ttatgtgatc cgttttagagg 960
tgcagctcca gaacgctatt caggcaggca ttatagctga gaaagatgca aaccggactc 1020
gcttgcaagca gctcctttta ggcggtgagc tgagttagga cctccgactc agacttaagg 1080
atthttctcag gatgtatgca aatgagcagg agcggtctcc caactttctg gagttaatca 1140
gaatggtaag ggaggaagag gattgggatg atgcttttat taaacgggaag cgtccaaaaa 1200
ggctctgagtc aatgggtggag agggcagtcg gccctgtggc atttcagggc tccccaccga 1260
tagtgatcgg cagtgtctgac tgcaatgtga tagagataga tgataccctc gacgactccg 1320
atgaggatgt gatcctgggtg gagtctcagg accctccact tccatcctgg ggtgccctc 1380
ccctcagaga cagggccaga cctcaggatg aagtgtgggt cattgattcc cccacaatt 1440
ccagggctca gtttccctcc accagtgggtg gttctggcta taagaataac ggtcctgggg 1500
agatgcgtag agccaggaag cgaaaacaca caatccgctg ttcgtattgt ggtgaggaag 1560
gccactcaaa agaaaacctgt gacaacgaga gtgacaaggc ccaggttttt gagaatttga 1620
tcatcactct ccaggagctg acccatactg agatggagag gtcaagagtg gcccctggcg 1680
aatacaatga cttctctgag ccactgtgaag ggaccacccc caggtttcag tgaaccctta 1740
cctatatcca gcatccagta gtgggaaaaac tgggggtggg gtgggggtgg gacttctaac 1800
tgcataaatt aatccacaaa gcggctatct tttgggggtgg agtagaaagg gtcttgata 1860
ccagcattt ggagggagat agcctgacct ctgtccttgc tccctctccc tgcagctac 1920
gggtctgttt tctgtgtgtg cccatttccct tgacagcttt attctttgtg aaagtggat 1980
aatttattgt taaatatttg aacaataaaa aaggtacaaa aagtgaagta caaattacc 2040
aaatctctcc acccttatat aatcattgtc aaccctttga tgagtatat tccctatac 2100
ctatgtacc agatagatat atgcatagat aaaagtgatg aaatataagt gctgttctat 2160
ctgtattttt tcaccaaaca atatattgtg tgagcttcta tgacaataaa tatatatatc 2220
act 2223

```

<210> 81

<211> 1370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1398816CB1

<400> 81

```

cccacgcgtc cggccggggag gactgggtgc gcctgcaggg atcggaagcc ggttgggggtg 60
tgagaggttt tctcgctcta gggagattct tcaagcaatc actatgtcaa cagacacagg 120
tggttccctt ccttcatatg aggaagatca gggatcaaaa ctcatcgaa aagctaaaga 180
ggcaccattc gtaccggttg gaatagcggg ttttgcagca attgttgcat atggattata 240
taaactgaag agcaggggaa atactaaaat gtccattcat ctgatccaca tgcgtgtggc 300
agcccaaggc tttgttgtag gagcaatgac tgttggatat ggctattcca tgtatcggga 360
attctgggca aaacctaaag cttagaagaa gagatgctgt cttggctctg ttggaggagc 420
ttgctttagt tagatgtctt attattaaag ttacattata ttgttgaaa taaactaatt 480
tgtatgggtt tagatggtaa catggcattt tgaatatgg cttcctttct tgcaggcttg 540
atthgcttgg tgaccgaatt actagtgact agtttactaa ctaggctcatt caaggaagtc 600
aagtttaact aaacatgtca cctaaatgca cttgatgggt ttgaaatgtc caccttctta 660
aatttttaag atgaacttag ttctaaagaa gataacaggc caatcctgaa ggtactccct 720
gtttgctgca gaatgtcaga tattttggat gttgcataag agtcctattt gcccagttta 780
attcaacttt tgtctgcctg ttttgtggac tggctggctc tgtagaact ctgtccaaaa 840
agtgcattga atataacttg taaagcttcc cacaattgac aatatatatg catgtgttta 900
aaccaaatcc agaaagctta aacaatagag ctgcataata gtatttatta aagaatcaca 960
actgtaaaca tgagaataac ttaaggattc tagtttagtt ttttgaatt gcaattata 1020
ttttgctgc tgatatatta gaataatttt taaatgtcat cttgaaatag aaatatgtat 1080
tttaagcact cagcgaagg taaatgaaca cgttttaaat gtgtgtgttg ctaatttttt 1140
ccataagaat tgtaaacatt gaactgaaca aattacctat aatggatttg gttaatgact 1200
tatgagcaag ctggtttggc cagacagtat acccaaactt ttatataata tacagaaggc 1260
tatcacactt gtgaaattct cttgtctaat ctgaatttgc attccatggg gttaacatgg 1320
tatatgtatt gttattaaag taagtgacct atgtcaaaaa aaaaaaaaaa 1370

```

<210> 82

WO 01/07471

PCT/US00/19948

<211> 1541
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1496820CB1

<400> 82
gtgttaagct gacaaaatct gtacagaata ttttaattttt ctttttattt ctgtgatata 60
aagatttgtt ttctttttcat agcaacatga accgtgaaga ccggaatgtg ctgcgtatga 120
aagaacggga aaggcggaat caggaaattc agcagggcga agacgccttc ccacctagct 180
ctcctctctt tgcagagcca tacaaagtta ctacgaaaga agataagtta tcaagtcgta 240
ttcagagtat gcttggaac tacgatgaaa tgaaggattt cataggagac agatctatac 300
caaagcttgt tgcaattccc aagcctacag taccaccatc agcagatgaa aaatctaacc 360
caaattttct tgaacagaga catggaggct ctcatcagag tagcaaatgg actccagtag 420
gacccgcacc cagcacttct cagtctcaga aacggtcctc aggcttacag agtggacata 480
gtagccagcg gaccagcgca ggtagcagta gtggcactaa cagtagtggt cagaggcacg 540
accgtgagtc atataacaat agtgggagca gtagccggaa aaaaggccag catggatcag 600
aacactccaa atcaggttct tccagccctg gaaaacccca ggctgtttct tcattaaact 660
ctagtcatte caggtctcat gggaatgatc accatagcaa ggaacatcaa cgctccaaat 720
cacctcggga ccttgatgca aactgggatt ctcttcccg tgtacctttt tcaagtgggc 780
agcactcaac tcaatctttc ccacctcat tgatgtcaaa gtccaattca atgttacaga 840
aaccactgc ctatgtgcgg cccatggacg gacaggagtc catggaacca aagctgtcct 900
ctgagcacta cagcagccaa tcccatggca acagcatgac tgagctgaag cccagcagca 960
aagcacatct caccaagctg aaaatacctt cccaaccact ggatgcatca gcttctgggt 1020
atgtgagctg tgtggatgaa atcctaaaag agatgacgca ttcatggcct cccctcttaa 1080
cggctattca tacaccatgc aaaacagaac ctcccaaatt tccttttcca actaaggtaa 1140
gtaataaaaa tgtatctttc ataattgtaag aaaactctaa atggcttgac taaaatcata 1200
tggattaaaa attgtcttgc cattcctatt ctagtgggag acagacagta aataagtga 1260
taaatagata aattcagata gtgacaactg ttatgaagat aattagcagg gtaatggaac 1320
tgagagcatc ttggatcaag aggtattaag aaagctttga aggcaatatg cgagagagat 1380
ttaaagagca ttaatacagc cggacacggg ggctcactcc tgtaatccca gcactttgga 1440
aggctgagcc aagagactct cttgaggcca ggagtttgcg accagcctgg tcagcatggc 1500
aagaccctgt ctctacaaaa aattggaagg aaaaaaaaaa a 1541

<210> 83
<211> 1372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1514559CB1

<400> 83
cggctcgagc agctgccgaa gtcagttcct tgtggagccg gagctgggag cggattcgcc 60
gaggcaccga ggcactcaga ggaggcgcca tgtcagaacc ggctggggat gtccgtcaga 120
acccatgcgg cagcaaggcc tgccgcggcc tcttcggccc agtggacagc gacgagctga 180
gccgcgactg tgatgcgcta atggcgggct gcatccagga ggcccgtag cgatggaaact 240
tcgactttgt caccgagaca cactggagg gtgacttcgc ctgggagcgt gtgcggggcc 300
ttggcctgcc caagctctac cttcccactt ggtccgctgg gtggtaccct ctggaggggg 360
gtggctcctt cccatcgctg tcacaggcgg ttatgaaatt caccctctt cctggacact 420
cagacctgaa ttctttttca tttgagaagt aaacagatgg cactttgaag gggcctcacc 480
gagtgggggg atcatcaaaa actttggagt cccctcacct cctctaagg tgggcagggt 540
gacctggaag tgagcacagc ctagggtcga gctggggacc tgggtaccct ctggctcttg 600
ataccccct ctgtcttggt aaggcagggg gaaggtgggg tccctggagca gaccaccccg 660
cctgcctcca tggccctct gacctgcact ggggagcccg tctcagtggt gagcctttc 720
cctctttggc tccctgtac cttttgagga gcccagcta cccttcttct ccagctgggc 780
tctgcaatte cctctgctg ctgtccctgc cccttgctct tcccttcag taccctctca 840
gctccagggt gctctgaggt gctgtccca cccccaccc cagctcaatg gactggaagg 900
ggaagggaaga cacaagaaga agggcacct agttctacct caggcagctc aagcagcgac 960
cgccccctcc tctagctgtg ggggtgaggg tcccatgtgg tggcacaggc ccccttgagt 1020

WO 01/07471

PCT/US00/19948

```

gggggttatct ctgtgttagg ggtatatgat gggggagtag atctttctag gagggagaca 1080
ctggcccttc aaatcgtcca gcgaccttc tcatccacc catccctccc cagttcattg 1140
cactttgatt agcagcggaa caaggagtc gacattttaa gatggtggca gtagaggcta 1200
tggaacagggc atgccacgtg ggctcatatg gggctgggag tagttgtctt tcctggcact 1260
aacgttgagc ccctggaggc actgaagtgc ttagtgtact tggagtattg gggctcgacc 1320
ccaaacacct tccagctcct gtaacatact ggctgggact gttttctctc gg 1372

```

<210> 84
 <211> 868
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1620092CB1

```

<400> 84
cattgagctc accagcgcca ccgtccccgg cgaagttctg cgttggtcgg cggagtagca 60
agtggccatg gggagcctca gcggtctgcg cctggcagca ggttggttca tgtgacctg 120
gttaatggaa cataagttag attttatggg tgacagggag agagatcagg cttgacttga 180
gagcacgtgg gaaaagaagg gggctatctc ttcgcaaaga tttaagtatc ttataagaac 240
tgtttgccag tgcaattatg agaagctggt ttaggttatg tgaaagagat gtttcctcat 300
ctctaaggct taccagaagc tctgatttga agagaataaa tggattttgc acaaaaccac 360
aggaaagtcc cggagctcca tcccgcactt acaacagagt gcctttacac aaacctacgg 420
attggcagaa aaagatcctc atatggtcag gtcgcttcaa aaaggaagat gaaatcccag 480
agactgtctc gttggagatg cttgatgctg caaagaacaa gatgagagtg aagatcagct 540
atctaattgat tgccctgacg gtggtaggat gcattctcat ggttattgag ggcaagaagg 600
ctgcccacaa acacgagact ttaacaagct tgaacttaga aaagaaagct cgtctgaaag 660
aggaagcagc tatgaaggcc aaaacagagt agcagaggta tccgtgttgg ctggattttg 720
aaaatccagg aattatgtta taacgtgcct gtattaaaaa ggatgtggta tgaggatcca 780
tttcataaag tatgatttgc ccaaacctgt accatttccg tatttctgct gtagaagtag 840
aaataaattt tcttaaataa aaaaaaaaa 868

```

<210> 85
 <211> 3388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1678765CB1

```

<400> 85
aactgtgtct gcaagcagtt tgtactcagt ttgtcaagag agcagctttc tgttttgatt 60
atataccttc atctctgaaa aaagacatgc tagttaaatt tcaagatggt ttacttagaa 120
gatgacaagg aagatgaggt ggtttgtaaa ggctcattaa gtaaaactca agatgtttac 180
catgacaagt cccctcctgg tatcttgtct caaacatga attatgtggg acagctggct 240
gggcaggtga ttgtcactgt gaaggaactc tacaagggca ttaaccaggc caccctctct 300
gggtgcattg atgtcatcgt ggtacagcag caggatggca gctatcagtg ttcacctttt 360
cacgttcggt ttggaaagct gggagtccct agatccaaag agaaagtgat tgatatagaa 420
atcaacggca gtgcagtgga tcttcacatg aagttgggtg ataacggaga agctttcttt 480
gttgaggaga ctgaagaaga atatgaaaag ctctctgctt accttgccac ctcaccaatt 540
cctactgaag atcagttctt taaagatatt gacaccctt tggtgaaatc ggggtggagat 600
gaaacaccat ctcagagttc agacatctca cacgtcttgg aaacagagac aatttttact 660
ccaagttctg tgaaaaagaa aaaacgaagg agaaagaaat acaaacagga cagtaagaag 720
gaagagcagg ccgcactctg tgctgcagaa gacacatgtg atgtaggcgt gagctccgat 780
gatgacaagg gggcccaggc agcacgagga tcttcaaatt ctctccttgaa agaagaagaa 840
tgtaaaagag ctttgcctt ccattctggg gatcattacc ccttatctga tggagattgg 900
tcccctttag agaccaccta tcccagaca gcgtgtccta agagtgttcc agagctggag 960
gtgaaacctg cggagagcct gctcagatca gagtatcaca tggagtggac gtggggcgga 1020
ttcccagagt ccaccaaggt cagcaaaaaga gaacgatctg accatcatcc taggacagct 1080
acaattacac catcagaaaa tactcatttt cgggtaattc ccagtggaga caacctcatc 1140
agtgaagttg agaaggatgc ttccatggaa gacactgtct gtaccatagt gaagcccaaa 1200

```


WO 01/07471

PCT/US00/19948

```

gccggcgggg tccacagtgg gggcagtggg gatggggccg gcagcggggg cccgggagca 960
cagaaccacg tgaaggagag atgagccccc cgggcccggac aggggcacac gtgtgcaaag 1020
agacggtggt gtgtgttctc tcctgcatct gcgtgtgcac acatgtgctg ggcacgcgtg 1080
tgggtgaggtc tgagagggcc ccgggctgca ctgggtgtggg ctgcacaggc acagacgcag 1140
acggcccccg ccgtgtcctg tggccccctg tcggatggat gcgtgccgtt tgtagagaag 1200
agcctttggg cccattcact cgttcagcag acacgcacat gactgatgct ttgagttttc 1260
ttctgtgggg ttttcttttc tctggtctcc gtgcagcccc tgccctccct cgggtgctgc 1320
tggccgcaaa ggaggaactc gtggggggag ggtgtgattt gcagacctgg gtctctgctc 1380
tgctctgggg gtggggcttg ctatcacaga gacctcctt ccctctcacc cctcctctcc 1440
caggcctcgc caggagtctt ggctgttggc agctcagagg tgggggaggc ctgtggtgtg 1500
agtgcctgc acctgctctt gctcctgtca ccccttctctg ctgcctcctc catgcccaag 1560
gaacacccat ggtgcagtcc tcaggcaagg ccaggacggg gctgaggccc tgcgtggaga 1620
tgctgcacca gcggaaggct gagccccgct taccttagtt catctgttca ctcgtaataa 1680
aaagaattct ctcagaaaaa aaaaaaa 1707

```

<210> 87

<211> 1752

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1806454CB1

<400> 87

```

cccgggtgcg ccgcggcgct gggggcgcca ggttgcggcg gcgccggagc gggctctccag 60
gctggcgagc gcccaggaca ggcatgttgt tgggactggc ggccatggag ctgaagggtg 120
gggtggatgg catccagcgt gtggtctgtg gggctcaga gcagaccacc tgccaggaag 180
tggtcatcgc actagcccaa gcaataggcc agactggccg ctttgtgctt gtgcagcggc 240
ttcgggagaa ggagcggcag ttgctgccac aagagtgtcc agtggcgccc caggccacct 300
gcggacagtt tgccagcgat gtccagtttg tcctgaggcg cacagggccc agcctagctg 360
ggaggccctc ctcagacagc tgtccacccc cggaaacgtg cctaattcgt gccagcctcc 420
ctgtaaagcc acgggctgcg ctgggctgtg agccccgcaa aacactgacc cccgagccag 480
ccccagcct ctcacgccct gggcctggcg cccctgtgac acccacacca ggctgctgca 540
cagacctgcg gggcctggag ctcaggggtgc agaggaatgc tgaggagctg ggccatgagg 600
ccttctggga gcaagagctg cgccgggagc agggccggga gcgagaggga caggcacgcc 660
tgcaggcact aagtgcggcc actgctgagc atgccgccc gctgcaggcc ctggacgctc 720
aggcccgctg cctggaggct gagctgcagc tggcagcggg gggccctggg ccccccctcac 780
ctatggcatc tgccactgag cgcctgcacc aggacctggc tgttcaggag cggcagagtg 840
cggagggtga gggcagcctg gctctggtga gccgggccc ggaggcagca gagcgagcct 900
tgcaggctca ggtcaggag ctggaggagc tgaaccgaga gctccgtcag tgcaacctgc 960
agcagttcat ccagcagacc ggggctgcgc tgccaccgcc cccacggcct gacaggggcc 1020
ctcctggcac tcaggctcga gtggttcttg ggggaggctg ggagggtgagg acctggccca 1080
gccccactcc aagctgactt cccaaccac agggccctct gcctccagcc agagaggagt 1140
cctcctggg cgtccctctt gagtcccatg ctggtgccca gcctaggccc cgagggtatg 1200
tetgtgeccc acctccccct ggggcaccgg gccctcctgt ggctgcagcc acctcagcct 1260
gtgtcctccc gcagtggccc ccatgacgca gaactcctgg aggtagcagc agtccctgcc 1320
ccagagtggg gtctcttggc agcccagccc caggctctgt gacagcctag tgagggctgc 1380
aagaccatcc tgcccggacc acagaaggag agttggcggc cacagagggc tctctgcca 1440
ggcagtggga agccctgggt ttggcctcag gagctggggg tgcagtgggg gactgcccta 1500
gtccttgcca ggtgcgcagc accctggaga agcatggggc gtagccagct cggaaacttg 1560
caggccccaa aggccacgac tgcctgttgg ggacaggaga tgcattggaca gtgtgctcaa 1620
gctgtgggca tgtgcttggc tgcgggagag gtccttact gtgtgtacac agcaagagca 1680
tgtgtgtgcc acttccccca cccaacgtg aaaacctcaa taaactgccc gaagcagctt 1740
gaaaaaaaaa aa 1752

```

<210> 88

<211> 2461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

WO 01/07471

PCT/US00/19948

<223> Incyte ID No: 1806850CB1

<400> 88

```

ctgaaagaga gattggaggc ttttacaaga gattttcttc ctcacatgaa agaggaagag 60
gagggttttc agcccatggt aatggaatat tttacctatg aagagcttaa gtatattaaa 120
aagaaagtga ttgcacaaca ctgctctcag aaggatactg cagaactcct tagaggctct 180
agcctatgga atcatgctga agagcgacag aagtttttta aatattccgt ggatgaaaag 240
tcagataaag aagcagaagt gtcagaacac tccacaggta taaccctatc tcctcctgag 300
gtaatgctgt caatttttcag ctatcttaat cctcaagagt tatgtcgatg cagtcaagta 360
agcatgaaat ggtctcagct gacaaaaacg ggatcgcttt ggaaacatct ttaccctgtt 420
cattggggcca gaggtgactg gtatagtggg cccgcaactg aacttgatac tgaacctgat 480
gatgaatggg tgaaaaatag gaaagatgaa agtcgtgctt ttcatgagtg ggatgaagat 540
gctgacattg atgaatctga agagtctgag gaggaatcaa ttgctatcag cattgcacaa 600
atggaaaaac gtttactcca tggcttaatt cataacgttc taccatattg tggtaacttc 660
gtaaaaacct tagtattagc atacagctct gcagtttcca gcaaaatggg taggcagatt 720
ttagagcttt gtcctaacct ggagcatctg gatcttacct agactgacat ttcagattct 780
gcatttgaca gttggctctg gcttgggttg tggcagagtc ttcggcatct tgatctgtct 840
ggttggtgaga aaatcacaga tgtggcccta gagaagattt ccagagctct tgggaattctg 900
acatctcatc aaagtggctt tttgaaaaca tctacaagca aaattacttc aactgcgtgg 960
aaaaataaag acattaccat gcagtcacac aagcagtatg cctgtttgca cgatttaact 1020
aacaagggca ttggagaaga aatagataat gaacacccct ggactaagcc tgtttcttct 1080
gagaatttca cttctcctta tgtgtggatg ttagatgctg aagatttggc tgatattgaa 1140
gatactgtgg aatggagaca tagaaatgtt gaaagtcttt gtgtaatgga aacagcatcc 1200
aactttagtt gtccacctc tgggtgtttt agtaaggaca ttggtggact aaggactagt 1260
gtctgttggc agcagcattg tgcttctcca gcctttgcgt attgtgggtc ctcattttgt 1320
tgtacaggaa cagctttaag aactatgtca tcactcccag aatcttctgc aatgtgtaga 1380
aaagcagcaa ggactagatt gcctagggga aaagacttaa tttactttgg gagtgaaaaa 1440
tctgatcaag agactggacg tgtacttctg tttctcagtt tatctggatg ttatcagatc 1500
acagaccatg gtctcagggt tttgactctg ggaggagggc tgccctattt ggagcacctt 1560
aatctctctg gttgtcttac tataactggg gcaggcctgc aggatttggg ttcagcatgt 1620
ccttctctga atgatgaata cttttactac tgtgacaaca ttaacgggcc tcatgctgat 1680
accgccagtg gatgccagaa tttgcagtggt ggttttcgag cctgctgccg ctctggcgaa 1740
tgacccttga cttctgatct ttgtctactt catttagctg agcaggcttt ctttcatgca 1800
ctttactcat agcacatttc ttgtgttaac catccctttt tgagcgtgac ttgttttggc 1860
cccatttctt acaacttcag aaatcttaat ttaccagtga attgtaatgt tgtttctctt 1920
gcaaattata cttttggttt agaaagggat taggtctttt caaaagggtg agaacagtct 1980
tacatttttc ttttaaatga aatgctttaa agaatgttgg taatgccatg tcatttaaaag 2040
tatttcatag ataattttga gttttaaagt ccatggaggt gattgggtct ctttacacat 2100
taacactgta ccaagctttg cagatctttt ccgacacaca tgtctgaaga cttattttca 2160
aagacagcac atttttggaa actaatctct tttccgtaat atttccctta tttcaatgat 2220
tctcagaagg ccaattcaaa caaacccaca ttttaagggtc tttaggatta tagaataaaa 2280
tggcttctga gtgttagctc agtgagctag gaaagcacca atcgatattt gtttctttaa 2340
gggatacttt gttctcacca ctgtccctat gtcatcaaat ttgggagaga ttttttaaaa 2400
taccacaatc atttgaagaa atgtataaat aaaatctact ttgaggactt taaaaaaaaa 2460
a

```

<210> 89

<211> 965

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1851534CB1

<400> 89

```

ctttcagaaa aacccttggt gctgctgtaa caaattacaa caaacttaat ggcttaaaac 60
gacacagatt tattctttta catttcttga tgtctgacat gggactaaaa tcaagggtgtc 120
agcggcagag gcccgatgag agaaaggga agttaaggat gctggagcag aacaatggat 180
ttctctttct ctttcatgca agggatcatg ggaaacacaa ttcagcaacc acctcaactc 240
attgactccg ccaacatccg tcaggaggat gcctttgata acaacagtga cattgctgaa 300
gatgggtggc agacaccata tgaagctact ttgcagcaag gctttcagta ccagctaca 360
acagaagatc ttcctccact cacaaatggg tatccatcat caatcagtgt gtatgaaact 420

```

WO 01/07471

PCT/US00/19948

caaacc	aaat	accagtcata	taatcagtat	cctaattgggt	cagccaatgg	ctttggtgca	480
gttagaa	act	ttagcccccac	tgactattat	cattcagaaa	ttccaaacac	aagaccacat	540
gaaattct	tg	aaaaaccttc	ccctccacag	ccaccacctc	ctccttcggt	accacaaact	600
gtgattccaa		agaagactgg	ctcacctgaa	attaaactaa	aaataaccaa	aactatccag	660
aatggcaggg		aattgtttga	gtcttccctt	tgtggagacc	ttttaaatga	agtacaggca	720
agtgagcaca		cgaaatcaaa	gcatgaaagc	agaaaagaaa	agaggaaaaa	aagcaacaag	780
catgactcat		caagatctga	agagcgcaag	tcacacaaaa	tccccaatt	agaaccagag	840
gaacaaaata		tgaccaaata	agaggggtga	cactgtatca	gaaaaaccaa	gggaagaacc	900
agtactaaaa		gagggaagcc	ccagttcagc	caatactatc	ttctgttcca	acaacggtag	960
tgcc							965

<210> 90

<211> 2555

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1868749CB1

<400> 90

agcacgtccc	actctatgac	cagtgggagg	atgtgatgaa	agggatgaag	gtggaggtgc	60
tcaacagtga	tgctgtgctc	cccagccggg	tgtactggat	cgctctgtc	atccagacag	120
cagggatcgc	ggtgctgctt	cggatgaag	gctttgaaaa	tgacgccagc	catgacttct	180
ggtgcaacct	gggaacagtg	gatgtccacc	ccattggctg	gtgtgccatc	aacagcaaga	240
tcctagtgcc	cccacggacc	atccatgcca	agttcaccca	ctggaagggc	tacctcatga	300
aacggctggt	gggctccagg	acgttcccg	tggatttcca	catcaagatg	gtggagagca	360
tgaagtaccc	ctttaggcag	ggcatgcggc	tggaagtggg	ggacaagtcc	caggtgtcac	420
gcactcgcat	ggctgtggtg	gacacagtaa	tcgggggtcg	cctacggctc	ctctacgagg	480
atggtgacag	tgacgacgac	ttctggtgcc	acatgtggag	ccccctgatc	caccagtggt	540
gttggtcacg	acgtgtgggc	cacggcatca	agatgtcaga	gaggcgaagt	gacatggccc	600
atcacccccac	cttccggaag	atctactgtg	atgccgttcc	ttacctcttc	aagaaggtag	660
gagcagtcta	cacagaaggc	ggttggtttg	aggaagggat	gaagctggag	gccattgacc	720
ccctgaatct	gggcaacatc	tgctgtggcaa	ctgtctgtaa	ggttctctctg	gatggatacc	780
tgtatgactg	tgtggacggg	gggccctcca	cagatggctt	ggaactgggtc	tgctaccatg	840
cctcttcccc	cgccatcttc	ccggccacct	tctgtcagaa	gaatgacatt	gagctcacac	900
cgccaaaagg	ttatgaggca	cagacttttca	actgggagaa	ctacttggag	aagaccaagt	960
cgaaagccgc	tccatcgaga	ctctttaaca	tggattgccc	aaacccatggc	ttcaagggtg	1020
gcatgaagct	ggaggccgtg	gacctgatgg	agccccggct	catctgtgtg	gccacgggtga	1080
aacgagtggt	gcacgggctc	ctcagcatcc	actttgacgg	ctgggacagc	gagtacgacc	1140
agtgggtgga	ctgcgagtc	ccagacatct	accccgctcg	ctggtgtgag	ctcaccggct	1200
accagctcca	gcctctctgtg	gccgcagaa	cggccacacc	gctgaaggcc	aaagaggcca	1260
caaagaagaa	aaagaaacag	tttgggaaga	aaaggaaaag	aatcccgcgc	actaagacgc	1320
gacccctcag	acaggggtcc	aagaagcccc	tgctggagga	cgaccctcag	ggtgccagga	1380
agatctcgtc	ggagcctgtt	cctggcgaga	tcattgctgt	gcgtgtgaag	gaagagcatc	1440
tagacgtggc	ctcgcccgac	aaggcttcaa	gtccagagct	gcctgtctcc	gtcgagaaca	1500
tcaagcagga	aacagacgac	tgagccttcc	gtcctccagc	ctggcttcta	gctggaagcc	1560
agcccagcgt	ttctctacca	ccaccaccat	gcctccacct	gactttggct	tggagactga	1620
tcctctctgt	gtaaattctg	cccgggtgctg	tgaaggctgg	acgggtggagg	acctgctggg	1680
gtctcctggg	acccgcctgt	tgtctctgcc	ctcccctgtg	gaaaggtcta	tatgacgggc	1740
cgcttgaggc	cccagaactc	gtctgtgaac	caccttttcc	agccagagtt	cccaaagctg	1800
gaacgctagc	tgcctgctct	tccttaagat	ggcctcccc	cgacccgcca	agccacctcag	1860
ttgccagggg	tggggccacc	actgtcacac	tgtggaatac	aagacagtga	actctgtctg	1920
cctgaacgag	tcattgtaaat	taagttctag	agcagctctc	tgagcaggat	aaggtccctc	1980
gacagtgagt	tgtgtggtgg	gggcagcctc	tgccctcaaaa	attcaccaag	cagaatgcct	2040
ctcagcctca	tgtgttggtc	ctctgtctct	cctagctccc	cagggatgtt	ggggacccag	2100
cttgtctcgg	cagctaagaa	gcagtgaacca	ggatgtggat	tttggcgacc	tgtgtggtgg	2160
ccttgagctg	ctttctgtgt	ttgtgaggac	tgactcccat	ttcctaaagg	aaatgcccc	2220
ggggaggaca	ttgggaggaa	gatggcctga	gtgtgcactt	tggtctgtct	acctgtctct	2280
gaagccccgc	taaaaataat	tcattccaaga	ttccttttga	gttaaagggt	ccagttctga	2340
ctggagcctc	tagagagctg	ggcttgtatg	ttcttttggc	cttttgttcc	tacctaaatg	2400
aagaaacctc	gccgtgaggg	gccgtgaaca	cagaaccctc	aagacaagga	tgacagagct	2460
ggaggacaca	tctagctgcc	attgcaacct	cactgggctc	cccagactct	gtgtgtgaga	2520

WO 01/07471

PCT/US00/19948

aattaaaccc cctgcttgct tgagaaaaaa aaaaa

2555

<210> 91

<211> 4172

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1980010CB1

<400> 91

```

ccacaaagct tcatgacatg gtagaccaac tggaaacaaat tctcagtgtg tcagagcttt 60
tggaaaaaca tggactcgag aaaccaatth catttgtaa aaacactcaa tctagctcag 120
aagaggcacg caagctgatg gttagattga cgaggcacac tggccggaag cagcctcctg 180
tcagtgaagtc tcatggaga acgttgctgc aagacatggt aactatgcag cagaatgtat 240
acacatgtct agattctgat gcctgctatg agatatttac agaaagcctt ctgtgtctta 300
gtcgccctga aaacatccac ctggctggac agatgatgca ctgcagtgtg tgttcagaaa 360
atcctccagc tggatatagcc cataaaggga acccccacta cagggtcagc tacgaaaaga 420
gtattgactt tgagaaccca gaagaaaggc agtacttcaa ttcttctacc aacctcactg 480
atagctgcat ggatctagcc aggtgctgct tacaactgat aacagacaga cccctgcca 540
ttcaagagga gctagatctt atccaagccg ttggatgtct tgaagaatth ggggtaaaaga 600
tcttgccctt gcaagtgcga ttgtgcccctg atcggatcag tctcatcaag gagtgtatth 660
cccagtcctc cacatgctat aaacaatcca ccaagcttct gggccttgct gagctgctga 720
gggttgacag tgagaaccca gaagaaaggc ggggacaggt tctaactcct ttagtggagc 780
aggcacttcg ctcccatgac tacaagcag ccagtatgca ttgtcaggag ctgatggcca 840
caggttatcc taaaagttgg gatgtttgta gccagttagg acaatcagaa ggttaccagg 900
acttgccac tcgtcaagag ctcatggctt ttgctttgac acattgccct cctagcagca 960
ttgaacttct tttggcagct agcagctctc tgcagacaga aattctttat caaagagtga 1020
attccagat ccatcatgaa ggaggggaaa atatcagtgc ttcaccatta actagtaaag 1080
cagtacaaga ggatgaagta ggtgttccag ttagcaattc agctgacctt ttgcgtgga 1140
ccactgctac caccatgaaa gtcctttcca acaccacaac caccaccaa gcggtgctgc 1200
aggccgtcag tgatgggcag tgggtggaaga agtctttaac ttaccttcca ccccttcagg 1260
ggcaaaaatg tgggtgtgca tatcaaatcg gaactacagc caatgaagat ctagagaaac 1320
aagggtgtca tctttttat gaactgtcca tctcaaatcc tttgtcgtc gagtctgaag 1380
ggacctatga cacctatcag catgttccag tggaaagctt tgcagaagta ttgctgagaa 1440
ctggaaaatt ggcagaggct aaaaataaag gagaagtatt tccaacaact gaagtctct 1500
tgcaactagc aagtgaagcc ttgccaaatg acatgacctt ggctcttgct tacttctctg 1560
ccttaccaca agtggttagat gctaaccggt gctttgaaaa gcagtcctcc tctgcattat 1620
ctctccagct ggcagcgtat tactatagcc tccagatcta tgcccgattg gccccatgtt 1680
tcagggaaca gtgccatcct ctttacaggg ctgattccca agaactaatc aagatgggta 1740
ccaggcatgt gactcgacat gagcacgaag cctggcctga agacctatt tcactgacca 1800
agcagttaca ctgctacaat gaacgtctcc tggatttcac tcaggcgcag atccttcagg 1860
gccttcggaa ggggtgtggac gtgcagcggg ttactgcaga tgaccagtat aaaagggaaa 1920
ctatccttgg tctggcagaa actctagagg aaagcgtcta cagcattgct atttctctgg 1980
cacaacgtta cagtgtctcc cgctgggaag tttttatgac ccatttgag ttctcttcta 2040
cggacagtgg tttgtccaca ctagaaattg aaaatagagc ccaagacct catctctttg 2100
agactttgaa gactgatcca gaagcctttc accagcacat ggtcaagtat atttacccta 2160
ctattgggtg ctttgatcac gaaaggctgc agtattatth cactctctct gaaaactgtg 2220
gctgtgcaga tttggggaac tgtgccatta aaccagaaac ccacattcga ctgctgaaga 2280
agtttaaggt tgttgcatca ggtcttaatt acaaaaagct gacagatgaa aacatgagtc 2340
ctcttgaaagc attggagcca gttctttcaa gtcaaaatat cttgtctatt tccaaacttg 2400
ttcccaaaat cctgaaaag gatggacaga tgctttcccc aagctctctg tacaccatct 2460
ggttacagaa gttgttctgg actggagacc ctcatctcat taaacaagtc ccaggctctt 2520
caccggagtg gcttcatgcc tatgatgtct gcatgaagta ctttgatcgt ctccaccag 2580
gtgacctcat cactgtgta gatgcagta cattttctcc aaaagctgtg accaagctgt 2640
ctgtggaagc cgtaaaagag atgactagaa agctatttaa gacagtcaaa catthtattg 2700
agaagccaag gaaaagaaac tcagaagacg aagctcaaga agctaaggat tctaaagtta 2760
cctatgcaga tactttgaat catctggaga aatcacttgc ccacctggaa accctgagcc 2820
acagcttcat cctttctctg aagaatagtg agcaggaaac actgcaaaaa tacagtcacc 2880
tctatgatct gtcccgatca gaaaaagaga aacttcatga tgaagctgtg gctatttgtt 2940
tagatgggtc gcctctagca atgattcagc agctgctaga ggtggcagtt ggccctcttg 3000
acatctcacc caaggatata gtgcagagtg caatcatgaa aataatttct gcattgagtg 3060

```

WO 01/07471

PCT/US00/19948

```

gtggcagtgc tgaccttggt gggccaaggg acccactgaa ggtcctggaa ggtgttgttg 3120
cagcagtcca cgccagtgtg gacaaggggt aggagctggg ttacacctgag gacctgctgg 3180
agtggctgcg gcctttctgt gctgatgacg cctggccggg gcggcccccgc attcacgtgc 3240
tgcagatttt ggggcaatca ttacacctga ctgaggaggga cagcaagctc ctgctgttct 3300
ttagaactga agccattctc aaagcctcct ggccccagag acaggtagac atagctgaca 3360
ttgagaatga agagaaccgc tactgtctat tcatggaact cctggaatct agtcaccacg 3420
aggctgaatt tcagcacttg gttttacttt tgcaagcttg gccacctatg aaaagtgaat 3480
atgtcataac caataatcca tgggtgagac tagctacagt gatgctaacc agatgtacga 3540
tgaggagaaca ggaaggattg ggggaatgaag ttttgaaaat gtgtcgctct ttgtataaca 3600
ccaagcagat gctgcctgca gagggtgtga aggagctgtg tctgctgctg cttaaccagt 3660
ccctcctgct tccatctctg aaactctctc tcgagagccg agatgagcat ctgcaacaga 3720
tggcactgga gcaaatcacg gcagtcacta cgggtgaatga ttccaattgt gaccaagaac 3780
ttctttccct gctcctggat gccaaagctgc tgggtgaagtg tgtctccact cccttctatc 3840
cacgtattgt tgaccacctc ttggctagcc tccagcaagg gcgctgggat gcagaggagc 3900
tgggcagaca cctgcgggag gccggccatg aagccgaagc cgggtctctc cttctggccg 3960
tgagggggac tcaccaggcc tcagaacgc tcagtacagc cctccgcgca gcacagcat 4020
gggtgtgagg gccacctgtg gccctgctcc tttagcagaaa aagcatctgg agttgaatgc 4080
tgttcccaga agcaacatgt gtatctgccc attgttctcc atggttccaa caaattgcaa 4140
ataaaactgt atggaaacga tgaaaaaaaa aa 4172

```

<210> 92

<211> 4037

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2259032CB1

<400> 92

```

tcggagtgcc gcccgcgccc ccgagtcggt ctcgagccgc cggccggccg tgccggtgtc 60
cgtaggcgct gcgccctcgg cggggcccat gtgtgtgcgg cccgcccag gccgcccggg 120
ctttgcctcc accagcgccc tggcctccgc tcgggctccc acacgggcct ccgaagagct 180
gccgcgacgc ccggcccgca gggcaggtaa agagattata aatcttccac tgaatgaaaa 240
aaattttctt aaagctgcat atactccaag aaaaaaacca caaatgtttt tctgttttgc 300
ctgaatacat gatttaaaca agagatttcc acagaagctc tgccggccgtc acgatgttct 360
ggaagtttga cttgaacacc acgtcccatg ttgacaagct gctggacaag gagcatgtga 420
cgctgcagga gttaatggat gaagatgaca tcttgcaagg gtgtaaggct cagaaccaga 480
agctgctgga ctctctgtgc aggcagcagt gcatggaggga gctgggtgag ctcatcacac 540
aggatccgcc cctggacatg gaggagaagg tccgcttcaa atatccaaac acagcctgtg 600
agcttctgac ttgtgatgtg ccgcagatca gcgaccgctt cggtgggggac gagagcctgc 660
tgagcctcct gtacgacttc ttggaccatg agccgcctct caatcctctg ctgcgccagt 720
ttttcagcaa gaccattggc aatctcattg caagaaaaac cgaacagggtg attacgtttt 780
tgaagaagaa ggacaagttc atcagcctgg tgttgaagca catcggcacc tcagcgctta 840
tggaacctgt gctgcgcctg gtcagctgtg tggagccagc cgggctccgg caggacgtcc 900
tgcactggct gaataagag aaggtcatcc agaggcttgt ggagttgate caccgagcc 960
aggatgaaga taggcagtca aatgcttctc agactctctg tgacatagtt aggttgggca 1020
gagaccaggg cagtcagctg caagaggctc tggagccaga cccgctcctc acagcgctgg 1080
agtccaggca ggactgtgtg gagcagcttc tgaagaacat gtttgatgga gaccggacgg 1140
agagctgcct cgtcagtggt actcaggtgt tactacctt gctggaaacc aggcgggttg 1200
ggacagaggc cttggtggac tcctttctc agggactgga aaggtcatac gctgtcagca 1260
gcagcgtact acacggcatc gagcctcggc tgaaggactt ccaccagctc ctgctcaacc 1320
cgcccaagaa gaaagcgatc ctgaccacca ttggtgtgct ggaggagccc ctggggaatg 1380
cccgtctgca tggcgcccgc ctcatggcag cactgctgca cacaacaca cccagcatca 1440
accaggagct ctgccggctc aacacgatgg acttactgct ggaactgttc tttaatgata 1500
cctggaataa ctttttgca tccaagtgg aactatgcat agccgctatt ctctcccacg 1560
ctgcccggtg ggagaggaca gaagccagcg gatccgagag cagggtggag cctccgcatg 1620
agaacgggaa ccggagcctg gagactcccc agccggccgc cagcctccct gacaacacaa 1680
tggtgacca cctgttccag aagtgtgcc tgggtgcagag gatcctggag gcctgggaag 1740
ccaacgacca cagcgaggca gccgggtggc tgagacgtgg gaacatgggc cacctcacac 1800
ggatcgccaa cgcggtggtg cagaacctgg agcggggccc tgtgcagacg cacatcagcg 1860
aggtcatccg agggctccct gcggaactgc gtggccgctg ggagagcttc gtggaggaga 1920
cgctgacgga gacgaaccgc aggaacactg tggacctggc cttctctgac taccagatcc 1980

```

WO 01/07471

PCT/US00/19948

```

agcagatgac agccaacttc gtggatcagt ttggcttcaa tgatgaggag tttgccgacc 2040
aggacgacaa catcaatgcc ccgtttgaca ggatcgacaga gatcaacttc aacatcgacg 2100
ctgacgagga cagtcaccagc gcagctctgt ttgaggcctg ctgcagtgcg cgcaccagc 2160
cctttgatga tgatgaggac gaggacatct cccatgcttc agagagtgc tcaaagaatg 2220
gggtgatggc cagacccagg tttggagccc cccatgcttc agagagtgc tcaaagaatg 2280
gcccagagcg tggaggccag gatgggaagg cgagcttggg agcacacaga gatgcacctg 2340
gggcagggtgc cccaccggcc cccgggaaga aggaagcccc cctgtggag ggtgactcag 2400
aagcaggcgc catgtggacg gcagtgtttg atgagccagc gaactcaacg cccacagccc 2460
caggagtggg gagggacgtg ggttccagtg tgtgggcagc tggcacctca gctccagagg 2520
agaaaggctg ggccaagtgc actgacttcc aacctttctg ctgctccgag tcaggggccc 2580
ggtgcagctc tccggtggac acagaatgca gccatgctga gggcagccgg agccaaggcc 2640
ctgagaaagc cttcagcccc gcttctccat gtgcctggaa cgtgtgtgtc accaggaagg 2700
ccccctgct ggctcttgac agtagctcct ctgggggctc ccacagcgag gatggcgacc 2760
agaaggcagc gagtgccatg gatgcggtga gcaggggtcc cggccgggag gccccccgc 2820
tgcccacagt ggccaggaca gaggaggctg tcggcagggt cgggtgtgtc gacagccggc 2880
tgttaagccc tgcttcccc gcgccaaagg aagtgactgc tgcccagcc gtggctgtgc 2940
cccccgaggc tactgtggcc atcaccacag cactgagcaa ggctggcccc gccataccca 3000
ccccagcagt ctcttctgca ctggccgtgg cggccccctc agggcccatc atggcagtca 3060
cagcagcccc agccatgggt gccaccctgg ggacagtgc aaaggacggg aagacagatg 3120
ccccgcagag aggagctgcc ttaaattggc cagtgtgat ctgctgccgc ccggccacgg 3180
ccccccctgg tcaggctgcc tccttaatcg agaaaactac ctggtgatgc aatctttttt 3240
tttttaattt aatttaattt taaaataaat gctgcattgg taaagctggc agttgaaacc 3300
agttggacgg cccagcttgc gtctcttctg cctgagtggg cctctcaggt cactcgtgcc 3360
ctgctggagg acagaggggc acctcagccg cccccaagcc cagagcacag caataaggtc 3420
ggcctgcagg agccgggggt ggggtggggg tggggggggc aggaccctga gatgccacca 3480
ggacctgatg ggccaggaag ggcgtggaca tggaggctgt ttttacagtt ttttttgtt 3540
gttgttttgt ttttaagaa tacagaagga gccaaagctt tttgcacttt gtatccagct 3600
gcaagctcag ggcagagtca agggcctggg ttggaaaaac ctgactcaca ggaatgcata 3660
attgacctt gcagctaccc aatagccctt ggagctggca ctgaaccagg ctgcaagatt 3720
tgactgcctt aaaaacacaa ggccctctag gcctggcagg gatgtccctg tgcccagcac 3780
aggggtgctg gcagggggag accacaggtg gtcaggtggg gggacatggt gtggcactgc 3840
gggctcgaag actggtttct agcactaccg gtcacggcca tgtcgtccta gaagggtcca 3900
gaagattatt ttacgttgag tccattttta atgttctgat cacctgacag ggcaccccaa 3960
accccaact cccaataaaa gccgtgacgt tcggacaaaa aaaaaaaaaa aaaaaaaaaa 4020
aaaaaaaaa aaaaaaa 4037

```

<210> 93

<211> 2031

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2359526CB1

<400> 93

```

ggcggggctc ggctcgggct ccgcgggcgg gcgggcgagc atggcgggcca acatgtaccg 60
ggtcggagat tatgtctact ttgagaattc ctccagcaac ccatacctaa taagaaggat 120
agaagaactc aacaagactg caagtggcaa cgtggaagca aaagtagtat gcttttatag 180
acgacgtgat atttccaaca cacttataat gctcgcagat aagcatgcta aagaaattga 240
ggaagaatct gaaacaacag ttgaggctga cttgaccgat aagcagaaac atcagttgaa 300
acatagggaa ctctttttgt cagccagta tgaatctctg cccgcaacac atatcagggg 360
aaagtgcagt gttgccttc tgaatgagac agaactcagta ttgtcatatc ttgataagga 420
ggataccttc ttctactcat tggcttatga cccctcattg aaaacactat tagctgacaa 480
aggtgaaatc agagtgggac ctagatatca agcagacatt ccagaaatgc tgttagaagg 540
agaatcagat gagagggaac aatcaaaatt ggaagttaaa gtttgggac caaatagccc 600
acttacggat cgacagattg accagttttt agttgtagca cgtgctgttg ggacattcgc 660
cagagccctg gattgcagca gttctgtgag gcagcctagt ttgcatatga gtgctgctgc 720
agcttccccg gacatcacct tgtttcacgc tatggataca ttgtatagac acagctatga 780
tttgagcagt gccattagt tcttagtacc actcggagga cctgttttat gcagagatga 840
aatggaggaa ttgtcagcct ctgaagctag cttatttgaa gaggcactgg aaaaatatgg 900
caaagacttc aatgacatac ggcaagattt tcttccttgg aaatcattga ctgacatcat 960
tgaatattat tacatgtgga aaactactga cagatatgtg caacagaaac gtctaaaagc 1020

```


WO 01/07471

PCT/US00/19948

```

ggctacacta tgataccctg gcaactggaa taatttattt tcatcgcttc tatatgtttc 360
attccttcaa gcaattccca agatatgtga caggagcctg ttgcctcttt ctggctggga 420
aagtagaaga aacaccaaaa aaatgtaaag atatcatcaa aacagctcgt agtttattaa 480
atgatgtaca atttggccag tttggagatg acccaaagga ggaagtaatg gttctggaga 540
gaatcttact gcagaccatc aagtttgatt tacaggtaga acatccatac cagttccctac 600
taaaatatgc aaagcaactc aaaggtgata aaaacaaaat tcaaaagtgt gttcaaatgg 660
catggacatt tgtaaattgac agtctctgca ccaccttgct actgcagtgg gaaccagaga 720
tcatagcagt agcagtgatg tatctcgcag gacgtttgtg caaatttgaa atacaagaat 780
ggacctccaa acccatgtat aggagatggt gggagcagtt tgttcaagat gtcccggtcg 840
acgttttggg agacatctgc caccaaattc tggatcttta ctcaacaagga aaacaacaga 900
tgctcatca cccccccat cagctgcaac agccccatc tcttcagcct acaccacaag 960
tgccgcaagt acagcagtca cagccgtctc aaagctccga accatcccag cccagcaga 1020
aggaccccca gcaaccagcc cagcagcagc agccagccca acagcccaag aaacctctc 1080
cgcagcccag ttctccccga cagggttaagc gagccgtggt tgtttctccc aaagaagaga 1140
acaaagcagc agaaccacca ccacctaaaa tccccaaaat tgagaccact ctccaccgt 1200
tgctccagc ccacctacct ccagaccgga agctccccct cgctgctgcc ttaggtgagg 1260
ctgagccgcc gggccctgtg gatgccactg acctcccca agtccagatt cccctccgg 1320
cccacccggc cctgtgac cagccaccgc cgctgccaca ccggcccccg ccccccccc 1380
cctccagcta catgaccggg atgtccacca ccagctccta catgtctgga gagggtacc 1440
agagcctgca gtccatgatg aagaccgagg gacctccta cggtgccctg cccccgcct 1500
acggccacc tgcacacctg cctaccacc ccatgtcta cccgcccaac ccgcccccgc 1560
cacctgtgcc tctccccca gctccttcc cccacctgcc atccccccc ctactcctgg 1620
ctacccccaa cccccacca cctacaacct caacttcca ccccccccc cagcctccc 1680
gctacccac gcagtccccc ctcatcctcc tccagggttg ggctgcccgc cagccagcta 1740
ccacctcct cccgtcccc ctggaggaca gcctcctgtg ccccgccca ttccccacc 1800
cggcatgcct ccagttggag gggctggggc gggcagcctg gatgagataa cgtgagcctt 1860
tttccctct ttgtttttt aacaagattt tctaatacgc ttgcagagta gttgaagtgg 1920
gtaagcagca gggtagcttg tataatgcac gacagttgca gtatgggaag aatggaccgg 1980
gcccctggga taaaatcaga gtggtcctca cacctagagg acggggacaa ccagctttca 2040
gagtagcctc atcagtgncc ttgcagnctg
2070

```

<210> 96

<211> 2046

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2683225CB1

<400> 96

```

tgacatggat ggggatgact tctgggcta acatttctct tgctaaagga tgattttgca 60
ccaccttgaa tgcccatgat taagacataa acaagaaaag agatatctga ggagaatgca 120
gttgaaacta attttgtgga tagagaaact gttggaactg ctttacaag tattttaaca 180
gcccacctga ggatattgac cataaggact catatctcat tacaagaagc atcatggccg 240
agccagacta catagaagat gacaatctg aactcattag gcctcagaaa ctgatcaatc 300
ctgtaaaaac ctcccgaac catcaagatc ttcacagaga acttcttatg aatcaaaaaa 360
ggggtcttgc tctcagaac aaaccagaat tgcagaaggt gatggaaaaa agaaaacgag 420
accaagtaat aaagcagaag gaagaagaag cacagaagaa gaaatctgac ttggaaatag 480
agctattaaa acggcagcag aagttggagc agcttgaact tgagaagcag aaattgcaag 540
aagagcaaga aaatgcccc gagttctgta aggtgaaagg caatctcagg agaacaggcc 600
aagaagtgc ccaagcccag gagtcctagg ctgaggctgc accaagacct cgtgtgtcac 660
cccacagagc tgtctgtggg tgcttctca atctcagggc aaaagccccct ggagaatatt 720
tcagccagca gagaattttg acttgacagta ggatttggtt tgattttcct acgatctggg 780
tggtatgcctt gcctgtgaca gttgcagttc ctattcgcca aatgaagggc agtgccccgc 840
acgtaagtgt gaattgatga cctgtgttca gagacttaac agaaccaaca agcaaaaaca 900
gtgagaacag gaaaaaggaa gaggacactg gaatcaattc ttgagagttg cactactttg 960
ttttcttcc attccaagtt tctgtggacc cagagccttt tttcttttaa aagctaaaaa 1020
acaagtgtt aattcctctt ttgttatct gttagataat tgagatcacc tagaaatgcg 1080
tttaatctgt tcaactcactg taaattttga ggaccagaa ttgtcttgtt taatttatac 1140
tttcacccct gttgcagtta acaccagaga aggaacgtga atgtcgagca cagccactac 1200
ccttggtggc acttaattta gaaatagggt gagaagttta aaagcccatc ttgattttat 1260
tttcattcct tttggttctc tgtgtaataa tagcaggcta catagtgaca ttccagttcc 1320

```

WO 01/07471

PCT/US00/19948

```

aagaagggtac atcctgtcca ttcattaatt gctttgatta ctaggagggt ttctgttcag 1380
ttttgttttt aaatgtcttg ctgatctagt tctttcagat ggaataacct tccagtcctt 1440
tagagagtgg aactagtcca tataacccag cttcagtagc aaaagtagaa gccgccacat 1500
cttttcattt ctccaagagg agagtgggga aggttcccat gaccagctgg gcagtcagga 1560
tttctctagg cattctaatt tgaaataagt gtagactgct gtcaaggagg cttcatcaga 1620
agatgtatag catttgaatg tctaataata atgcatatca ttagaatcca agctttgaaa 1680
atctctgatt aatgctcatg tatttcttta tctttgtttt tccttgtgaa gaaagacttt 1740
caccactgtc tgagtgtatg tgctgttgat aaggatgatg tcgatgacta ctatattgca 1800
tctctcagga acagctgatg ggaagggagg ggctgctgag ttcccttgtt ctagctagca 1860
gcacgctcct cagagagggg gccgagttac agacagcagc cgcattctca tgcaaaatta 1920
gttttaaaact gctagtgtgg gcatcggtac cttttgcctg ggtgataccg aagaattgtt 1980
gaggatttag tatgctccgt agagacagtt cagccagtca tttctgcatt ggagagactt 2040
ctcata

```

2046

<210> 97

<211> 2660

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2797839CB1

<400> 97

```

gtggcgagtg ccggccgaaa gctaggtccg gattgcacgt ggagggccgc ccgaagggca 60
ctctcggaca ttaacccgca ttctgtacca tggggcgcaa gttggaccct acgaaggaga 120
agcggggggc aggccgaaag gcccggaagc agaaggggtg cgagacagaa ctctgcagat 180
tcttgccctg agtaagtgc gaaaattcca agaggctgtc tagtctgtct cgaaagaggg 240
cagccaagag gagattgggc tctgttgaag cccctaagac aaataagtct cctgaggcca 300
aaccattgct tggaaagcta ccaaaaggga tctctgcagg agctgtccag acagctggta 360
agaagggacc ccagtcctta ttaatgtct ctcgaggcaa gaagcgcca gcacctggca 420
gtgatgagga agaggaggag gaagactctg aagaagatgg tatggtgaac cacggggacc 480
tctggggctc cgaggacgat gctgatacgg tagatgacta tggagctgac tccaactctg 540
aggatgagga ggaaggtgaa gcgttgcctg ccattgaaag agctgtctcg aagcagaagg 600
cccgggaagc tgctgctggg atccagtgga gtgaagagga gaccgaggac gaggaggaa 660
agaaagaagt gacccctgag tcaggccccc caaaggtgga agaggcagat gggggcctgc 720
agatcaatgt ggatgaggaa ccatttctgc tgccccctgc tggggagatg gacagggatg 780
cccaggtctc agacctgcaa cgagttcaca agcggatcca ggatattgtg ggaattctgc 840
gtgatttttg ggctcagcgg gaggaagggc ggtctcgttc tgaataacct aaccggctca 900
agaagacctt ggccatttac tactcctatg gagacttctt gcttggcaag ctcatggacc 960
tcttccctct gtctgagctg gtggagtctt tagaagctaa tgaggtgcct cggcccgtca 1020
ccctccggac caataccttg aaaacccgac tcgagagacc tgcacaggct ctaatcaatc 1080
gtgggggttaa cctggatccc ctgggcaagt ggtcaaagac tggactagtg gtgtatgatt 1140
cttctgtgce cattgggtgt acccccagat acctggctgg gcactacatg ctgcagggag 1200
cctccagcat gttgcccgtc atggccttgg caccacagga acatggccca gctgatgaag aacacgggtg 1320
tgtgttgtgc cctgggagga aagaccagct acatggccca tgttgtgggc aacttgcac 1380
tgatccttgc caatgacgcc aatgctgagc ggctcaagag actatgatgg gcgccagttc cccaaggtgg 1440
ggctgggagt caccaacacc attatcagcc actatgatgg tggcactggg gtcactctca 1500
tggggggctt tgaccgagta ctgctggatg ctccctgcag tggcactggg gtcactctca 1500
aggatccagc cgtgaagact aacaaggatg agaaggacat cctgcgctgt gctcacctcc 1560
agaaggagtt gctcctgagt gctattgact ctgtcaatgc gacctccaag acaggaggtt 1620
acctggttta ctgcacctgt tctatcacag tagaagagaa tgagtgggtg gtagactatg 1680
ctctgaaaaa gaggaatgtg cgactggtgc ccacgggcct agactttggc caggaaggtt 1740
ttacccgctt tcgagaaagg cgcttcacc ccagctctgc ttctacccga cgcttctacc 1800
ctcataccca caatatggat ggggttcttca ttgccaagtt caagaaattt tccaattcta 1860
tccctcagtc ccagacagga aattctgaaa cagccacacc tacaatgta gacttgcctc 1920
aggatcatcc caagtctgag aacagcagcc agccagcaa gaaagccaag ggggctgcaa 1980
agacaaagca gcagctgcag aaacagcaac atcccaagaa ggcctccttc cagaagctga 2040
atggcatctc caaaggggca gactcagaat tgtccactgt accttctgtc acaaagacct 2100
aagcttcttc cagcttccag gatagcagtc agccagctgg aaaagccgaa gggatcaggg 2160
agccaaaggt gactgggaag ctaaagcaac gatcacctaa attacagtc tccaagaaag 2220
ttgcttcttc caggcagaat gccctccca agggcacaga cacacaaaca ccggctgtgt 2280
tatccccatc caagactcag gccaccctga aacctaaagg ccatcatcag ccccttggaa 2340

```

WO 01/07471

PCT/US00/19948

```

gggccaaggg ggttgagaag cagcagttgc cagagcagcc ttttgagaaa gctgccttcc 2400
agaaacagaa tgataccccc aagggggcctc agcctcccac tgtgtctccc atccgttcca 2460
gccgcccccc accagcaaaag aggaagaaat ctcagtccag gggcaacagc cagctgctgc 2520
tatcttagat ggttgaaaac tagacgggtg gctcactgcc attgtcacca ggttggaaact 2580
cttgccctctg tgaggatgcc ttctctactg tgcataccca tgaaatttaa tacacatttt 2640
aaaaacctctg aaaaaaaaaa

```

2660

<210> 98

<211> 4610

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2959521CB1

<400> 98

```

ggggcccgga cgcattgaggg ggggtcggcgc gcgtgtctac gcggacgcac cggctaaget 60
gcttctgccc ccgccggccg cctgggacct tgcggtgagg ctgcgcgggg ccgaggccgc 120
ctccgagcgc caggtttatt cagtcaccat gaagctgctg ctgctgcacc cggccttcca 180
gagctgcctc ctgctgacct tgcttggtt atggagaacc accctgagg ctcacgcttc 240
atccctgggt gcaccagcta tcagcgtctg ctcctcctg caggatctaa tacatcggtg 300
tgccgagggg gacagcctca ctctgcagca gctgaaggcc ctgctcaacc acctggatgt 360
gggagtgggc cggggtaatg tcaccagca cgtgcaagga cacaggaacc tctccacgtg 420
ctttagttct ggagacctct tcaactgccc caatttcagc gagcagtcgc ggattgggag 480
cagcgagctc caggagtctt gcccaccat cctccagcag ctggattccc gggcctgcac 540
ctcggagaac caggaaaacg aggagaatga gcagacggag gaggggcggc caagcgtgt 600
tgaagtgtgg ggatacggtc tcctctgtgt gaccgtcacc tccctctgct cctcctggg 660
ggccagcgtg gtgcccttca tgaagaagac cttttacaag aggtgctgc tctacttcat 720
agctctggcg attggaacct tctactccaa cgccctcttc cagctcatcc cggaggcatt 780
tggtttcaac cctctggaag attattatgt ctccaagtct gcagtgggtg ttgggggctt 840
ttatcttttc tttttcacag agaagatctt gaagattctt cttaaagcaga aaaatgagca 900
tcatcatgga cacagccatt atgcctctga gtcgttccc tccaagaagg accaggagga 960
gggggtgatg gagaagctgc agaacgggga cctggaccac atgattcctc agcactgcag 1020
cagtgaagctg gacggcaagg cgcccatggt ggacgagaag gtcattgttg gctcgtctc 1080
tgtgcaggac ctgcaggctt ccagagtgct ttgctactgg ctgaaagggtg tccgctactc 1140
tgatatcggc actctggcct ggatgatcac tctgagcgac ggcctccata atttcctg 1200
tgccctggcc atcgggtgctt ccttcaactgt gtcagttttc caaggcatca gcacctgggt 1260
ggccatcctc tgtgaggagt tcccacatga gctaggagac tttgtcatcc tgctcaacgc 1320
tggtgatgac atccaacaag ctctcttctt caacttctt tctgcctgct gctgctacct 1380
gggtctggcc tttggcatcc tgccggcgag ccacttctct gccaaactgga tttttgcgct 1440
agctggagga atgttcttgt atatttctct ggctgatatg ttccctgaga tgaatgaggt 1500
ctgtcaagag gatgaaagga agggcagcat cttgattcca tttatcatcc agaacctggg 1560
cctcctgact ggattcacca tcatggtggt cctcaccatg tattcaggac agatccagat 1620
tggttagggc tctgccaaga gcctgtggga ctggaagtcg ggccctgggc tgcccgatcg 1680
ccagcccgag gacttaccat ccacaatgca ccacggaaga ggccgttcta tgaaaaactg 1740
acacagactg tattcctgca ttcaaagtgc agcgtttgt aaaatgctgt atcctaggaa 1800
taagctgccc tggttaaccag tctctagcta gtgcctcttg cctctcctc acctcctttt 1860
ctctcagtga ctctggaacc tgaatgcagc ttacaagaca agcctgactt ttttctctga 1920
ttacctggc ctcctcttgg aaccagtgtt gaaaggtttt gaatccttta cccaacaatg 1980
caaaaataga gccaatggtt ataacttggc tagaaatc aagagttgaa tccataggtg 2040
ggggcccatg actctagctg ggcaccttgg acctccagct ggccaataga agagacagga 2100
gacaggaagc cttcccattt tttcaaagtc tgtttaattg cctattactt ctctcaaaga 2160
gaacctgaag tcagaacaca tgagcagggg gagaggtgag gcaagggttca tctgaatgg 2220
gagaggaagt cgaaccactg ctgtgtgtct tgtcaggatg ctcacttggt cctactgaga 2280
tgctggatat tgattttgta acagcaccgg gtgtttcacg gctgtccgag tgagctaacg 2340
tgccggtgtg gctgcctgga cctcctcttt caggttaacg ctgacagaat ggaggctcag 2400
gctgtctgca agaaaacagt tggtttggct gtgattttga cctcctcttc cccactgcca 2460
tcttctaaga gactttgtag ctgcctccta gaagcacatt ctgagcacat ttgagacctc 2520
tgtgttagag gggagactgc acaaactatc cccccagg ttgagacgtc tgcagagtgg 2580
caagctgact tgtagaaatg gggtgccatt tatgtctctac ttagacaagg gtaatcagaa 2640
atggaatcag tgcaggcaaa atttaggatt tgccgcttcc ataaatcaaa gcatgactaa 2700
taggggggtct ctgaaatgta agggcacaaa cttcacttag ggcacgcag atgtttgcag 2760

```

WO 01/07471

PCT/US00/19948

```

aatggttggc ctaatgatta tgctacagat ggggttttaa tgaccegtct aggttactgc 2820
ttccttgcaa aaaaagtcga atcctgcatt gaattgaata tgaatttctc taactctctc 2880
cagaaaatgg atggagataa cttgtcttta aaactgtagg ccagccttag ccactgtgga 2940
gcccttgcc cccagctctg gcttcaaggg gagctcttct ccagggtcac taggtgaatt 3000
gatttattat tatcatattg ataatgtgag attcttttag cactttgggg agctgtctc 3060
tccagaagcc tttcttagtg gtgcccacag ttggagccca ggggccaatg ttgcaaaactg 3120
attcatgtgc atggctgaca ggagtactgg ttcactacca atgcctgagc ttttctctta 3180
catagaaaaa ctgtccgctc tcagtaatca caagcagcat ccgttttggt ttctcttctt 3240
gggagacatc tgtcaaacca ggaatattct tgaaaagaac gtgagcagga aaaactgctg 3300
gtgatacttt ttttaagttt tgtttttatc ttgcctgttg gcttcaatac atttgagaat 3360
acgctgaaga gggaaaattt cagtgtatga gattctagat taaatatcag gactgatttc 3420
ctgggtgggag gattatgggtc cagttttacc aaagaaccaa ttccttgaat gttggaatct 3480
aactttttat attgtcatta ttattgttgt ttttaaaccg ttctttgtct tttctgtttt 3540
atttttctca agctgctttc aggagctagc agaaaataac tcaaagttga agactctgga 3600
agattttgct ttaacctaac tcgcattgat gtattaaatt tataatttta gcattcccaa 3660
tagatcctat cattccttaa acataatacc ctttgtcttg gactagaata ctaagttaga 3720
gttagtggat ttctagttaa ggagaggagc tcaaaactat aatctttaac aaattgaaaa 3780
atgaaatagg gtgttttccc tttttgtgca cacctatatt accttaagaa atttccctcc 3840
atagacagct gcctcaaagg gaaatcctct ttaaaccgta gttggcgag aggtcagtc 3900
tagtcggagc ttaggagggg cggagacgct cacatcgtct gacttgagtc gccactgatt 3960
gtggcaacag ctttgccctca tgagtcaaaa attggcaatt tcttttgatt ttagttgtt 4020
gaatttgctg tttcaagcat ttgtacatat tagaagtcta aggagtagca agtcagtggtg 4080
aggacttttt cacccttggtc attagcagct tcgacctcat tttccagatg caccagctcc 4140
tattaataag ttagcaagga aagtgtatgt cacgtgcagg aacagtgagg cagggacagg 4200
ggttctgctc cttctcactt caccaccggc acacagcttg cccctgtctt tgcccccaaa 4260
ggtattttgt gctcagtgtc aaattggagc tattcttcac tggtccttaa ccttggttt 4320
taaaaagaag gcttctctgt ttgggtagcg taagagctga gtatagtaag tctcttcca 4380
aagagatggc aatatgctgg gcactactt taaaacaaag ttgtctgatt ttgcaagag 4440
aggttaggat tttattgttc ttatttccct ttacagttct gcagttccat cacagtattt 4500
ttttaataaa ctcaggtgta tgagaagaaa ttagaaaaga aaattaactt atgtggactg 4560
taaagtgttt atttgaaga ttctataaat aaagctatat tctgtaaaac 4610

```

<210> 99

<211> 1889

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3082014CB1

<220>

<221> unsure

<222> 1809, 1848, 1853, 1880

<223> a, t, c, g, or other

<400> 99

```

acgtagaaga tggagagaag gaggtggtat tgagagatgc tgtggggagg gagagtgggg 60
ctcaccgggg ttttccaatc tctctcctat aggggggaaat gcagtgtgac cctcttgaat 120
gagacagata tcttgagcca gtacctggaa aaggaggact gcttttttta ctactggtg 180
tttgaccccg tgcagaagac acttctcgct gatcagggcg agattagagt tggttgcaaa 240
taccaagctg agatcccaga tcgcctagta gagggagaat ctgataatcg gaaccagcag 300
aagatggaga tgaaggtctg ggacccagac aacctctca cagaccggca gatcgaccag 360
tttcttggtg tggcccgagc tgtgggaacc tttgcaagag ccctagattg tagcagctcc 420
attcggcagc caagcttgca catgagtgc gctgctgcct ccgagatat cactctgttt 480
cacgccatgg ataccttgca aaggaacggc tacgacctgg ctaaggccat gtcgaccctg 540
gtaccccagg gaggcccggt gctgtgtcgg gatgagatgg aggaatggtc agctcagag 600
gccatgctat ttgaggaggc cctagagaag tatgggaagg acttcaatga tattecgag 660
gattttctac cctggaagtc acttgccagc atagtccagt tttattacat gtggaaaacc 720
acagaccggt atattcagca gaaaagggtt aaagctgctg aagcagacag caaactgaaa 780
caggtctaca ttcccaccta cactaagcca aaccttaacc agatcatttc tgtgggttca 840
aaacctggca tgaatggggc tggatttcag aagggcctga cttgtgagag ttgccacacc 900
acacagtctg ctgagtggtg tgccctggggc ccacctaaac tgcagtgcg cctctgtgct 960

```


WO 01/07471

PCT/US00/19948

```

tctctgttggg tctactggaa gaagtatggg ggactgaaga ccccaactca gcttgagggg 1020
gccactcggg gcaccacgga gccacactca aggggtcatt tatccagacc tgaagctcaa 1080
agtctctctc cttacacaac cagcgccaac agggccaagc tactggctaa gaacagacaa 1140
actttcctgc ttcagaccac aaagctgacc cgtcttgcca gacgcattgt cagggaccta 1200
ttacagccaa ggagggcgc cgcacggcct tatgctccta tcaatgccaa tgccatcaa 1260
gcagagtgtc ccattcgact tcctaaggcc gccaaagactc cattgaagat tcacctctg 1320
gtgcggtgtc ccctggcaac tatcgtcaaa gatctgggtg cccaggcacc cctgaaacca 1380
aaaacacctc ggggtaccaaa gacaccgatc aacagaaacc agctgtccca gaaccgggga 1440
ctggggggga ttatgggtgaa acgggcctat gagactatgg caggggcagg ggttcctttc 1500
tctgccaatg gaaggcctct ggcttcaggg attcgttcaa gctcacagcc agcagccaag 1560
cgtcagaaac taaaccacagc tgatgcccc aatcctgtgg tgtttgtggc cacaaggat 1620
accagggccc tacggaaggc tctgacccat ctggaaatgc ggagagctgc tcgccgaccc 1680
aacttgcccc tgaaggtgaa gccaacgctg attgcagtgc ggccccctgt cctctacct 1740
gcacctcac atcctgccag caccaatgag cctattgtcc tggaggactg agcactgttg 1800
ggaaaggang tgggctgaga aggtagagg ggatgccag ggcaccanac ctnccttcc 1860
tttctgtctg aaggagtgan gaggatga 1889

```

<210> 100

<211> 2032

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3520701CB1

<400> 100

```

gccggggccg agccgctgtt cggttgacag ttgaggatgg ccggagccga gggcgccgct 60
ggcgggcagt cggagctgga gcccggtggt tctgttggtc acgtccttga ggaggacgag 120
gagctggaga atgaggcgtg cgctgtcctg ggcggcagcg actccgagaa gtgctcctac 180
tctcagggct cagtaaagag acaagcacta tatgcctgta gtacctgcac cccagaggga 240
gaagaaccag caggaatttg tttagcttgc agttatgaat gtcattggaag tcacaaacta 300
tttgagctat acacaaaaag aaattttcgt tgtgattgtg gaaacagcaa gtttaaaaaat 360
ttggaatgca aattacttcc tgacaaagca aaggtaaatt ctggcaataa gtacaatgac 420
aacttttttg gattgtactg catttgcaag agaccttacc ctgatcctga agacgagatt 480
ccagatgaga tgatccagtg cgtagtctgt gaagactggg tccatggaag gcattctggg 540
gccattcccc ctgagagtgg ggattttcag gagatgggat gccaggcctg catgaaacgt 600
tgttcttttt tgtgggctta tgctgcacaa ttggcagtaa ccaaaatacc cactgaggat 660
gatggattgg tgcggaacat tgatggaata ggtgatcagg aagttatcaa acctgaaaat 720
ggagagcatc aagatagtag cctcaaagag gatgttccag aacagggaaa ggatgatgtc 780
cgggagggtta aagtagagca gaacagtga ccatgtgcc gctctagttc tgaatctgat 840
ctccagacag tgtttaagaa tgaaagcctc aacgcagaat caaaatctgg ctgcaaactt 900
caggagctta aagctaagca gcttataaag aaagacactg ccacctattg gcccctgaac 960
tggcgtagca agttgtgtac ctgccaagac tgtatgaaaa tgtatggaga tctagatgtc 1020
ttattcctga cagatgaata cgacacagtt ctggcttatg aaaacaaagg gaagattgcc 1080
caggccactg acaggagcga tcccctaatt gataccctta gcagcatgaa tagagtccag 1140
caagtggaa ccatcttgta atacaatgat ttgaagactg aacttaaaga ctatctcaag 1200
agatttgctg atgaaggcac ggttggttaag agagaggaca ttcagcagtt ctttgaagag 1260
tttcagtcaa aaaagagaag aagagtggat gggatgcagt attactgcag cttagagtga 1320
gtatgaagct ttctcattca agccaatgaa aatgcgcttc ccattcttgg aataaaagag 1380
gtgtgggtca catttggtcc ctttccgtc ctctctgtt tggagaggcc tcgcgctccc 1440
ttcattctct ttagctgcag tagccaccgt ctggatgctg acttcacagc cagcgtcttc 1500
tgtgactcag ctgatgcagc tcattccaca gacttcgcca gtgtactcct actccagtgc 1560
acccaggggt atttgcatag tttttaagtt tgattttgtt ttgagaaagc aaattgggtg 1620
cttgtttaat gatctgttat ttcactccca gatgtgtgtg ttttgccaca gagctgttgc 1680
cttccagaac ctctccgca ggcacacgg aaggctctct tcccgtcacc tagaacctct 1740
acagggtccc tcgccccat gattgtgggt ccttgggtca aagcttctc aagcctggtc 1800
tgctccttct ttcacgtccc tgttttctga ggtttggtca tagcttagaa aggatcttgg 1860
ggcttggttt ctctaggccc aacctccaga gtagccagga ctgatgggtt tctgggtctg 1920
atgtctgtca caggcgga gattaacaga tgacagggtt gaggaagcaa gcctttgtta 1980
tgaattttac taatacagtt caagtgaat tttcgttcat gattctattg gc 2032

```

<210> 101

WO 01/07471

PCT/US00/19948

<211> 1356
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <223> Incyte ID No: 4184320CB1

<400> 101
 aatgaaagca acaggagctg ctccggggac tgcttttggc agtaccacaga atcagtgtctc 60
 aggtctcagaa atcctggata gaaagagcat ttataaaaag agaattgtgtc cacatcatatc 120
 ccagcaccaa agaccccat aggtgttgtc gtgggcgtct gataggccag catgttggcc 180
 tcaccccccag tatctccgtg cttcagaatg agaaaaatga aagtcgcctc tcccgaatg 240
 acatccagtc tgaaaagtgg tccatcagca aacacactca actcagccct acggatgctt 300
 ttgggaccat tgagttccaa ggaggtggcc attccaacaa agccatgtat gtgcgagtat 360
 cttttgatac aaaacctgat ctctctttac acctgatgac caaggaatgg cagttggagc 420
 ttcccaagct tctcatctct gtccatgggg gcctgcagaa ctttgaactc cagccaaaac 480
 tcaagcaagt ctttgggaaa gggctcatca aagcagctat gacaactgga gcgtggatat 540
 tcaactggagg ggttaacaca ggtgttattc gtcattgttg cgatgccttg aaggatcatg 600
 cctctaagtc tcgaggaaa atagtcacca taggtattgc cccctgggga attgtggaaa 660
 accaggagga cctcattgga agagatgttg tccggccata ccagaccatg tccaatccca 720
 tgagcaagct cactgttctc aacagcatgc attcccactt cattctggct gacaacggga 780
 ccactggaaa atatggagca gaggtgaaac ttcgaagaca actggaaaag catatttcac 840
 tccagaagat aaacacaaga tgccctgccgt tttctctctc tgactcccg cttgttttatt 900
 cattttgggg tagttgccag ttagactcag ttggaatcgg tcaagggtgtt cctgtgggtg 960
 cactcatagt ggaaggagga cccaatgtga tctcgattgt ttggagtagc cttcgagaca 1020
 cccctcccggt gccagtgggt gtctgtgatg ggagtgagc ggcatcggac atcctggcct 1080
 ttgggcataa atactcagaa gaaggcgggt aggttaactt ccaggcccca tgggaagaacc 1140
 ctaaagcctg tttggaaaac aggggtatgag tggattatgt ttccagtagc tcaaccaaga 1200
 cctcaaataa aaacaagcta tgaacaaatt gtctaaaaaa tgtctgtcat gggagggctg 1260
 tgggtgaagaa cagagaaaac tattctaaat gtccgtgtga gtgggaaatt ctatgaaagc 1320
 tacacggata ataaaaaggg tgaggaaaag agagga 1356

<210> 102
 <211> 580
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4764233CB1

<400> 102
 cacaacgcag gcaccgactt cagtgtgcat gttccttggg cacctgcctc agtgtgcatg 60
 ttcactgggc atcttccctt cgaccccttt gccacgtgg tgaccgctgg ggagctgtga 120
 gagtgtgagg ggcaggttcc agcgtctgg actctttctc tctactgag acgcagccta 180
 taggtccgca ggccagtcct ccaggaact gaaatagtga aatatgagtt ggcgaggaag 240
 atcaacatat aggcctaggc caagaagaag ttacagcct cctgagctga ttggggctat 300
 gcttgaaccc actgatgaag agcctaaaga agagaaaacca cccactaaaa gtcggaatcc 360
 tacacctgat cagaagagag aagatgatca ggggtgcagc gagattcaag tgcctgacct 420
 ggaagccgat ctccaggagc tatgtcagac aaagactggg gatggatgtg aaggtgggtac 480
 tgatgtcaag gggaagattc taccaaaagc agagcacttt aaaatgccag aagcaggtga 540
 agggaaatca caggttttaa ggaagataag ctgaaacaac 580

<210> 103
 <211> 1487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4817352CB1

WO 01/07471

PCT/US00/19948

<400> 103

```

ccgggaggcc ggggtctcgg gtggccgccc gccagggcgc tggacggcag caggatgggg 60
aaggcgagg tccccgcctc caagcgcgcc ccgagcagcc ccgtggctaa gccgggtcct 120
gtcaagacgc tcaactcgga gaaaaacaag aagaaaaaaa gggtttggaa aagcaaggcg 180
cgggaagtaa gcaagaagcc agcaagcggc ccgggtgctg tggcgcgacc tccaaaggca 240
ccagaagact tttctcaaaa ctggaaggcg ctgcaagagt ggctgctgaa acaaaaatct 300
caggccccag aaaagcctct tgtcatctct cagatggggt ccaaaaagaa gcccaaat 360
atccagcaaa acaaaaaaga gacctcgctt caagtgaagg gagaggagat gccggcagga 420
aaagaccagg aggccagcag gggctctgtt ccttcagggt ccaagatgga caggaggggcg 480
ccagtacctc gcaccaaggc cagtggaaac gagcacaata agaaaggaac caaggaaagg 540
acaaatgggt atattgttcc agaacgaggg gacatcgagc ataagaagcg gaaagctaag 600
gaggcagccc cagccccacc caccgaggaa gacatctggt ttgacgacgt ggacccagcg 660
gatatcgaa ctgccatagg tccagaggcg gccaaagatag cgaggaaaca gttgggtcag 720
agcgaggggc gcgtcagcct cagcctcgtg aaagagcagg ccttcggcgg cctgacaaga 780
gccttagcct tggactgtga gatgggtggc gtggggcccta agggggaggga gagcatggcc 840
gcccgtgtgt ccatcgtaaa ccagtatggg aagtgcgttt atgacaagta cgtcaaacca 900
accgagcccc tgacggacta taggacagcg gtcagtggga ttcggcctga gaacctcaag 960
caggggagaag agcttgaagt tgttcagaag gaagtggcag agatgctgaa gggcagaatt 1020
ctagtggggc acgctctgca taatgacctt aagggtactat ttcttgatca tccaaaaaag 1080
aagattcggg acacacagaa atataaacct ttcaagagtc aagtaaagag tgggaaggccg 1140
tctctgagac tactttcagac gaagatccct gggtccagg tccagcaggc ggagcactgt 1200
tcaattcagg atgcccaggc agcaatgagg ctgtacgtca tgggtgaagaa ggagtgggag 1260
agcatggccc gagacaggcg cccctcgtg actgtccag accactgcag tgacgacgcc 1320
tagcagtcct gccctgctgc tgcgtccgcc ccgctacaga ggcaatgtga ccagtcacag 1380
ggacagatca catctcccca gagtggcaac tctggtgaaa ctttttcaga atcatggcag 1440
agggcggtgg cgtggtgcta ctgagaagac ctcttcgtg ttgacga 1487

```

<210> 104

<211> 2257

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5040573CB1

<400> 104

```

gcgcccggctc cggctgcagt tccccgggtcc ctccggccacc gaagccaccc tgccctgggtg 60
aaaggggtccc cgcaccgccc ggtgtccccc atctgcctgg cgttgtgcgc agagctggaa 120
agcatggctg ttataaatga attctgattt tggggagcag atgccaaact agagcctcgt 180
accaatctct ctgtctttaa aagatgaggt gactttgtga ttttcttga aaattatagg 240
tgcccagcta agacctgaat gccatcaccc tccccaggc tctgcagttt tctcgtgggtg 300
aacccttgat ggatttgttg ttgcttgaga aatggcgatg atcgaattgg ggtttggaa 360
acagaatttt catccattaa agaggaagag ttcattgctg ttgaaactca tagctgttgt 420
ctttgctgtg cttctatatt gtgaattttt aatctattac ttacgcatct ttcagtgtaa 480
ttggcctgaa gtgaaaacca cagcctctga tgggtgaacag accacacgtg agcctgtgct 540
caaagccatg tttttggctg acacccattt gcttggggaa ttcctaggcc actggctgga 600
caaattacga aggggaatggc agatggagag agcgttccag acagctctgt ggttgcgtgca 660
gccggaagtc gtcttcatcc tgggggatat ctttgatgaa ggggaagtga gcacccctga 720
ggcctggggc gatgatgtgg agcgttttca gaaaatgttc agacacccaa gtcagtaca 780
gctgaaggta gttgctggaa accatgacat tggcttccat tatgagatga acacatacaa 840
agtagaacgc tttgagaaag tgttcagctc tgaaagactg ttttcttga aaggcattaa 900
ctttgtgatg gtcaacagcg tggcgctgaa cggggatggc tgtggcatct gctctgaaac 960
agaagcagag ctcatgaa tttctcacag actgaactgc tcccagagag aggcacgtgg 1020
ctccagccgg tgtggacctg ggcctctgct gccacgtct gccctgtcc tctgcagca 1080
ttatcctctg tatcggagaa gtgatgctaa ctgttctggg gaagacgtg ctctccaga 1140
ggaaagggac atcccattta aggagaacta tgacgtgctt tcacgggagg catcacaata 1200
gctgctgtgg tggctccagg cgcgctggg tctcagtggc cacacgcaca cgcctgcga 1260
ggtgcaccac gggggccgag tccccgagct cagcgtccca tctttcagtt ggaggaacag 1320
aaacaacccc agtttcatca tgggtagcat cagccccaca gactacaccc tctccaagt 1380
ctacctccca cgtgaggatg tggttttgat catctactgt ggagtgggtg gcttcttgt 1440
ggtcctcaca ctcaactcact ttgggcttct agcctcacct tttctttctg gtttgaactt 1500
gctcggaaag cgtaagacaa gatgaagagc aggcgccatt ataaatatca aagcccaaga 1560

```

WO 01/07471

PCT/US00/19948

```

aatggaactt tgggcagaga tcatgttaga atcaagtgga tgatgagacc aattacaggc 1620
cgtctctctg cacagcacag aaattctcaa tcaactgaaat gagtaactgc aaaataaata 1680
gttgattgta ctgttctcat gctataaaag tggacaggta ctctacaaca aatctgtttt 1740
ctcattttta tcaaataatat gtatcatcaa aggttgcac tgtacagtat gtaaagtcta 1800
ttaatgtcgt cactcacatg cacgacagtc cttgttcccc caggaaggcc ctggtggccc 1860
cagcacacac ttgggattat gtgtatacat aaataaatat tgggctgttt cctcttctct 1920
gtgaagtggg tctcaaattc ctatgtactg taaagctgta cccttaaaag tacagatgtg 1980
gccgggcaca gtggctcaca cctgtaatcc cagcactttg ggaggctgag gcgggtggat 2040
cacttgaggt caggagtcca agaccagcct ggccaacatg gtgaaacctc gtctccgcta 2100
gaaatacaaa aattagccaa gcatggtagc aagtgcctat aataccagct gaggtgagg 2160
caggagaatc ccttgagccc gggaggcgga ggttgacgtg agccaagatc atgccactgc 2220
actctagcct gggcaacaga gtgagtcctg ctcaaac 2257

```

<210> 105

<211> 2550

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5627029CB1

<400> 105

```

cggaagtatt cccattttgc gttgtctggg ctcggcgcca gccgggctcg gactggacgt 60
gccactatgg ggtcgctcca gaagcatcgc ggagagaagg aggcggccgg gacgacggcg 120
gcggccggga ccgggggtgc caccgagcag ccgcccgcc accgggaaca caaaaaacac 180
aagcaccgga gtggcgccag tggcggtagc ggtggcgaa gacggaagcg gagccgggaa 240
cgtggggggc agcgcgggag cggcgggcgc ggggcccga ctgaggcccc gagcagcacg 300
cacgggcccc agcgcagcca ggcagagccc tccgagcggc gcgtgaagcg ggagaagcgc 360
gatgacgggt acgaggccgc tgccagctcc aaaactagct caggcgatgc ctctcactc 420
agcatcgagg agactaaca actccgggca aagttggggc tgaaaccctt ggaggttaat 480
gccatcaaga aggaggccgg caccaaggag gagcccgtga cagctgatgt catcaaccct 540
atggcccttg gacagcgaga ggagctgcgg gagaagctgg cggctgcca ggagaagcgc 600
ctgctgaacc aaaagctggg gaagataaag accctaggag aggatgacct ctggctggac 660
gacactcgag cctggatcga gaggagccgg cagctgcaga aggagaagga cctggcagag 720
aagagggcca agttactgga ggagatggac caagagtgtg gtgtcagcac tctggtggag 780
gaggagtctg ggcagaggcg gcaggacctg tacagtcccc gggacctgca gggcctcact 840
gtggagcatg ccattgattc ctcccgagaa ggggagacaa tgattcttac cctcaaggac 900
aaaggcgtgc tgcaggagga ggaggacctg ctggtgaacg tgaacctggt ggataaggag 960
cgggcagaga aaaatgtgga gctgcggaag aagaagcctg actacctgcc ctatgccgag 1020
gacgagagcg tggacgacct ggcgcagcaa aaacctcgct ctacctgtc caagtatgac 1080
gaagagcttg aaggggagcg gccacattcc ttccgcttgg agcagggcgg caggctgat 1140
ggcctgcggg agcgggagct ggaggagatc cgggccaagc tgcggctgca ggctcagtc 1200
ctgagcacag tggggccccg gctggcctcc gaatacctca cgcctgagga gatggtgacc 1260
tttaaaaaga ccaagcggag ggtgaagaaa atccgcaaga aggagaagga ggtagtagtg 1320
cgggcagatg acttgctgcc tctcggggac ccgagtgtcc gaagtggagg aggagaagga gcctgtgcct 1440
ctgcggggac ggggtcgccc ccgagtgtcc gagaacatgg acatcagtga tgaggaggaa 1500
cagccccctg cgtcggacga cacccgagtg gtagctggagg aggacgaggc ggagctggag 1560
ggtggagctc caccgccggc gtccccgcag gtgctggagg ctgacagagt tacagcagct acagcagctg 1620
ctgcagaagc agctggagaa gggacgccgg ctgcaagaagc tggagtctcg ccagcggggc 1680
cgagacagtg gcgagaaggt ggtggagatt ggggccatcg tgttcaacgc cagctccgag 1740
tgggaggagg atgaggatcc cgagcggaa gggggctgg tacgggctgg ctggcaatcg cgaggagcag 1800
ttctgccgca ccttggggga gatccccacc gagcgctcag ccaacgggtg ctccgaatct 1860
gaggagctca tggactttga acgggatgag gtgaacctgg acgaggagaa gcagcagcag 1920
gacggggagg agaacatcgg ctggagcacg gacgaggaac cgatcgtgaa tagggggctg 1980
gatttctctg ctctctccac caccatcctg gcgctgctgg agaccacagt gcagaagggtg 2040
gcagctgccc tgctcctgtg tcagaacaaa ccctcagccg tgactgcat caggaagggtg 2100
gcccgggtga agggccccaa caagtcgctg gaggaatacc gaggtctcac acaggacttc 2160
atggccatcg atgacaagta cagccggagg aagatcgaat acgtggatga gacgggcccg 2220
aaggagaagg acggctacaa acccgacgtt tttccggcag ctgtcgcacc gcttccatgg caagggctca 2280
aaactcacac ccaaggaggc tttccggcag ctgtcgcacc gcttccatgg caagggctca 2280
ggcaagatga agacagagcg gcgagtgagg aagctggacg aggaggcgct cctgaagaag 2340
atgagctcca gcgacacgcc cctgggcacc gtggccctgc tccaggagaa gcagaaggct 2400

```

WO 01/07471

PCT/US00/19948

cagaagaccc cctacatcgt gctcagcggc agcggcaaga gcatgaacgc gaacaccatc 2460
 accaagtgc agcgcctcc cgcggcgcc ctgcctcaac cttcatatta aataaagctc 2520
 cctccttatt ttttcaaaaa aaaaaaaaaa 2550

<210> 106
 <211> 2566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 5678487CB1

<400> 106
 cggctcgagg tgaggactac aactcccgac gtgcaaagcg agggccagtg ggtgggaaga 60
 gcccccaaga gctctgtgcg ggattctagg ctcccctgtg acagccgcgg caggaagcag 120
 gcgggcgctc cccggccaca ggctgttgt tctcggaagg gagaaagctg gacatttccc 180
 cacgtaactc ccagctctgg gcctagagtg cgtgcatggc gaagtccccg gagaactcta 240
 ccctggagga gattctgggg cagtatcaac ggagtctccg ggaacatgcc agcagaagca 300
 ttcaccaact gacatgtgcc ctgaaagaag gcgatgtcac tattggagaa gatgcacca 360
 atctttcttt tagcaccagt gtgggaaatg aggacgccag gacagcctgg cccgaattac 420
 aacagagcca tgctgttaat cagctcaaa agttgttgcg ccaacaagca gataaggaaa 480
 gtgaagtatc tccgtcaaga agaagaaaaa tgtccccctt gaggtcatta gaacatgagg 540
 aaaccaatat gcctactatg cacgaccttg ttcatactat taatgaccag tctcaatata 600
 ttcattcatt agaggcagaa gttaagtctt gcaaggagga actctctgga atgaaaaata 660
 aaatacaagt agttgtgctt gaaaacgaag tggatgcac ccaacaagca cacaattctt 720
 aagaggagac actgagggaa caaacacttc tggatgcac cgaacacatg cacaattctt 780
 ggattacaac aggtgaagat tctgggggtg gcgaaacctc caaaagacca ttttcccatg 840
 acaatgcaga ttttggcaaa gctgcatctg ctgggtgagca gctagaactg gagaagctaa 900
 aacttactta tgaggaaaag tgtgaaattg aggaatccca attgaagttt ttgaggaaacg 960
 acttagctga atatcagaga acttgtgaag atcttaaaga gcaactaaag cataaagaat 1020
 ttcttctggc tgctaatact tgtaaccgtg ttgggtgtct ttgtttgaaa tgtgctcagc 1080
 atgaagctgt tctttcccaa acccatacta atgttcatat gcagaccatc gaaagactgg 1140
 ttaaagaaa agatgacttg atgtctgcac tagtttccgt aaggagcagc ttggcagata 1200
 cgcagcaaa agaaagcaagt gcttatgaac aggtgaaaca agttttgcaa atatctgagg 1260
 aagccaattt tgaaaaaacc aaggctttaa tccagtgtga ccagttgagg aaggagctgg 1320
 agaggcaggc ggagcgactt gaaaaagatc ttgcatctca gcaagagaaa agggccattg 1380
 agaaagacat gatgaaaaag gaaataacaa aagaaagggg gtacatggga tcaaagatgt 1440
 tgatcttgtc tcagaatatt gcccaactgg agggccaggt ggaaaagggt acaaaggaaa 1500
 agatttcagc tattaatcaa ctggaggaaa ttcaaagcca gctggcttct cgggaaatgg 1560
 atgtcacaaa ggtgtgtgga gaaatgcgct atcagctgaa taaaaccaac atggagaagg 1620
 atgaggcaga aaaggagcac agagagttca gagcaaaaac taacagggat cttgaaatta 1680
 aagatcagga aatagagaaa ttgagaatag aactggatga aagcaaaca cacttggaa 1740
 aggagcagca gaaggcagcc ctggccagag aggagtgcct gagactaaca gaactgctgg 1800
 gcgaatctga gcaccaactg cacctcacca gacaggaaaa agatagcatt cagcagagct 1860
 ttagcaagga agcaaaaggc caagcccttc agggccagca aagagagcag gagctgacac 1920
 agaagataca gcaaatggaa gccagcatg acaaaactga aaatgaacag tatttgttgc 1980
 tgacctccca gaatacattt ttgacaaaag taaaggaaga atgctgtaca ttagccaaga 2040
 aactggaaca aatctctcaa aaaaccagat ctgaaatagc tcaactcagt caagaaaaaa 2100
 ggtatacata tgataaattg ggaaagttac agagaagaaa tgaagaattg gaggaacagt 2160
 gtgtccagca tgggagagta catgagacga tgaagcaaag gctaaggcag ctggataagc 2220
 acagccaggc cacagcccag cagctggtgc agctcctcag caagcagaac cagcttctcc 2280
 tggagaggca gagcctgtcg gaagaggttg accggctgcg gacccagtta cccagctgc 2340
 cacaatctga ttgctgacct ggatggaaca gagtgaata aatgatttac aaagagatat 2400
 ttacattcat ctggtttaga cttaatatgc cacaacgcac cacgaccttc ccagggtgac 2460
 accgctcag cctgcagtgg ggctggctct catcaacgcg ggcgctgtcc ccgcacgcag 2520
 tcgggctgga gctggagtct gactctagct gagcagagct cctggt 2566

<210> 107
 <211> 3022
 <212> DNA
 <213> Homo sapiens

WO 01/07471

PCT/US00/19948

<220>

<221> misc_feature

<223> Incyte ID No: 5682976CB1

<400> 107

```

gcttttcctta ttttttttaaa tgttctataa tgatatcaag actatagaac tatctgtttt 60
atgacactttt gaaaagattc aggtagggtc tccccctcca cccggctcag gcagagccat 120
gtctcgggggt ggctcctgcc cacacctgtt gtgggacgtg agggaaagggt ccctcgggct 180
ggaggaccg tccccggctgc ggagtcgcta cctgggaaga agagaattta tccaaagatt 240
aaaacttgaa gcaaccctta atgtgcatga tgggtgtgtt aatacaatct gttggaatga 300
cactggagaa tatattttat ctggctcaga tgacaccaa ttagtaatta gtaatcctta 360
cagcagaaag gttttgacaa caattcgctt agggcaccga gcaaacatat ttagtgcaaa 420
gttcttacct tgtacaaatg ataaacagat tgtatcctgc tctggagatg gagtaatt 480
ttataccaac gttgagcaag atgcagaaac caacagacaa tgccaattta cgtgtcatta 540
tggaactact tatgagatta tgactgtacc caatgacctt tacacttttc tctctgtgtg 600
tgaagatgga actgttaggt ggtttgatac acgcatcaaa actagctgca caaaagaaga 660
ttgtaaagat gatattttta ttaactgtcg acgtgctgcc acgtctgttg ctatttgccc 720
accaatacca tattaccttg ctgttggttg ttctgacagc tcagtacgaa tatatgatcg 780
gcgaatgctg ggcacaagag ctacagggaa ttatgcaggt cgagggacta ctggaatgg 840
tgccccgtttt attccttccc atcttaataa taagtcttgc agagtgcacat ctctgtgtta 900
cagtgaagat ggtcaagaga ttctcgttag ttactcttca gattacatat atctttttga 960
cccgaaagat gatacagcac gagaacttaa aactccttct gcggaagaga gaagagaaga 1020
gttgcgacaa ccaccagtta agcgtttgag acttcgtggg gatttggtcag atactggacc 1080
cagagcaagg ccggagagtg aacgagaacg agatggagag cagagtccca atgtgtcatt 1140
gatgcagaga atgtctgata tgttatcaag atggtttgaa gaagcaagtg aggttgca 1200
aagcaataga ggacgaggaa gatctcgacc cagaggtgga acaagtcaat cagatatttc 1260
aactcttctt acggctccat caagtccctg tttggaagt agtgaaactg caatggaagt 1320
agatactcca gctgaacaat ttcttcagcc ttctacatcc tctacaatgt cagctcaggc 1380
tcattcgaca tcatctccca cagaaagccc tcattctact cctttgctat ctctccaga 1440
cagtgaacaa aggcagtctg ttgaggcatc tggacaccac acacatcatc agtctgattc 1500
tccttcttct gtggttaaca aacagctcgg atccatgtca cttgacgagc aacaggataa 1560
caataatgaa aagctgagcc ccaaaccagg gacaggtgaa ccagttttta gtttgacta 1620
cagcacagaa ggaacaacta caagcacaat aaaactgaac tttacagatg aatggagcag 1680
tatagcatca agttctagag gaattgggag ccattgcaaa tctgagggtc aggaggaatc 1740
tttcgtccca cagagctcag tgcaaccacc agaaggagac agtgaaacaa aagctcctga 1800
agaatcatca gaggatgtga caaaatatca ggaaggagta tctgcagaaa acccagttga 1860
gaaccatata aatataacac aatcagataa gttcacagcc aagccattgg attccaactc 1920
aggagaaaga aatgacctca atcttgatcg ctcttggtgg gttccagaag aatctgcttc 1980
atctgaaaaa gccaaaggaa cagaaacttc agatcagact agcactgaga gtgctacca 2040
tgaaaataac accaatcctg agcctcagtt ccaaacagaa gccactgggc cttcagctca 2100
tgaagaacaa tccaccaggg actctgctct tcaggacaca gatgacagt atgatgacc 2160
agtctgtatc ccagggtgaa ggtatcgagc aggaacctgt gatagacgt ctgctgttgc 2220
ccgtattcag gagttcttca gacggagaaa agaaaggaaa gaaatggaag aattggatac 2280
tttgaacatt agaaggccgc tagtaaaaat ggtttataaa ggccatcgca actccaggac 2340
aatgataaaa gaagccaatt tctggggtgc taactttgt atgagtgggt ctgactgtgg 2400
ccacattttc atctgggatc ggcacactgc tgagcatttg atgcttctgg aagctgataa 2460
tcatgtggtt aactgcctgc agccacatcc gtttgaccca attttagcct catctggcat 2520
agattatgac ataaagatct ggtcaccatt agaagagtca aggattttta accgaaaact 2580
tgctgatgaa gttataactc gaaacgaact catgctggaa gaaactagaa acaccattac 2640
agttccagcc tctttcatgt tgaggatgtt ggcttcactt aatcatatcc gagctgaccg 2700
gttgagggtt gacagatcag aaggctctgg tcaagagaat gaaaatgagg atgaggaata 2760
ataaactctt tttggcaagc acttaaatgt tctgaaattt gtataagaca ttattatat 2820
ttttttcttt acagagcttt agtgcaattt taaggttatg gtttttgagg tttttccctt 2880
tttttggtat aacctaacat tggtttgtaa tgattgtgtg catgaatttg ggagattgta 2940
taaaacaaaa ctagcagaat gtttttaaaa ctttttgccg tgtatgagga gtgctagaaa 3000
atgcaaagtg caatattttc cc 3022

```

<210> 108

<211> 2787

<212> DNA

<213> Homo sapiens

<220>

WO 01/07471

PCT/US00/19948

<221> misc_feature

<223> Incyte ID No: 5992432CB1

<400> 108

```

gtcgtcgaaa agaagtcaat aacgtggggc tgtccgtcaa aaatgattta accaatagaa 60
aacgggtctg gctcggaggg gcggggccgtc agtggttagac gtcataagcg cgcgactctc 120
tcctgtacct gggcatccag aaaaatggtg gtgatggcgc gacttttcgcg gcccgagcgg 180
ccggaccttg tcttcgagga agaggacctc ccctatgagg aggaaatcat gcggaaccaa 240
ttctctgtca aatgctggct tcgctacatc gagttcaaac agggcgcccc gaagcccagg 300
ctcaatcagc tatacgagcg ggcactcaag ctgctgccct gcagctacaa actctggtac 360
cgataacctga aggcgcgtcg ggcacaggtg aagcatcgct gtgtgaccga cctgcctat 420
gaagatgtca acaactgtca tgagagggcc tttgtgttca tgcacaagat gcctcgtctg 480
tggctagatt actgccagtt cctcatggac caggggcgcg tcacacacac ccgccgcacc 540
ttcgaccgtg ccctccgggc actgcccac acgcagcact ctgaatttg gcccctgtat 600
ctgcgcttcc tgcgctcaca cccactgcct gagacagctg tgcgaggcta tggcgcttc 660
ctcaagctga gtctgagag tgcagaggag tacattgagt acctcaagtc aagtgaccgg 720
ctggatgagg ccgcccagcg cctggccacc gtggtgaacg acgagcgttt cgtgtctaag 780
gccggcaagt ccaactacca gctgtggcac gagctgtgcg acctcatctc ccagaatccg 840
gacaaggtag agtccctcaa tgtggacgcc atcatccgcg ggggcctcac ccgcttcacc 900
gaccagctgg gcaagctctg gtgttctctc gccgactact acatccgcag cggccatttc 960
gagaaggctc gggacgtgta cgaggaggcc atccggacag tgatgaccgt gcgggacttc 1020
acacaggtgt ttgacagcta cgcccagttc gaggagagca tgatcgctgc aaagatggag 1080
accgcctcgg agctggggcg cgaggaggag gatgatgtgg acctggagct gcgcctggcc 1140
cgcttcgagc agctcatcag ccggcggccc ctgctcctca acagcgtctt gctgcgccaa 1200
aaccacacc acgtgcacga gtggcacaag cgtgtcgccc tgcaccaggg ccgcccccg 1260
gagatcatca acacctacac agaggctgtg cagacggtgg acccctcaa ggccacagg 1320
aagccccaca ctctgtgggt ggcgtttgcc aagttttatg aggacaacgg acagctggac 1380
gatgcccgtg tcatcctgga gaaggccacc aaggtgaact tcaagcaggt ggatgacctg 1440
gcaagcgtgt ggtgtcagtg cggagagctg gagctccgac acgagaacta cgatgaggcc 1500
ttgcccgtgc tgcgaaaggc cacggcgctg cctgcccgcc gggccgagta ctttgatggt 1560
tcagagcccg tgcagaaccg cgtgtacaag tcaactgaagg tctggtccat tctgggccag 1620
ctggaggaga gctcggcac cttccagtc accaaggccg tgtacgaccg catcctggac 1680
ctgcgtatcg caacacccca gatcgtcatc aactatgcca tgttcttgga ggagcacaag 1740
tacttcgagg agagcttcaa ggcgtacgag cgccgcatct cgctgttcaa gtggcccaac 1800
gtgtccgaca tctggagcac ctacctgacc aaattcattg cccgctatgg gggccgcaag 1860
ctggagcggg caccggacct gtttgaacag gctctggacg gctgcccccc aaaatatgcc 1920
aagaccttgt acctgctgta cgcacagctg gaggaggagt ggggcctggc ccggcatgcc 1980
atggccgtgt acgagcgtgc caccagggcc gtggagcccg cccagcagta tgacatgttc 2040
aacatctaca tcaagcgggc ggccgagatc tatggggtca cccacacccg cggcattctac 2100
cagaaggcca ttgaggtgct gtcggacgag cacgcgcgtg agatgtgcct gcggtttgca 2160
gacatggagt gcaagctcgg ggagattgac cgcgccccgg ccactctacag cttctgctcc 2220
cagatctgtg acccccggac gaccggcgcg ttctggcaga cgtggaagga ctttgaggtc 2280
cggcattgga atgaggacac catcaaggaa atgctgcgta tccggcgag cgtgcaggcc 2340
acgtacaaca cgcagggtcaa cttcatggcc tcgcagatgc tcaaggctctc gggcagtgcc 2400
acgggcaccg tgtctgacct ggcccctggg cagagtggca tggacgacat gaagctgctg 2460
gaacagcggg cagagcagct ggcggtgag gcggagcgtg accagccctt gcgcgcccag 2520
agcaagatcc tgttcgtgag gactgacgcc tccgggagg agctggcaga gctggcacag 2580
caggtcaacc ccgaggagat ccagctgggc gaggacgagg acgaggacga gatggacctg 2640
gagcccaacg aggttcggct ggagcagcag agcgtgccag ccgcagtgtt tgggagcctg 2700
aaggaagact gacccgtccc tccccctcc cccctcccca cccctccccc aatacagcta 2760
cgtttgtaca tcaaaaaaaaa aaaaaaa 2787

```